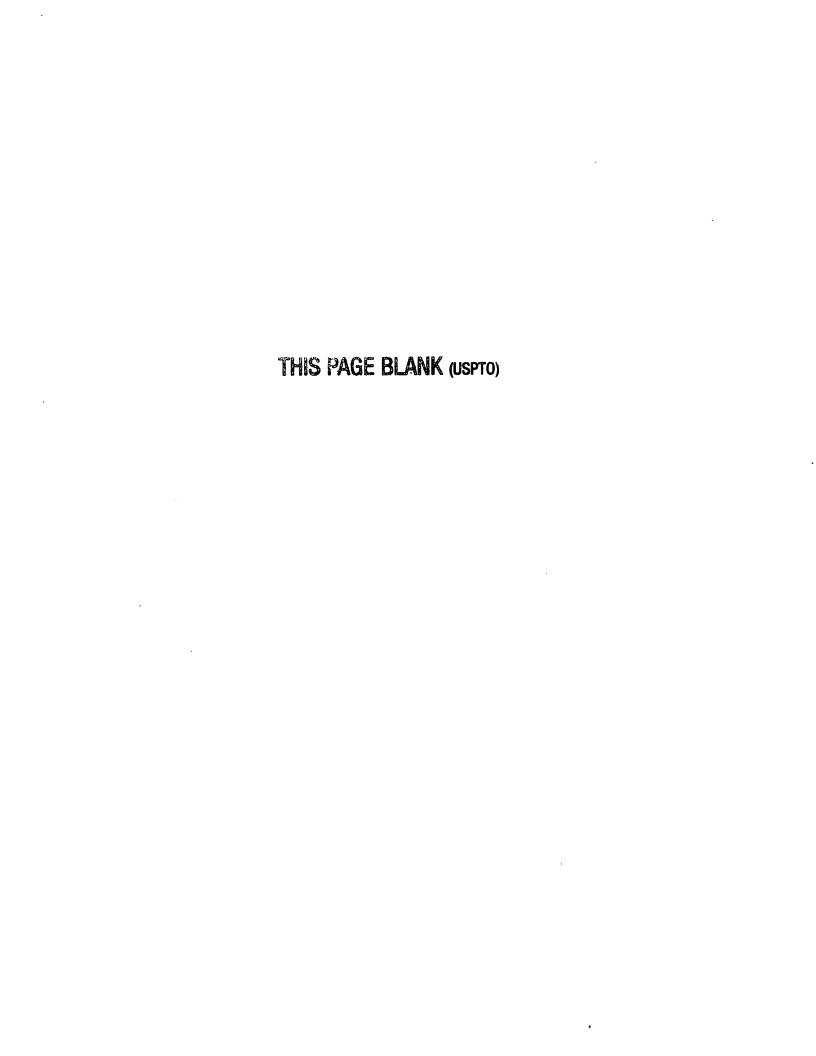
Searches run against the **Published_Applications** AA database on any Compugen machine between Feb 18 – Mar 16, 2004 had incomplete results.

The incomplete results were due to problem with the program that moves new applications into the Published_Applications_AA database. This problem was detected and corrected on Mar 17, 2004.

We have determined that a search was done for you on case in the Published_Applications_AA database between Feb 18 – Mar 16, 2004. This search has been rerun. The new results are attached.

STIC Database tracking # $\frac{1/4522}{1/4627}$ original search completed $\frac{2/18}{1}$



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RESULT 2
US-09-847-946A-19
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                                                                                                                                 ; Search time 77.9211 Seconds (without alignments) 75.239 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_MEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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11 US-09-847-940B-18
10 US-09-847-940B-18
11 US-09-847-940B-18
15 US-10-097-175-101
9 US-09-731-023A-12
12 US-10-229-915-1
15 US-10-229-915-1
15 US-08-610-220A-11
15 US-09-150-623-11
15 US-10-116-275-190
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15 US-10-116-275-190
17 US-10-116-275-190
18 US-10-116-275-190
19 US-09-171-023A-11
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                                                                                                                                                                                                                                                                                                                                                                                       801455 seqs, 209382283 residues
                                                                                                                                                                                                                                                148
1 DRQIKIWFQNRRMKWKKTALDASALQTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                 February 18, 2004, 14:36:10
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Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                              US-09-643-260-19
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Match Length DB
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                                                                                                                                                                                                                                                                          Sequence:
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Sequence 1169, Applisequence 1169, Apple Sequence 6, Applisequence 9, Applisequence 38, Applisequence 10, Applisequence 10, Applisequence 11, Applisequence 2, Applisequence 3, Applisequence 4, 
Sequence 44, Appl
Sequence 129, App
Sequence 4, Appli
Sequence 4, Appli
Sequence 50, Appli
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Sequence 10, 2
Sequence 3, Al
Sequence 6, Al
Sequence 54, Al
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                                                                                                                                    US-09-214-371-9

US-09-225-299-1169

US-09-925-299-1169

US-09-925-299-1169

US-09-925-299-1169

US-09-925-299-1169

US-09-925-299-1169

US-09-925-299-1169

US-09-925-299-1169

US-09-731-023A-10

US-09-731-023A-10

US-09-731-023A-10

US-09-731-023A-10

US-09-732-480-29

US-09-732-480-29

US-09-785-802A-2

US-09-785-802A-2

US-09-785-802A-2

US-09-785-802A-3

US-09-981-286A-3

US-09-981-286A-3
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Gaps
Sequence 19, Application US/09847940B
Fatent No. US20020156000A1
GENERAL INFORMATION:
APPLICANT: May, Michael J.
APPLICANT: GAOB, Sankar
TITLE OF INVENTION: ANTI INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REPERENCE: PPI-117CP
CURRENT APPLICATION NUMBER: US/09/847,940B
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR PLILNG DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Description of Artificial Sequence: NBD peptides US-09-847-940B-19
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                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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1 DRQIKIWFQNRRMKWKKTALDASALQTE

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Sequence 19, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION:
APPLICANT: May, Michael J

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Gaps

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SQUENCE 101, Application US/10097175

Publication No. US20030045680A1

GENERAL INFORMATION:
APPLICANT: USA, USBA B.
APPLICANT: OZA, UIBHA B.
TITLE OF INVENTION: PEPTIDIC MODULATORS OF THE ANDROGEN RECEPTOR
FILE REFERENCE: PPI-110

CURRENT APPLICATION NUMBER: US/10/097,175

CURRENT APPLICATION NUMBER: 60/275,240

PRIOR APPLICATION NUMBER: 60/275,240

PRIOR PILING DATE: 2001-03-12

PRIOR PILING DATE: 2001-03-12

PRIOR PILING DATE: 2001-03-12

PRIOR PILING DATE: 2001-03-12

PRIOR PILING DATE: 2001-03-12
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APPLICANT: Sessa, William
TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics
FILE REFERENCE: 44574-5076-US
CURRENT APPLICATION NUMBER: US/09/731,023A
CURRENT FILING DATE: 2000-12-07
                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-18
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INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 134; DB 11;
Pred. No. 6e-12;
0; Mismatches 2;
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Pred. No. 2.4e-07;
                                     CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR PAPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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73.9%;
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Best Local Similarity 92.9%;
Matches 26; Conservative
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Best Local Similarity 73.9
Matches 17; Conservative
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LENGTH: 26
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LENGTH: 28
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     APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
ITILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR PLING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SEQ ID NO 19
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: NBD peptides
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APPLICANT: May, Michael J.
APPLICANT: Ghosh, Sankar
TITLE OF INVENTION: AATT-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-117CP
CURRENT APPLICATION NUMBER: US/09/847,940B
CURRENT FILING DATE: 2001-05-02
PRIOR FILING DATE: 2000-08-22
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Best Local Similarity 100.0%; Pred. No. 6.6e-14;
Matches 28; Conservative 0; Mismatches 0;
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Phillips, Kathryn
Hannig, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
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Matches 26; Conservative
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APPLICANT: Ghosh, Sankar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-847-946A-19
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LENGTH: 28
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Sequence 11, Application US/08610220A

Publication No. US20030099638A1

GENERAL INFORMATION:

APPLICANT: Troy, Carol M.

TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL

TITLE OF INVENTION: DEATH AND USES THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      // Sequence 11, Application US/09150623
// Patent No. US20020044931A1
// CENERAL INFORMATION:
// APPLICANT: Troy, Carol M.
// IITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
                                                                                                                                                                             ch 66.2%; Score 98; DB 15; Length 17; 1 Similarity 100.0%; Pred. No. 4.1e-07; 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 64.2%; Score 95; DB 8; Length 21; Best Local Similarity 94.4%; Pred. No. 1.3e-06; Matches 17; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SITABLE IN THE ANIMAL OF THE ANIMALICARY STATE: New York COUNTRY: U.S.A.

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk COMPUTER: PLOPPY disk COMPUTER: PLOPPY disk COMPUTER: PREDICT PROPERTIES PATENT PC-DOS/MS-DOS SOFTWARE: PATENTIN RELEASING SYSTEM: PC-DOS/MS-DOS CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/610,220A FILING DATE: MAR-04-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. REGISSTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 48332/JPW/JML
TELEPONMULCATION: TELEPONDE: 212-278-0400
                                                                                                       ; OTHER INFORMATION: anti-inflammatory compound US-10-229-915-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RQIKIWFQNRRMKWKKQA 18
                                                                                                                                                                                                                                                                                                                  DRQIKIWFQNRRMKWKK 17
                                                                                                                                                                                                                                                                                  1 DRQIKIWFQNRRMKWKK 17
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INFORMATION FOR SEQ ID NO: 11:
                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-610-220A-11
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          LENGIH: 17
                                                                                     FEATURE:
                                                                                                                                                                                                                                 Matches
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Publication No. US20030165510A1

GENERAL INFORMATION:

APPLICANT'S Seesa, William

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/358,365

CURRENT APPLICATION NUMBER: US/00/31,023

PRIOR APPLICATION NUMBER: US 60/731,023

PRIOR APPLICATION NUMBER: US 60/231,327

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 12

SEQ ID NO 12

LENGTH: 36
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APPLICANT: Lazarus, Gerhard
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING INFLAMMATORY
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: PPI-127
CURRENT APPLICATION NUMBER: US/10/229,915
CURRENT FILING DATE: 2002-08-27
PRIOR FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 39
SOFFWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                         Query Match 67.6%; Score 100; DB 9; Length 36; Best Local Similarity 69.2%; Pred. No. 4.5e-07; Matches 18; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Antennapedia-cav-X fusion peptide
US-09-731-0238-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Antennapedia-cav-X fusion peptide US-10-358-365-12
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PRIOR APPLICATION NUMBER: US 60/231,327
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 12
LENGTH: 36
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Publication No. US20030083262A1
GENERAL INFORMATION:
                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-229-915-1
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; OTHER INFORMATION: TIRAP/Antennapedia fusion protein
US-10-188-947-11
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Brayden, David
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Best Local Similarity 67.9%;
Matches 19; Conservative
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Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                   Query Match
Best Local Similarity 78.3%;
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-499-79
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APPLICANT: HORNG, TIFFANY
TITLE OF INVENTION: TOLL/INTERLEUKIN-1 RECEPTOR ADAPTER PROTEIN (TIRAP)
FILE REPERENCE: 044574-510108
CURRENT APPLICATION NUMBER: US/10/188,947
CURRENT FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: 60/289,738
PRIOR PILICATION NUMBER: 60/289,738
PRIOR PILICATION NUMBER: 60/289,815
PRIOR PILICATION NUMBER: 60/289,866
PRIOR PILING DATE: 2001-05-09
PRIOR PLING DATE: 2001-05-09
PRIOR PLING DATE: 2001-05-09
PRIOR PLING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VETSION 3.1
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OTHER INFORMATION: TIRAP/Antennapedia fusion protein
NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/150,623
                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/610,220
FILING DATE: MAR-04-1996
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 48332/JPW/JML
TELECOMOUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFRX: 212-391-0525
INFORMATION FOR SEQ ID NO: 11:
LENGTH: 21 amino acids
      DEATH AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                   ADDRESSEE: Cooper & Dunham LLP
STRET: 1185 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/10188947
Publication No. US20020023993A1
GENERAL INFORMATION:
APPLICANT: MEDHITOV, Ruslan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ROIKIWFONRRMKWKKTA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 94.4
Matches 17; Conservative
    TITLE OF INVENTION: DE.
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: si
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ZIP: 10036
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LENGTH: 30
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APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Indeed
APPLICANT: Indeed
APPLICANT: Higgins, Lisa
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
FILE REFERENCE: E1067/20087
CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
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Pred. No. 3e-06;
  Length 30;
                                                4; Indels
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Publication No. US20030044427A1
GENERAL INFORMATION:
APPLICANT: Howley, Peter M.
APPLICANT: Benson, John
APPLICANT: Rasukawa, Hiroaki
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 94.5; DB 12;
Pred. No. 2e-05;
3; Mismatches 5;
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                                                Mismatches
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CURRENT APPLICATION NUMBER: US/10/161,499
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US/09/347,504
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.1
LENGTH: 34
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                                                                                                                                                                                                                                                                                                                                   APPLICANT: Blan Pharmaceutical Technology APPLICANT: O'Mahony, Daniel J
Score 95;
Pred. No.
                                                                                                2 RQIKIWFQNRRMKWKKTALDASA 24
                                                                                                                                             1 ROIKIWFONRRMKWKKLOLRDAA 23
                                                                                                                                                                                                                                                            Sequence 190, Application US/10116275 Publication No. US20030211476A1 GENERAL INFORMATION:
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Job time : 77.9766 secs

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US-10-358-365-11

Sequence 11, Application US/10358365

Publication No. US20030165510A1

GENERAL INFORMATION:

APPLICATION Caveolin Peptides and Their Use as Therapeutics
FILE REFERENCE: 44574-5076-US

CURRENT APPLICATION NUMBER: US10/358,365

CURRENT APPLICATION NUMBER: US 09/731,023

PRIOR PILING DATE: 2000-12-07

PRIOR PLING DATE: 2000-12-07

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.1
                                                                                     RESULT 14
US-09-731-0234-11
Sequence 11, Application US/09731023A
Fatent No. US20020077283A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics
TITLE OF INVENTION: 2000-10-07
FILE REFERENCE: 44574-5076-US
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/231,327
FRIOR FILING DATE: 2000-9-08
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 36
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Antennapedia-caveolin-1 scaffolding domain fusion
OTHER INFORMATION: peptide
US-10-358-355-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 63.5%; Score 94; DB 9; Length 36; Best Local Similarity 65.4%; Pred. No. 3.1e-06; Matches 17; Conservative 3; Mismatches 6; Indels
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1 ERQIKIWFONRRMKWKK 17
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LENGTH: 36
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| SIDSI/godata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/godata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/godata/geneseq/geneseqp-embl/AA1982.DAT:*
| SIDSI/godata/geneseq/geneseqp-embl/AA1982.DAT:*
| SIDSI/godata/geneseq/geneseqp-embl/AA1985.DAT:*
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| SIDSI/godata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/godata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/godata/geneseq/geneseqp-embl/AA1981.DAT:*
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| SIDSI/godata/geneseq/geneseqp-embl/AA1993.DAT:*
| SIDSI/godata/geneseq/geneseqp-embl/AA1999.DAT:*
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                                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1107863 segs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148
1 DRQIKIWFQNRRMKWKKTALDASALQTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	•	-	Description	Mutated IKKbeta NE	NBD peptide SEQ ID	Human mutant NEMO	IKKbeta NEMO bindi	NBD peptide SEQ ID	Wild-type human NE	Androgen receptor	Antennapedia-caveo	Synthetic alpha sm
SUMMAKIES		;	TD	ABB08741	AAM48524	ABU08435	ABB08740	AAM48523	ABU08434	AAE31836	AAU79345	AAB13423
			<u>n</u> .	23	23	24	23	23	24	24	23	21
		Query	Length	28	28	28	28	28	28	26	36	20
,	* P (- 1	100.0	100.0	100.0	90.5	90.5	90.5	68.2	67.6	66.2
			Score	148	148	148	134	134	134	101	100	98
	,	Kesuit	NO.	-	8	m	4	ហ	ø	7	æ	6

/note= "Wildtype Trp substituted by Ala"
24
/note= "Wildtype Trp substituted by Ala"

Location/Qualifiers

Misc-difference 22 /n Misc-difference 24

SXELLLLXXXX

Key

WO200183547-A2

10	98	66.2			AAW11630	Anti-apoptotic pro
11	86	66.2			AABB0924	r SIM peptide
12	98	66.2			AAB80925	Mixer SIM mutant p
13	95				AAW45976	Cysteine protease
14	95	4			AAW82957	gen r
15	9 9 1				ABP58107	Mouse TIRAP-Antenn
917	D C	•	•		AAY78416	Drosophila antenna
7.8	υ ο υ 4	63.2	230	7 6	AAX58610 AAW11629	Protein regulating Anti-apoptotic pro
13	4 6	'n			AAY27444	Antennapedia inter
20	94	m			ABB83151	Transduction domai
21	94	m			AAY79919	Human papillomavir
22	94	m i			AAU79344	Antennapedia-caveo
23	46	m (ABP53779	Antennapedia helix
24	94	m (AAY42291	Drosophila antenna
25	4.	m (AAY27403	D. melanogaster pA
7 6	4.0	n (AAY04364	Drosophila antenna
7 0	2, 0	ים כ			ABB844 / U	s. cerevisiae Ancp
0 O	, Q	2			AAEOOSII	Drennanedia Clabi.
S &	76	"	•		ABB99729	Amino acid seguenc
3 6	. 46	3 (1)	, .,		AAE10922	Human HOXB7 varian
35	9.6	m			ABG96337	Human ovarian canc
33	94	(1)			AAE32047	Clostridium botuli
34	94	m	(~)		ABB72035	Drosophila melanog
35	94	m	4		ABB57755	Drosophila melanog
36	94	m	41		ABB58929	Drosophila melanog
37	93	N			AAW91049	Internalization se
38	66	N I	,		AAB27063	Beta-catenin deriv
68	66 6	62.8			AAB21030	Human nucleic acid
* 4 0 +	n 0	40	-		AAB53823	י וייין סר
4.2	9 6	10			AAM39701	200
43	83	~			AAW48885	Amino acid sequenc
44		62.8	257		AAE32048	Clostridium botuli
45	92.5	62.5	4.2		ABP53778	Antennapedia helix
					ALIGNMENTS	
RESULT 1						
ABBOB741	14790	ר מיקר מיקר	otenderd. nentide.	9	44 85	
		Carren	i dod i	,	,	
•	ABB08741;					
14	-JUN-2002		(first entry)	₹		
DE Mut	Mutated IKKbeta NEMO binding	Kbeta	NEMO bir	ding	domain peptide SEO ID	NO 19.
				1		
	IKKbeat; I	IKKalpha,	a; NEMO	NEW	NEMO; NEMO binding domain; NBD; N	록.
	lase act.	ivatio	n; leuk	ocyte	; inflammation; E-select	in; osteoclast;
	oimmune	disea	se; tra	ıspla	autoimmune disease; transplant rejection; osteoporosis; cancer;	•
	heimer	e dise	ase, vi	ral;	infection; asthma; anapr	lylaxis; psoriasis;
	umatoid	arthr	itie; C	cohn,	s disease; multiple scie	
	ticoste	roid;	1 mmunosı	appre	corticosteroid; immunosuppression; antiinflammatory; immunosuppressive	immunosuppressive;
	eopathi	c; cyt	ostatic	 60	tropic; neuroprofective;	anti-HIV; numan;
	iarteri	oscler	otic, v	iruci	de; antiasthmatic; antia	antiallergic;
	matolog	cal;	antibaci	ceria	dermatological; antibacterial; antipsoriatic; antiro	eumacıc;
	larchri	נוני ס	всеораст	, 210	anciulcer; murant; murein.	h.
	o sabie	ns.				
	Synthetic.	į				

NBD peptide SEQ ID NO 19.

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differentiation. The compound is useful in treating Userconsist of the compound is useful in treating Userconsist conditions, where the condition is an inflammatory disorder, an autoimmune disease, transplant rejection, osceoporosis, cancer, Alzheimer's disease, atherosclerosis, a viral infection or ataxia telangiectasia. The inflammatory disorder is asthma, allergies, urticaria, anaphylaxis, categorathitis, postiatio, sepsies, psoriatis, inflammatory bowel disease, chronic obstructive pulmonary disease, vasculitis and burstitis. The inflammatory disorder may also be dermatitis, eczema, psoriasis, osteoarthritis, psoriatic arthritis, lupus and spondylarthritis, also for Crohn's disease, ulcerative colitis, polymylalgia, scleroderma, Wagner's granulomatosis, temporal arteritis, croyoglobulinaemia or multiple sclerosis. For chronic viral infections caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral diseases include HIV and infiluenza. The compound may also be useful for treating anaphylaxis, dury and food sensitivity, contact dermatitis, unburn or aging. The compound may be used to replace corticosteroids in munosurnorsesion in transplant and cancer therever.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunosuppression in transplants and cancer therapy. Also for identifying antiinflammatory compounds and for diagnosis of an inflammatory disorder. The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of a mutated NEMO binding domain of IKKbeta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to modulating NF-kappaB (NF-kB) induction in a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting a cell with an anti-inflammatory compound comprising at least one NEMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprises contacting a cell with an anti-inflammatory compound (ABB08725-ABB08742) comprising at least one NEMO binding domain (ABB77313). The compound has acts through selective inhibition of cytokine-mediated NF-kB activation by blocking the interaction of NEMO with IKKDeta at the NEMO binding domain. Blockage of IKKDeta-NEMO interaction results in inhibition of IKKDeta kinase activation and subsequent decreased phosphorylation of IkKDeta kinase activation and act (directly or indirectly) by blocking the recruitment of leukocytes into sites of acute and chronic inflammation, by down-regulating the expression of E-selectin on leukocytes or by blocking osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 23; Fig 5; 82pp; English.
                                                                                               02-MAY-2001; 2001WO-US40654.
                                                                                                                                                                                    02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
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Best Local Similarity 100.00
Thes 28; Conservative
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                                                                                                                                                                                                                                                                                                                                      (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                Ghosh S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           binding domain
08-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     May MJ,
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AMA 8620-AAAM 8645), comprising a membrane translocation domain (AAA48620-AAAM 8645), comprising a membrane translocation domain (AAA48620-AAAM 862) ro AAAM 8651) which comprises from 6-15 amino acid residues, fused to a NEWO binding sequence (AAA48619). The antiinflammatory compounds have antiasthmatic, antipacterial, immunosuppressive, dermatological, neuroprotective, cartibacterial, immunosuppressive, dermatological, neuroprotective, noctropic, antiatheroscleresive, dermatological, neuroprotective, notropic, antiatheroscleresive, dermatological, neuroprotective, noctropic, antiatheroscleresive, dermatological, neuroprotective, noctropic, antiatheroscleresive, dermatological, neuroprotective, notropic, antiatheroscleresive, dermatological, neuroprotective, notropic, antiatheroscleresive, dirangless kinase beta (IKKObeta) at the NEWO binding domain that results in inhibition of IKAOpea (IKKOpeta) at the NEWO binding domain that results in inhibition of IKAOpea The compounds are useful for treating inflammation or cancer, psoriasis, rheumatoid arthritis, unglammatory bowel disease, sepsis, vasculitis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; transplants scleroderma, profit inflammatory resonness such as allowed, if treating profit in franting anaphylaxis and ataxia anaphylaxis, profit in the anaphylaxis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                             Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatheroscalerotic; antiallergic; membrane translocation domain; NEWO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an antiinflammatory compound (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phillips K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5; Fig 5; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Findeis MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAY-2001; 2001WO-US14346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PRAE-) PRAECIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-121889/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ghosh S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 AA;
                                                                                                                                                                                                                                                                                                                                                         WO200183554-A2.
                                                                                                                                                                                                                                                                                                                                                                                                      08-NOV-2001.
                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                May MJ,
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RESULT 3

DRQIKIWFQNRRMKWKKTALDASALQTE 28

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Gaps

, 0

Length 28; Indels

100.0%; Score 148; DB 23; 100.0%; Pred. No. 5.6e-15; ive 0; Mismatches 0;

58

1 DRQIKIWFONRRMKWKKTALDASALOTE 28 1 DRQIKIWFONRRMKWKKTALDASALQTE

ò d AAM48524 standard; Peptide; 28 AA.

RESULT 2 AAM48524 20-MAR-2002 (first entry)

AAM48524;

Kinase activation; leukcyte; inflammation; B-selectin; osteoclast; autoimmune disease; transplant rejection; osteoporosis; cancer; Alzheimer; disease; transplant rejection; osteoporosis; cancer; rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; antiinflammatory; immunosuppressive; osteopathic; cytostatic; noctropic; neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antiasthmatic; antiallergic; dermatological; antibaccerial; antibacc

IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;

IKKbeta NEMO binding domain peptide SEQ ID NO 18

(first entry)

14-JUN-2002

ABB08740;

ABB08740 standard; peptide; 28 AA.

```
Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta; IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB; nuclear factor-kappaB induction; inflammatory disorder; autoimmune disease; osteoporosis; cancer; Alzheimer's disease; atherosclerosis; viral infection; Ataxia telangiectasia; transplantation detection; immunosuppressive; osteopathic; cytoetatic; nootropic; neuroprotective; antiatherosclerotic; virucide; vasotropic; antirheumatic; antiatheritic; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel antiinflammatory peptide compounds comprising NEMO binding domain, useful for modulating NF-kappaB induction in a cell and for treating NF-kappaB-mediated inflammation disorders e.g., asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                telangiectasia, and for transplantation detection. The compounds of the invention block NF-kappaB induction by IKK but do not inhibit the basal activity of NF-kappaB. The present sequence represents a human mutant NBD peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 148; DB 24;
100.0%; Pred. No. 5.6e-15;
tive 0; Mismatches 0;
                                                                                     Human mutant NEMO binding site (NBD) peptide.
          ABU08435 standard; peptide; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 22; Fig 5A; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
                                                                                                                                                                                                                                                                                                                        02-MAY-2001; 2001US-0847940
                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     psoriasis, vasculitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-209142/20.
                                                                                                                                                                                                                                                                                                                                                                                                                             May MJ, Ghosh S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 AA;
                                                                                                                                                                                                                                                                                                                                                                                      (MAYM/) MAY M J. (GHOS/) GHOSH S.
                                                                                                                                                                                                                                                                      JS2002156000-A1.
                                                                                                                                                                                                                                  Homo sapiens.
                                                             12-JUN-2003
                                                                                                                                                                                                                                                                                                24-OCT-2002.
                                                                                                                                                                                                                                                Synthetic.
                                    ABU08435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
ABU08435
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Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting a cell with an anti-inflammatory compound comprising at least one NEMO

WPI; 2002-179350/23.

domain

binding

Ghosh S;

May MJ,

(UYYA) UNIV YALE.

02-MAY-2001; 2001WO-US40654. 02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.

WO200183547-A2.

08-NOV-2001.

Homo sapiens.

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The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB008725-ABB08725) comprising at least one NEMO binding domain (ABB07313). The compound has acts through selective inhibition of (ABB07313). The compound has acts through selective inhibition of cytokine-mediated NF-kB activation by blocking the interaction of NEMO interaction results in inhibition of IKADpaB. The compound may also act (directly or indirectly) by blocking the recruitment of Leukocytes into sites of acute and chronic inflammation, by blocking the recruitment of Leukocytes into sites of acute and chronic inflammation, by blocking osteoclast of Eselection on leukocytes or by blocking osteoclast of differentiation. The compound is useful in treating osteoclast conditions, where the condition is an inflammatory disorder. an autoimmune disease, transplant rejection, osteoprosis, cancer, Alzheimer's disease, atheroscolerosis, a viral infection or ataxia telangiectasia. The inflammatory disorder may also be dermatitis, inflammatory disorder may also be dermatitis, eczema, bowel disease, chronic obstructive pulmonary disease, vasculitis and bursitis. The inflammatory disorder may also be dermatitis, coloriasis, osteoarthritis, psociatic arthritis, luque and bursitis. The inflammatory disease, ulcerative colitis, polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis, polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis, polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis, cursed by Epstein-barr, cytomegalovirus or herpes simplex. Other craning anaphylaxis, drug and food sensitivity, contact dermatitis, any application in which controcercine to replace corticosteroids in munuosuppression in transplants and cancer therapy. Also for identifying immunosuppression in transplants and cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 23; Fig 5; 82pp; English.
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Gaps

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Indels

1 DROIKIWFONRRMKWKKTALDASALQTE 28 DROIKIWFONRRMKWKKTALDASALQTE 28

ò a RESULT 4 ABB08740

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Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                    12-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-OCT-2002.
                                                                                                                arthritis
                                                                                                                                                                                                                                                                                                                             ABU08434;
                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         May MJ,
                                                                                                                                                                                                                                                                            RESULT 6
                                                                                                                                                                                                                                                                                       ABU08434
ID ABU
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                                                                                                                                                                                                                                     요.
                                                                                                                ö
                                                                                                                                                                                                                                                                                                                         Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; anticheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
antiinflammatory compounds and for diagnosis of an inflammatory disorder. The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of the NEWO binding domain of IKKDeta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an antiinflammatory compound (especially AAM46628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48651), comprising a membrane translocation domain cardian areasons. The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antisheumatic, antiarhritic, osteopathic, antibacterial, immunosupprestory, dermatological, neuroprotective, noctropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IxappaB kinase beta (IXKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel antiinflammatory compound comprising membrane translocation
                                                                                                                ö
                                                                                      Length 28;
                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            ataxia telangiectasia, allergy, anaphylaxis, arthritis.
                                                                                       23;
                                                                                      Score 134; DB 23;
Pred. No. 6.7e-13;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phillips
                                                                                                                                                        1 DROIKIWFONRRMKWKKTALDASALQTE 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Findeis MA,
                                                                                                                                                                                                                           AAM48523 standard; Peptide; 28
                                                                                       90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAY-2001; 2001WO-US14346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-2000; 2000US-201261P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-AUG-2000; 2000US-0643260.
                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PRAE-) PRAECIS PHARM INC.
                                                                                                                                                                                                                                                                                                    NBD peptide SEQ ID NO 18.
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-121889/16.
                                                                                   Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            May MJ, Ghosh S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNIV YALE.
                                                               28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200183554-A2.
                                                                                                                                                                                                                                                                            20-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                   AAM48523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   psoriasis
                                                                Sequence
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                                                                                                                                                                                                     RESULT 5
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compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, seppis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis, transplant rejection; osteoporosis, Alzheimer's disease; atherosclerosis, viral infections, and ataxia relangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta; IkappaB kinase-alpha; IKKalpha; NF-kappaB; nuclear factor-kappaB linduction; inflammatory disorder; autoimmune disease; osteoporosis; cancer; Alzheimer's disease; atherosclerosis; viral infection; Ataxia telangiectasia; transplantation detection; immunosuppressive; osteopathic; cytostatic; nootropic; neuroprotective; antiatherosclerosic; virucide; vasotropic; antirheumatic; antiathritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to antiinflammatory compounds comprising NEMO binding domain (NBD) peptides. The NEMO binding domains are found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha (IKKalpha) proteins. The antiinflammatory compounds of the invention are useful for modulating nuclear factor kappaB (NF-kappaB) induction in a cell, where the compounds are capable of blocking the interaction between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel antiinflammatory peptide compounds comprising NEMO binding domain, useful for modulating NF-kappaB induction in a cell and for treating NF-kappaB-mediated inflammation disorders e.g., asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 90.5%; Score 134; DB 23; Best Local Similarity 92.9%; Pred. No. 6.7e-13; Matches 26; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wild-type human NEMO binding site (NBD) peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DRQIKIWFQNRRMKWKKTALDWSWLQTE 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DRQIKIWFONRRMKWKKTALDASALQTE 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU08434 standard; peptide; 28
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22-AUG-2000; 2000US-0643260.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        psoriasis, vasculitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-209142/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 AA;
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an androgen receptor binding peptide
                                                                                       Local Similarity
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                                       26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                       02-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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                                       Sequence
                                                                      Query Match
                                                                                                       Matches
                                                                                                                                                                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to novel peptide modulators of androgen receptor. The peptides of the invention are useful for treating androgen-associated disorders such as prostate cancer, particularly hormonally refractive prostate cancer, colon cancer, lung cancer, benign prostatic hypertrophy, acne, hirsutism, male pattern baldness, Stein-Leventhal syndrome, androgen insensitivity syndrome, infertility, endometrial cancer and X-linked spinal bulbar muscular atrophy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Androgen receptor; androgen-associated disorder; prostate cancer; acne; benign prostatic hypertrophy; hirsutism; androgen insensitivity syndrome; male pattern baldness; Stein-Leventhal syndrome; infertility; cytostatic; X-linked spinal bulbar muscular atrophy; antiseborrheic; dermatological; depilatory; androgen receptor binding peptide.
                                                                                                                                                                                                                       Gaps
antiinflammatory compound further comprises at least one membrane translocation domain. The compounds are useful for treating inflammatory disorders, autoimmune diseases, osteoporosis, cancer, Alzhelmer's disease, atherosclerosis, viral infections, Ataxia telanglectasia, and for transplantation detection. The compounds of the invention block NF-kappaB induction by IKK but do not inhibit the basal activity of NF-kappaB. The present sequence represents an antinflammatory compound of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptide modulators of androgen receptor, useful for treating androgen-associated disorder, e.g. prostate cancer, particularly hormonally refractive prostate cancer, colon cancer, lung cancer,
                                                                                                                                                                                                                       ö
                                                                                                                                                                                      Length 28;
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                    Score 134; DB 24;
                                                                                                                                                                                                    Pred. No. 6.76
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "N-terminal acetyl"
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                                                                                                                                                                                                                                                                       1 DRQIKIWFONRRMKWKKTALDASALQTE 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Androgen receptor binding peptide #87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    AAE31836 standard; peptide; 26 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Page 30; 68pp; English.
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                                                                                                                                                                                    90.5%;
92.9%;
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28-JAN-2002; 2002US-352399P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-2002; 2002WO-US07487
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                                                                                                                                                                                                  Local Similarity 92.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Joyal JL, Mueller J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-067363/06.
                                                                                                                                                     28 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                     AAE31836;
                                                                                                                                                     Sequence
                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                     RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes an isolated caveolin scaffolding domain peptide (I). A fusion peptide (II) containing (I) and at least a membrane translocation sequence is useful for down regulating endothelial nitric oxide synthase (eNOS) activity in a cell, resulting in blockage of vasodilation. (II) is therefore useful for inhibiting inflammation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chronic inflammatory bowel disease; tumour growth; malignant neoplasm;
human; fruit fly; antennapedia internalisation signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Control peptide based on a human caveolin-1 scaffolding domain shown in AAU79340 residues 82-101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide having caveolin scaffolding domain, useful for modulating activity of endothelial nitric oxide synthase and inhibiting inflammation and tumour cell angiogenesis proliferation
                                                                 Gaps
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/label= Antennapedia_internalisation_signal
/note= "Specifically claimed in claim 9"
17..32
/label= Cav-X
Length 26;
                                                                 Indele
Score 101; DB 24;
Pred. No. 4.9e-08;
                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antennapedia-caveolin-X fusion peptide.
                                                                                                                                                                         Location/Qualifiers
                                                                                                                                   2 ROIKIWFONRRMKWKKTALDASA 24
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                                                                                                                                                                                                                                                                                                                                                                        AAU79345 standard; Peptide; 36
68.2%;
73.9%;
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                                                                     17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
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tumour cell angiogenesis/proliferation in an animal; and for blocking the interaction of caveolin with a protein in vivo. (II) may be useful in treatment of inflammatory conditions such as osteoporosis, rheumatoid arthritis, atherosclerosis, asthma and Alzheimer's disease. (I) and (II) are also useful for treating pathological processes associated with a pro-inflammatory response including allergies such as allergic rhinitis, cuticaria, anaphylaxis, dry sensitivity, food sensitivity, cutaneous inflammatory response including allergies such as allergic rhinitis, cuticaria, anaphylaxis, dry sensitivity, food sensitivity, cutaneous inflammation such as dermatitis, eccema, psoriatic arthritis, submurn, aging, arthritis, and chronic obstruction pulmonary disease and chronic inflammatory bowel disease. (I) and (II) are useful for immunosuppression in transplant and cancer patients. When administered along with one or more antinflammatory conticosteroids useful for immunosuppression in transplant and cancer patients. Mhen administered along with one or more antinflammatory captured (II) and (II) are useful for inhibiting tumour growth or malignant neoplasm including cellular angiogenetics, proliferation, invasiveness, and metastasis in biological systems. This sequence represents a fusion intransplant internaphedia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha smooth muscle actin; alpha-SM; wound contraction; hypertrophic scar; fibromatosis; Dupuytren disease; fibrotic condition; lung fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                       internalisation signal and control sequence Cav-X, based on the hn caveolin-1 scaffolding domain shown in AAU79340, residues 82-101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 100; DB 23; Length 36;
Pred. No. 9.9e-08;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic alpha smooth muscle actin inhibitor # 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ROIKIWFONRRMKWKKTALDASALOT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROIKIWFONRRMKWKKWGIDKAFFTT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB13423 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                      67.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 69.2
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB13423;
                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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The present invention relates to novel peptides comprising of a specific

Claim 7; Page 23; 31pp; English.

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A peptidic product for prevention and treatment of a disease related alpha-SM actin expression comprises a tetrapeptide associated with a chemical entity that is able to introduce the tetrapeptide into the

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tetrapeptide associated with an oligopeptide which allows the introduction of the tetrapeptide into the target cell. The present sequence is one such peptide. Residues 1 to 4 of the present sequence correspond to the specific tetrapeptide, while residues 5 to 20 correspond to the specific tetrapeptide, while residues 5 to 20 correspond to the oligopeptide. The specific tetrapeptide of the present sequence interferes with alpha smooth muscle (alpha-SM) actin organisation in stress fibers. The present sequence may be used in the prevention and/or treatment of a disease related to alpha-SM actin expression, e.g. wound contraction, hypertrophic scars, fibromatosis and fibrotic conditions. The present sequence may also be used to treat
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a cell permeable anti-apoptotic protein blocking peptide, which can be used to inhibit tumour growth, e.g. by ex vivo purging or (after stablihsation) in vivo administration. The peptide preferably blocks Bcl-2, and comprises a signal peptide mediating cell penetration and a functional sequence corresponding to a Bcl-2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell permeable, apoptotosis; blocking; inhibition; tumour growth; ex vivo purging; in vivo administration; Bcl-2.
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                                                                                                                                                                                                                     Score 98; DB 21; Length 20;
Pred. No. 1e-07;
); Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide(s) that block anti-apoptotic proteins - useful for inhibiting tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 18; Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-apoptotic protein blocking peptide FP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.2%; Score 98;
                                                                                                                                                        Dupuytren disease and lung fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kiehntopf M;
                                                                                                                                                                                                                                                                                                                                                                                            AAW11630 standard; peptide; 26 AA.
                                                                                                                                                                                                                        66.20
100.08; Pre-
                                                                                                                                                                                                                                                                                                    DRQIKIWFONRRMKWKK 20
                                                                                                                                                                                                                                                                                    1 DRQIKIWFQNRRMKWKK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 7; 7pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95DE-1026174.
                                                                                                                                                                                                     Query Match
Best Local Similarity 100.00
Best Local 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95DE-1026174
                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Herrmann F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-088160/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIEHNTOPF M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BRAC/) BRACH M. (HERR/) HERRMANN F.
                                                                                                                                                                                        20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JAN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                         AAW11630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brach M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                            RESULT 10
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85.0%;

Best Local Similarity

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The present invention relates to peptides capable of interacting with a smad protein, comprising a Smad Interaction Motif (SIM; amino acid sequence PP(TN)K). The present sequence is one such Smad interacting peptide. Smad proteins are a family of highly conserved, intracellular proteins that signal cellular responses downstream of Transforming Growth Factor-beta (TGF-beta) family serine/threonine kinase receptors. The SIM is thought to be necessary for interaction with the MH2 domain of Smad2. The peptides of the present invention are useful in the manufacture of a medicament for the treatment of a patient in need of modulation of activin or TGF-beta signalling; cancer; a patient in need of reducing extracellular matrix deposition, encouraging tissue repair and/or regeneration, tissue remodelling or healing of a wound, injury or surgery, or reducing scar tissue formation arising from injury to the surgery or reducing scar tissue formation arising from injury to the carin; a patient with or at risk of end-stage organ failure, pathologic extracellular matrix accumulation, a fibrotic condition, disease states associated with immunosuppression (such as different forms of malignancy, and the immunosuppression (such as different forms of malignancy).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                growth, kidney damage (for e.g. obstructive neuropathy, IgA nephropathy
or non-inflammatory renal disease) or renal fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptide capable of interacting with a Smad polypeptide, useful in the treatment of cancer and for tissue remodelling or healing of a wound, injury or surgery, comprises a Smad Interaction Motif and is
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                            Smad; Cytostatic; vulnerary; cerebroprotective; immunosuppressive; Anti-HUY, antidabetic; ophthalmological; antiinflammatory; SIM; Smad Interaction Motif; tissue repair; fibrotic condition; immunosuppression; diabetic nephropathy; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chronic degenerative diseases, and AIDS), diabetic nephropathy,
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                                     IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Biotin.Aminohexanoic acid-R"
1.46-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
                                   Mismatches
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       than 32 amino acids in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 16; Page 140; 179pp; English.
                 89.5%; Pred.
                                                                                                                                                                                                        AAB80924 standard; Protein; 41 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Howell MT;
                                 ä
                                                                                             1 DRQIKIWFQNRRMKWKKTA 19
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                                                                                                                                                                                                                                                                                    04-JUN-2001 (first entry)
                                 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hill CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-265836/27.
             Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                          Mixer SIM peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200114413-A2.
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001
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                                                                                                                                                                                                                                              AAB80924;
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The present invention relates to peptides capable of interacting with a Smad protein, comprising a Smad Interaction Motif (SIM; amino acid sequence is one such Smad interacting peptide. Smad proteins are a family of highly conserved, intraccillular proteins that signal cellular responses downstream of Transforming Growth reacher. Factor-beta (TGF-beta) family serine/fureconine Kinase receptors. The SIM is thought to be necessary for interaction with the MH2 domain of Smad2. The peptides of the present invention are useful in the manufacture of a medicament for the treatment of a patient in need of modulation of activin or TGF-beta signalling; cancer; a patient in need of modulation of extracellular matrix deposition, encouraging tissue repair and/or regeneration, tissue remodelling or healing of a wound, injury or surgery, or reducing scar tissue formation arising from injury or brain; a patient with or at risk of end-stage organ failure, pathologic extracellular matrix accumulation, a fibrotic condition, disease states associated with immunosuppression (such as different forms of malignancy, chronic degenerative diseases, and AIDS), diabetic nephropathy, tumour growth, kidney damage (for e.g. obstructive neuropathy, 1gA nephropathy
                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Wild-type Pro replaced by Ala. Wild-type sequence given in AAB80924."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide capable of interacting with a Smad polypeptide, useful in the treatment of cancer and for tissue remodalling or healing of a wound, injury or surgery, comprises a Smad Interaction Motif and is less than 32 amino acids in length -
                                     Gape
                                                                                                                                                                                                                                                                                                                                            Smad; Cytostatic; vulnerary; cerebroprotective; immunosuppressive; Atti-HIV; attidiabetic; ophthalmological; antiinflammatory; SIM; Smad Interaction Motif; tissue repair; fibrotic condition; immunosuppression; diabetic nephropathy; tumour; mutein.
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                                     Indels
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Pred. No. 2.3e-07;
                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 123; 179pp; English
                                                                                                                                                                                                   AAB80925 standard; Protein; 41 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Howell MT;
                                                                                               1 ROIKIWFONRRMKWKKLLMD 20
                                                                         21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-AUG-2000; 2000WO-GB03265.
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                                                                                                                                                                                                                                                                      (first entry)
                                     17; Conservative
                                                                                                                                                                                                                                                                                                          Mixer SIM mutant peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-265836/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200114413-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                      04-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
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                                     Matches
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AAW82957 standard; peptide; 24 AA
                         WPI; 1998-594522/50.
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Modified-site
                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                 14-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                        14-APR-1997;
                                                                                                                                                                                                                                                                                                                    WO9846250-A1
                                                                                                                                                                                                                                                                                                                                        22-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pietras RJ;
                                                                                                                                                                                                                                  Synthetic
                                                                                                                AAW82957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                 AAW82957
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                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lystrophy, stroke), cardiovascular disease and liver disorders.
The peptides should be more specific than pseudosubstrate inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New cysteine protease inhibiting peptide(s) for preventing cell death - in cases of neuro:degenerative, cardiovascular and liver diseases, and their peptidomimetics, and general method for identifying enzyme inhibiting peptides
                                                                                                                                                                                                                                               Cysteine protease inhibiting peptide for preventing cell death.
                                                                     ;
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                                                                                                                                                                                                                                                                    Neuronal cell death; neurodegenerative disorder; inhibition; cysteine protease; cardiovascular; liver disease.
                                                                                                                                                                                                                                                                                                                                                    /note= "N-3-nitro-2-pyridyl-sulphenyl-Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 95; DB 18; Length 21; Pred. No. 3e-07; 0; Mismatches 1; Indels
                                              Length 41;
                                                                     Indels
or non-inflammatory renal disease) or renal fibrosis.
                                      Score 98; DB 22; Le
Pred. No. 2.3e-07;
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                           AAW45976 standard; peptide; 21 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Page 68; 112pp; English
                                                                                                         1 RQIKIWFQNRRMKWKKLLMD 20
                                                                                            2 RQIKIWFQNRRMKWKKTALD 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYCO ) UNIV COLUMBIA NEW YORK.
                                              66.2%;
85.0%;
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Best Local Similarity 94.4%;
Matches 17; Conservative
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                                                                                                                                                                                                                       01-JUL-1998 (first entry)
                                                      Local Similarity 85.0 es 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-489561/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 AA;
                        41 AA;
                                                                                                                                                                                                                                                                                                                                        Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAR-1997;
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                                                                                                                                                                                                                                                                                                        Synthetic.
                        Sequence
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                                              Query Match
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Matches
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                                                                                                                                                     RESULT 13
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                                                                                                                      Human; oestrogen receptor activity inhibitor; anti-oestrogen; diagnosis; breast cancer; estrogen; tumour; phosphotyrosyl peptide; malonyltyrosyl peptide; steroid receptor co-activator-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New anti-oestrogen peptide compositions - comprise sequences based on oestrogen receptor and steroid receptor co-activator-1 sequences, used for treating cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                            Oestrogen receptor activity inhibiting peptide #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 95; DB 19;
Pred. No. 3.5e-07;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "phosphotyrosine"
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 156; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP58107 standard; Peptide; 30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RQIKIWFQNRRMKWKKTALD 21
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85.0%;
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04-FEB-1999 (first entry)
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nes 17; Conservative
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ABP58107
ID ABP58
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0; Gaps

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Sequence
     Key
Peptide
      Peptide
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The present sequence is that of a fusion protein comprising an Antennapedia peptide and a mouse Toll/interleukin-1 receptor adapter protein (TRAP) inhibitor polypeptide (see ABPSB106) of the invention. Antennapedia, derived from Drosophila, is a cellular membrane transport protein and can be used to deliver the TIRAP inhibitor across the cell membrane so that it becomes the rappentically active within the cell membrane so that it becomes component signalling in response to TIRA ligation, and controls independent signalling in response to TIRA ligation, and controls dendritic cell meturation. Characterisation of TIRAP has led to the discovery of compounds that inhibit both the MyD88 independent pathway as well as the MyD88 dependent pathway of TIRAP by inhibiting TIRAP polypeptide emplaised signalling. Compounds that inhibit TIRAP activity are useful for preventing or reducing inflammation and septic shock, and especially for assisting in the prevention of graft rejection, which occurs, at least in part, because of cellular necrosis induced inflammation. The invention provides TIRAP inhibitor polypuctides (see ABPSB105-08). The TIRAP inhibit companies can inhibit both the MyD88 independent response in cells and mapp kinases, and the MyD88 dependent response in cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New toll/interleukin-1 receptor adapter protein (TIRAP) polynucleotides and polypeptides, useful for treating a disease state associated with TIRAP expression, e.g. inflammation, and for inducing and affecting immune response
                                                                                                                                                                                                                     Toll/interleukin-1 receptor adapter protein; TIRAP; mouse; inhibitor; Antennapedia; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..16
/note= "Antennapedia peptide"
17..30
/note= "mouse TIRAP inhibitor peptide"
                                                                                                                                              Mouse TIRAP-Antennapedia fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 74; 74pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-MAY-2001; 2001US-289738P.
09-MAY-2001; 2001US-289815P.
29-AUG-2001; 2001US-289866P.
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                                                                       28-MAR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                        Chimeric - Mus sp.
Chimeric - Drosophila sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medzhitov R, Horng T,
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29-AUG-2001;
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ABP58107;
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Search completed: February 18, 2004, 14:26:28 Job time : 106.289 secs

Query Match 64.2%; Score 95; DB 24; Length 30; Best Local Similarity 78.3%; Pred. No. 4.5e-07; Matches 18; Conservative 1; Mismatches 4; Indels

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

February 18, 2004, 14:12:09; Search time 30.7632 Seconds (without alignments) 87.531 Million cell updates/sec Run on:

US-09-643-260-18

162 1 DRQIKIWFQNRRMKWKKTALDWSWLQTE Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES	Description	antennapedia-like	antennapedia-like	homeotic protein			homeo box protein	homeotic protein	homeotic protein	homeotic protein	homeotic protein		homeotic protein	antennapedia prot	homeotic protein		homeobox protein	homeotic protein	homeo box protein	homeotic protein	homeotic protein	homeotic protein	homeotic protein						
SUMMARIES		PC2399	PC2400	A27471	A03314	A28329	151341	815536	B29585	A05266	C27176	S26400	31324	57235	165241	PC1216	I51439	S15538	JC1161	A60084	D34510	58852	C43559	I51342	S47605	18302	847603	990058	01275
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808303	800589	A03317	808639	A24779	A32167	S47602	S36448	B61045	T10775	A24777	JT0273	B24777	S20087	PC4071	млнизс
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86	87	88	96	97	103	105	106	107	113	118	118	118	138	148	153
58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0	58.0
94	94	94	94	94	94	94	94	94	94	94	94	94	94	94	94

ALIGNMENTS

C;Species: Styela clava
C;Species: Styela clava
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jul-2000
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jul-2000
R;Gc, T:; Lee, H.; Tomlinson, C.R.
Gene 147, 219-222, 1994
A;Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela c
A;Reference number: PC2399; MUD:95011617; PMID:7926803
A;Accession: PC2399
A;Accession: PC399
A;Accession: PC399; MUD:95011617; PMID:7926803
A;Accession: PC399
A;Accession: PC399
A;Accession: PC399
A;Accession: PC399
A;Accession: DNA
A;Residues: 1-60 cGET>
A;Cose-references: GB:S73920; NID:g693714; PIDN:AAB33061.2; PID:g7387472
A;Accession: PC399
A;Accession: DNA
A;Accession: Accession: Accession antennapedia-like homeotic protein AHox 2 - sea squirt (Styela clava) (fragment)

Gaps Score 97; DB 2; Length 60; Pred. No. 1.5e-06; 1; Mismatches 0; Indels 59.9%; Ouery Match Best Local Similarity 94.1 Matches 16; Conservative

ö 1 DROIKIWFONRRMKWKK 17 ઠે

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C;Species: Styela plicata
C;Species: Styela plicata
C;Date: 26-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 17-Oct-1997
C;Accession: PC2400
R;Ge, T.; Lee, H.; Tomlinson, C.R.
R;Ge, T.; Lee, H.; Tomlinson, C.R.
A;Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela c
A;Reference number: PC2399; MUID:95011617; PMID:7926803 antennapedia-like homeotic protein AHox 3 - sea squirt (Styela plicata) (fragment)

A;Accession: PC2400
A;Molecule type: DNA
A;Residues: 1-60 <GET>
A;Note: The authors translated the codon ATA for residue 47 as Glu
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox, nucleus; transcription regulation
F;2-58/Domain: homeobox homology <HOX>

Gaps ö 'Match 59.9%; Score 97; DB 2; Length 60; Local Similarity 94.1%; Pred. No. 1.5e-06; les 16; Conservative 1; Mismatches 0; Indels Matches

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1 DRQIKIWFQNRRMKWKK 17

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homeo box protein - Atlantic salmon)
C;Species: Salmo salar (Atlantic salmon)
C;Species: Salmo salar (Atlantic salmon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999
C;Accession: 15:341
R;Fjose, A.; Molven, A.; Eiken, H.G.
Gene 62, 141-152, 1988
A;Title: Molecular cloning and characterization of homeobox-containing genes from Atlant A;Reference number: 15:1341; MUID:88226009; PMID:2897318
A;Accession: 15:1341
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NyAlternate names: homeotic protein Hox 1A
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 31-58-1991 #sequence_revision 30-Sep-1991 #text_change 29-Aug-1997
C;Accession: 31-585
R;Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Stc Genome 31, 745-756, 1989
A;Title: Organization of human class I homeobox genes
A;Reference number: S1536
A;Accession: $15536
                                                                                                                                                                                                                                                                                                                                                                                 of the murine Hoxa-7 gene
A; LILLE: Primary structure and nuclear localization of a murine homeodomain protein.
A;Reference number: A28329; MUID:87260976; PMID:2885847
A;Accession: A28329
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A;Residues: 1-42, 'CAG', 46-229 <RES>
A;Cross-references: EMBL:U15972; NID:g664757; PIDN:AAC52160.1; PID:g664758
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                                                                                                                                                                    A, Molecule type: mRNA
A, Residues: 1-229 «KES>
A, Kroser-references: GB: M11192; NID: g193906; PIDN: AAA37833.1; PID: g309313
B, Parikh, H.; Shah, S; Hilt, D.; Peterkofsky, A.
Gene 154, 237-242, 1995
A, Title: Organization, sequence and regulation of expression of the murin
A, Reference number: 149131; MUID: 95197009; PMID: 7890170
A, Accession: 149131
A, Accession: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-75 < FJO>
A; Residues: 1-75 < FJO>
A; Residues: 1-75 < FJO>
A; Cross-references: GB: M18903; NID: G213797; PIDN: AAA49559.1; PID: G213798
C; Superfamily: unassigned homeobox proteins; homeobox homology
C; Keywords: DNA binding; homeobox; nucleus; transcription regulation
F; 2-58/Domain: homeobox homology < HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Introns: 126/1
C;Superfamily: homeotic protein Hox A7; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;130-186/Domain: homeobox homology cHOX>
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Pred. No. 6.2e-06;
1; Mismatches 7; Indels
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Pred. No. 2.6e-06;
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78.3%;
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Best Local Similarity 70.4%;
Matches 19; Conservative
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Best Local Similarity 78.33,
Conservative
18; Conservative
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A; Residues: 1-19 < COL.
B; R; Reference number: S13785; MUD:87053860; PMID:2877873
A; Reference number: S13785; MUD:87053860; PMID:2877873
A; Residues: 19-48, 'RI', 51-87 < BRE>
C; Genetics: Molecule type: DNA
A; Residues: 19-48, 'RI', 51-87 < BRE>
C; Genetics: Molecule type: Molecule type:
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Jul-1997
C;Accession: A03314; S14043
R;Colberg-Poley, A.M.; Voss, S.D.; Chowdhury, K.; Gruss, P.
Nature 314, 713-718, 1985
A;Title: Structural analysis of murine genes containing homoeo box sequences and their A;Reference number: A03314; MUID:85188311; PMID:2986010
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                                                                                                                                                                                                                                                  C;Species: Rattus norvegicus (Norvay rat)
C;Species: Rattus norvegicus (Norvay rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-May-1997
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-May-1997
C;Accession: A7471
R;Falzon, M.; Sanderson, N.; Chung, S.Y.
A;Fitle: Cloning and expression of rat homeo-box-containing sequences.
A;Reference number: A91576; MUD:87277429; PMID:2886401
A;Accession: A2771
A;Accession: A2771
A;Resiques: 1-105 < FAL>
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Superfamily: unassigned homeobox; nucleus; transcription regulation
F;6-62/Domain: homeobox homology < HOX>
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C;Species: Mus musculus (house mouse)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 20-Aug-1999
C;Accesion: A28329; 149131
R;Kessel, M.; Schulze, F.; Fibi, M.; Gruss, P.
Proc. Natl. Acad. Sci. U.S.A. 84, 5306-5310, 1987
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70.4%; Pred; No. 2.7e-06;
Mismatches 7; Indels
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                                                                 DROVKIWFONRRMKWKK 58
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homeotic protein Hox A7 - mouse
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Best Local Similarity 70.49
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Gaps

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homeotic protein Hox 2.2 (variant 1) - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Nov-2000
C;Accession: 826400; 826401
R;Shen, W.; Detmer, K.; Simonitch-Eason, T.A.; Lawrence, H.J.; Largman, C.
Rvicher, Acids Ree. 19, 539-545, 1991
A;Title: Alternative splicing of the HOX 2.2 homeobox gene in human hematopoietic cells
A;Reference number: S26400; MUID:91187672; PMID:1672751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Reywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulat
F;147-203/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and -2.4 homeo boxes: evolution
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A;Residues: 1-224 <SHE>
A;Residues: 1-224 <SHE>
A;Cross-references: EMBL;X58431; NID:g32369; PIDN:CAA41335.1; PID:g32370
A;Experimental source: tissue-type placenta
A;Note: the authors translated the codon ACT for residue 55 as Tyr, CGC for A;Accession: S26401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-139, 'E' cH2>
A; Cross-references: EMBL:X58431; NID:g32369; PIDN:CAA41336.1; PID:g32371
A; Experimental source: tissue-type placenta
A; Note: the authors translated the codon ACT for residue 55 as Tyr, CGC for A; Note: the authors did not translate the codons for residues 139, and 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Sep-1999
C;Accession: C27176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB: M18401; NID: 9193936; PIDN: AAC27130.1; PID: 93335322
         C;Superfamily: unassigned homeobox proteins; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;19-75/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: unassigned homeobox proteins; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;20-76/Domain: homeobox homology <HOX>
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Pred. No. 1.1e-05;
                                                                                                                                                                                          Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Hart, C.P.; Fainsod, A.; Ruddle, F.H.
Genomics 1, 182-195, 1987
A;Title: Sequence analysis of the murine Hox-2.2, -2.3,
A;Réference number: A27176; MUID:88085193; PMID:2891608
A;Accession: C27176
                                                                                                                                                                                          58.6%; Score 95; DB 2; 1
66.7%; Pred. No. 4.6e-06;
iive 2; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                       1 DRQIKIWFQNRRMKWKKTA--LDWSWLQTE 28
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59 ERQIKIWFQNRRMKWKKESKLLSASQLSAE
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C27176
homeotic protein Hox 2.2 - mouse
                                                                                                                                                                                                                               Local Similarity 66.7
1es 20; Conservative
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Matches 20; Conservative
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Best Local Similarity
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A; Residues: 1-97 < HAR>
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A.Accession: B29586
A.Accession: B29586
A.R. Residues: 1-81 < LON>
A.R. Residues: 1-81 
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R;Levine, M.; Rubin, G.M.; Tjian, R.
A;Title: Human DNA sequences homologous to a protein coding region conserved between hom A;Reference number: A05265; MUID:85024858; PMID:6091895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sta
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C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 17-Oct-1997
C;Accession: B29585
E;Lonai, P.; Arman, E.; Czosnek, H.; Ruddle, F.H.; Blatt, C.
DNA 6, 409-418, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homeotic protein Hox B6 - human (fragment)
N;Alternate names: homeotic protein Hox 2B; homeotic protein Hu2
C;Species: Homo sapiens (man)
C;Species: 05-Jun-1987 #sequence_revision 30-Sep-1991 #text_change 17-Oct-1997
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A;Residues: 1-66 <BON>
C;Genetics:
C;Genetics:
C;Genetics:
A;Gene.
C;BiHOXA7
A;Cene.
A;Gene.
C;BiHOXA7
A;Cene.
C;BiHOXA7
A;Cene.
C;BiHOXA7
A;Gene.
C;BiHOXA7
A;Gene.
C;BiHOXA7
A;Gene.
C;BiHOXA7
A;Gene.
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C;Genetics:
C;Gen
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A; Residues: 1-96 <LEV>
A; Cross-references EMBL: K02571
A; Note: this reading frame extends between two stop codons and does
B; Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma,
Genome 31, 745-756, 1989
A; Title: Organization of human class I homeobox genes.
A; Reference number: S15036; MUID: 90215256; PMID: 2576652
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Pred. No. 3.1e-06;
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66.7%; Pred. No. 3.8e-06;
Mismatches 6;
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2; Mismatches
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A;Map position: 17q21.3-17q21.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DRQIKIWFQNRRMKWKKTALD 21
                                                                                                                                                                                                                                                                                                                                                                                                                 58.6%;
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Best Local Similarity
Matches 17; Conserv
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Best Local Similarity
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A;Title: Structural changes in the antennapedia complex of Drosophila pseudoobscura.
A;Reference number: S57224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antennapedia protein (clone p1105) - fruit fly (Drosophila pseudoobscura) (fragment)
                                                                                                                                                                                                                                                                                                 C;Accession: A31324
R;Schughart, K.; Utset, M.F.; Awgulewitsch, A.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 85, 5582-5586, 198
A;Title: Structure and expression of Hox-2.2, a murine homeobox-containing gene.
A;Reference number: A31324; MUID:88289762; PMID:2899893
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                                                                                                                                                                                                                   homeotic protein Hox 2.2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Drosophila pseudoobscura
C;Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 15-Oct-1999
C;Accession: S57235
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 15-Oct-1999
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-224 «SCH»
A; Residues: 1-224 «SCH»
A; Cross-references: GB:J03782; NID:g193929; PIDN:AAA37843.1; PID:g387203
C; Superfamily: unassigned homeobox proteins; homeobox homology
C; Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;147-203/Domain: homeobox homology «HOX»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule Lype: DNA
A; Residues: 1-33 < RAN>
A; Cross-references: EMBL:X77711
C; Genetics:
A; Gene: FlyBase:Antp
A; Cross-references: FlyBase:FBgn0012693
C; Superfamily: unassigned homeobox proteins; homeobox homology
C; Keywords: DNA binding, homeobox; nucleus; transcription regulation
F; 1-22/Domain: homeobox homology (fragment) < HOX>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.6%; Score 95; DB 2; Length 224; 66.7%; Pred. No. 1.1e-05; ive 2; Mismatches 6; Indels
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  Indels
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Best Local Similarity 94.1%; Pred. No. 2e-06;
Matches 16; Conservative 1; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 ERQIKIWEQNRRMKWKKESKLLSASQLSAE 216
                                                                                             187 ERQIKIWFONRRMKWKKESKLLSASQLSAE 216
Mismatches
                                                 1 DROIKIWFONRRMKWKKTA--LDWSWLQTE 28
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Best Local Similarity 66.73
Matches 20; Conservative
Conservative
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A; Molecule type: mRNA
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20;
Matches
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Gaps

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1; Mismatches

58.0%; 94.1%;

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Rioliver, G.; Vispo, M.; Mailhos, A.; Martinez, C.; Sosa-Pineda, B.; Fielitz, W.; Ehrlic dene 121, 337-342, 1992
A.Title: Homeoboxes in flatworms.
A.Reference number: JC1386; MUID:93077050; PMID:1359988
                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Dugesia tigrina
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Oct-1997
C;Accession: PC1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                   C;Superfamily: unassigned homeobox proteins; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;1-40/Domain: homeobox homology (fragment) <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X66822
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;1-45/Domain: homeobox homology (fragment) <HOX>
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                                                                                                                                                                                                                                                                                                                                                                             58.0%; Score 94; DB 2; Length 42;
94.1%; Pred. No. 2.6e-06;
live 1; Mismatches 0; Indels
A;Reference number: 152340; MUID:95217128; PMID:7702549
A;Accession: 165241
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                         A;Cross-references: GB:S76290; NID:g913077
C;Genetics:
A;Gene: Hox-A; Hox-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 ERQIKIWFONRRMKWKK 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DRQIKIWFQNRRMKWKK 17
                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 94.1
Matches 16, Conservative
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                                                                                                                                   A; Residues: 1-42 < RES>
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Sequence 190, App Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 50, Appl Sequence 9, Appli Sequence 169, Ap Sequence 1169, Ap Sequence 1169, Ap Sequence 43, Appl Sequence 43, Appl Sequence 9, Appli Sequence 10, Appli Sequence 10, Appli Sequence 1, Appli Sequence 32, Sequence 10, Sequence 3, A Sequence 6, Al Sequence 6, Al Sequence 54, Sequence 8, 7 Sequence 29, Sequence 1 Sequence Sequence Sequence Sequence Sequence US-09-214-371-9
US-09-925-299-1169
US-09-925-299-1169
US-08-10-220A-9
US-09-10-220A-9
US-09-10-20A-10
US-09-10-20A-10
US-09-10-023A-10
US-09-10-023A-10 US-10-358-365-11 US-10-369-226-50 US-10-017-672-11

ALIGNMENTS

Gaps OTHER INFORMATION: Description of Artificial Sequence:NBD peptides Sequence 18, Application US/09847940B
Patent No. US20020156000A1
GENERAL INFORMATION:
APPLICANT: May, Michael J.
APPLICANT: Ghosh, Sankar
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FIETE REFERENCE: PPI-117CP
CURRENT APPLICATION NUMBER: US/09/847,940B
CURRENT FILING DATE: 2001-05-02
PRIOR PILING DATE: 2001-05-02
MINDED OF OF THE 2000-08-22 ö Length 28; Indels Query Match 100.0%; Score 162; DB 10; Best Local Similarity 100.0%; Pred. No. 3e-13; Matches 28; Conservative 0; Mismatches 0; TYPE: PRT ORGANISM: Artificial Sequence NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 18 LENGTH: 28 US-09-847-940B-18 US-09-847-940B-18

1 DROIKIWFONRRMKWKKTALDWSWLQTE 28

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RESULT 2
US-09-847-946A-18
Sequence 18, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

OM protein - protein search, using sw model

February 18, 2004, 14:36:10 ; Search time 77.9211 Seconds (without alignments) 75.239 Million cell updates/sec

Run on:

US-09-643-260-18

162 1 DRQIKIWFQNRRMKWKKTALDWSWLQTE Perfect score:

Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

801455 segs, 209382283 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published_Applications_AA:*

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(cgn2_6/ptcdata/1/pubpaa/USO08_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		. d p	•		SUMMARIES	•
Result No.	Score	Query	Query Match Length DB	DB	OI.	Description
-1	162	100.0	28	2	US-09-847-940B-18	Sequence 18, Appl
7	162	100.0	28	11	US-09-847-946A-18	Sequence 18, Appl
m	134	82.7	28	10	US-09-847-940B-19	Sequence 19, Appl
4	134	82.7	28	11	US-09-847-946A-19	Sequence 19, Appl
2	105	64.8	18	11	US-09-847-946A-131	
9	101	62.3	36	σ	US-09-731-023A-12	Sequence 12, Appl
7	101	62.3	36	12	US-10-358-365-12	Sequence 12, Appl
80	98	60.5	17	15	US-10-229-915-1	Sequence 1, Appli
σ	97	59.9	34	15	US-10-161-499-79	Sequence 79, Appl
10	96	59.3	26	15	US-10-097-175-101	_
11	95	58.6	21	80	US-08-610-220A-11	Sequence 11, Appl
12	95	58.6	21	σ	US-09-150-623-11	Sequence 11, Appl
13	94	58.0	30	15	US-10-188-947-11	Sequence 11, Appl
14	94	58.0	64	15	US-10-118-079-44	Sequence 44, Appl
15	40	58.0	217	15	US-10-097-340-129	Sequence 129, App

Gaps

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Sequence 12, Application US/09731023A
Patent No. US20020077283A1
GENERAL INFORMATION:
APPLICANT: Sessa, William
IITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics
FILE REFERENCE: 44574-5076-US
                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-19
      INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                  Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 18;
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                                                                                                                                                                                                                                                                                                                                                                Score 134; DB 11;
Pred. No. 8e-10;
0; Mismatches 2;
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Pred. No. 1.9e-06;
FILE REFERENCE: PPI-119
CURRENT APPLICATION UNBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 06/201,261
PRIOR PILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DRQIKIWFQNRRMKWKKTALDASALQTE 28
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                  82.7%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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Best Local Similarity 92.9
Matches 26; Conservative
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                     SEQ ID NO 19
LENGTH: 28
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                  APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT APPLICATION NUMBER: 60/201,261
PRIOR PILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: NBD peptides
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Patent No. US20020156000A1
GENERAL INFORMATION:
APPLICANT: May, Michael J.
APPLICANT: Ghosh, Sankar
ITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REPERBING: PPI-117CP
CURRENT APPLICATION NUMBER: US/09/847,940B
CURRENT FILING DATE: 2001-05-02
PRIOR PILING DATE: 2000-08-22
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100.0%; Score 162; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 3e-13;
Matches 28; Conservative 0; Mismatches 0; Indels
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Pred. No. 8e-10;
0; Mismatches 2; Indels
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Publication No. US20030054999Al
GENERAL INFORMATION: APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 82.7%;
Best Local Similarity 92.9%;
Matches 26; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Findeis, Mark A
Phillips, Kathry
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US-09-847-946A-19
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APPLICANT:
APPLICANT:
APPLICANT:
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Gaps

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APPLICANT: JOYAL, JOHN L.
APPLICANT: MUELLER, JOHN
APPLICANT: OZA, VIBHA B.
APPLICANT: OZA, VIBHA B.
TITLE OF INVENTION: PEPTIDIC MODULATORS OF THE ANDROGEN RECEPTOR
TITLE REFERENCE: PPI-110
CURRENT APPLICATION NUMBER: US/10/097,175
CURRENT PILING DATE: 2002-03-12
PRIOR PILING DATE: 2001-03-12
PRIOR PILING DATE: 2001-03-12
PRIOR PILING DATE: 2002-01-28
NUMBER OF SEQ ID NOS: 102
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PASKSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-161-499-79

i Sequence 79, Application US/10161499

i Sequence 79, Application US/10161499

i Publication No. US20030044427A1

GENERAL INFORMATION:

APPLICANT: Howley, Peter M.

APPLICANT: Rasukaw, Hiroaki

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING

TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS

FILE REPERENCE: HWV-041.01

CURRENT APPLICATION NUMBER: US/10/161,499

CURRENT FILING DATE: 2002-06-03

PRIOR APPLICATION NUMBER: US/09/347,504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 59.9%; Score 97; DB 15; Length 34; Best Local Similarity 64.3%; Pred. No. 3.3e-05; Matches 18; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                               Length 17;
                                                                                                                                                                                                                                                                                                    Indela
                                                                                                                                                                                                                                             Query Match 60.5%; Score 98; DB 15; L
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: anti-inflammatory compound
US-10-229-915-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DRQIKIWFQNRRMKWKKTALDWSWLQTE 28
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        SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 101, Application US/10097175; Publication No. US20030045680A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    1 DRQIKIWFQNRRMKWKK 17
                                                                                                                                                                                                                                                                                                                                                        1 DRQIKIWFQNRRMKWKK 17
                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 79
LENGTH: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT; ORGANISM: Homo sapiens
US-10-161-499-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-097-175-101
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LENGTH: 26
                                 SEQ ID NO 1
LENGTH: 17
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Sequence 1, Application US/10229915
Publication No. US20030083262A1
Bublication No. US20030083262A1
GENERAL INFORMATION:
APPLICANT: Lazarus, Douglas
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING INFLAMMATORY
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: PPL-127
CURRENT APPLICATION NUMBER: US/10/229,915
CURRENT FILING DATE: 2002-08-27
PRIOR FILING DATE: 2001-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sessa, William
TITLE OF INVENTION: Caveolin Peptides and Their Use as Therapeutics
FILE REPRENCE: 44574-5076-US
CURRENT APPLICATION NUMBER: US/10/358,365
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: US 69/731,023
PRIOR APPLICATION NUMBER: US 60/231,327
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VAR: 2.11
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
62.3%; Score 101; DB 9; Length 36;
Best Local Similarity 69.2%; Pred. No. 1.1e-05;
Matches 18; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Description of Artificial Sequence: ) OTHER INFORMATION: Antennapedia-cav-X fusion peptide US-10-358-365-12
                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence; ; OTHER INFORMATION: Antennapedia-cav-X fusion peptide US-09-731-023A-12
CURRENT APPLICATION NUMBER: US/09/731,023A
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/231,327
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RQIKIWFQNRRWKWKKWGIDKAFFTT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-358-365-12; Sequence 12, Application US/10358365; Publication No. US20030165510A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 12
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                       SEQ ID NO 12
LENGTH: 36
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US-09-150-623-11
is Sequence 11, Application US/09150623
j Patent No. US20020044931A1
j GENERAL INFORMATION:
j TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL
TITLE OF INVENTION: DEATH AND USES THEREOF
j NUMBER OF SEQUENCES: 11
correspondence Address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-610-220A-11

Sequence 11, Application US/08610220A

Publication No. US20030099638A1

GENERAL INFORMATION:

APPLICANT: Troy, Carol M.

TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL

TITLE OF INVENTION: DEATH AND USES THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
                                                                                                                                                   Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.6%; Score 95; DB 8; Length 21; 94.4%; Pred. No. 3.7e-05;
                                                                                                                                            59.3%; Score 96; DB 15; Length 26 ilarity 77.3%; Pred. No. 3.4e-05; Conservative 2; Mismatches 3; Indels
                               , OTHER INFORMATION: Androgen Receptor Binding Polypeptides US-10-097-175-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
CUUNTRY: U.S.A.
ZIP: 1003 A.
ZIP: 1003 A.
ZIP: 1003 A.
ZIP: 1003 A.
ZIP: 1004 A.
ZIP: 1005 A.
ZIP: 1005 A.
ZIP: 1006 A.
ZIP: 1006 A.
ZIP: 1006 A.
ZIP: 1007 A.
ZIP: 2007 A.

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                                                                                                                                                                                                                                                                                                                                           1 RQIKIWFQNRRMKWKKLTIESS 22
                                                                                                                                                                                                                                                                                                2 RQIKIWFQNRRMKWKKTALDWS 23
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Best Local Similarity 94.4
Matches 17; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                            Query Match
Best Local Similarity
Matches 17; Conserv
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FEATURE:
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Sequence 11, Application US/10188947

Sequence 11, Application US/10188947

Sequence 11, Application VS20030023993A1

GENERAL INFORMATION:
APPLICANT: HORNG, Tiffany
APPLICANT: HORNG, Tiffany
APPLICANT: HORNG, Tiffany
APPLICANT: BARTON, Gregory
TITLE OF INVENTION: TOLL/INTERLUXIN-1 RECEPTOR ADAPTER PROTEIN (TIRAP)
FILLS OF INVENTION: TOLL/INTERLUXIN-1 RECEPTOR ADAPTER PROTEIN (TIRAP)
FILLS REPERENCE: 044574-5101US
CURRENT PILING DATE: 2002-07-03
FRICK APPLICATION NUMBER: 60/289, 738
FRICK APPLICATION NUMBER: 60/289, 866
FRICK APPLICATION NUMBER: 60/289, 866
FRICK FILING DATE: 2001-05-09
FRICK FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 12
SEQ ID NO :
FRICK PAPELICATION VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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COTHER INFORMATION: TIRAP/Antennapedia fusion protein
NAME/KEY: MISC_PEATURE
COTHER INFORMATION: TIRAP/Antennapedia fusion protein
US-10-188-947-11
                                                                                                                ZIF: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/150,623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48332/JPW/JML
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                         PELLING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/610,220
FILING DATE: MAR-04-1996
ATTORNEY/AGBNT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
FREERENCE/DOCKET NUMBER: 48332/
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
TELEPHONE: 7212-391-0525
TELEPHONE: 7212-391-0525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                         New York
                                                 New York
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                                                                                                 COUNTRY:
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Query Match 58.0%; Score 94; DB 15; Length 217; Best Local Similarity 94.1%; Pred. No. 0.0004; Matches 16; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 129
LENGTH: 217
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR PELING DATE: 2001/09/26
PRIOR FILING DATE: 2001/09/31,732
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325, 102
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR PLING DATE: 2001-09-19
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US-10-097-340-129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Amino acid sequence of Antennapedia from C3APL
US-10-118-079-44
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0
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         58.0%; Score 94; DB 15; Length 30; 89.5%; Pred. No. 6.8e-05; tive 0; Mismatches 2; Indels
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TITLE OF INVENTION: FUSION PROTEINS
FILE REFERENCE: 60746-004-095-03
CURRENT PRILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: CA 2,367,636
PRIOR FILING DATE: 2002-01-15
PRIOR PILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
SEQ ID NOS: 48
SEQ ID NOS: 48
LENGRARE: PatentIn version 3.1
SEQ ID NO 44
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Publication No. US20030087250Al
GENERAL INFORMATION:
APPLICANT: John MONAHAN
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PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FLILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-118-079-44

; Sequence 44, Application US/10118079
; Publication No. US20030103957A1
; GENERAL INFORMATION:
                                                                                                                                                                                      2 RQIKIWFQNRRMKWKKTAL 20
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Sebastian HOERSCH
Shubhangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
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Robert C. BAST, Jr.
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Rosemarie SCHMANDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                             Best Local Similarity 89.5
Matches 17; Conservative
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Karen GLATT
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         Query Match
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February 18, 2004, 13:37:19; Search time 106.289 Seconds (without alignments) 41.814 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1107863 seqs, 158726573 residues
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1 DRQIKIWFQNRRMKWKKTALDWSWLQTE
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    OM protein - protein search, using sw model
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Gapop 10:0 , Gapext 0.5
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seg length: 200000000
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Perfect score:
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS1/gcgdata/geneseg/genesegp-emb1/AA2002.DAT:*/SIDS1/gcgdata/geneseg/genesegp-emb1/AA2003.DAT:*

	Description	IKKbeta NEMO bindi	NBD peptide SEQ ID	Wild-type human NE	Mutated IKKbeta NE	NBD peptide SEQ ID	Human mutant NEMO	Anti-inflammatory	Anti-inflammatory	Antennapedia-caveo
SUMMARIES	ai	ABB08740	AAM48523	ABU08434	ABB08741	AAM48524	ABU08435	AAM48628	AAM48629	AAU79345
	08	23	23	24	23	23	7	23	23	23
	Query Match Length DB	28	28	28	28	28	28	18	18	36
do	Ouery Match	100.0	100.0	100.0	82.7	82.7	82.7	64.8	64.8	62.3
	Score	162	162	162	134	134	134	105	105	101
	Regult No.	r 1	7	m	4	S	φ	7	80	σ

Mixer SIM peptide.		Synthetic alpha sm	Anti-apoptotic pro	Human papillomavir	Androgen receptor	Antennapedia helix	Cysteine protease	Oestrogen receptor	Drosophila antenna	Protein regulating	Anti-apoptotic pro	Antennapedia inter	Transduction domai	Mouse TIRAP-Antenn	Drosophila antenna	D. melanogaster pA	Drosophila antenna	S. cerevisiae Antp	D. melanogaster an	Antennapedia C3APL	Amino acid sequenc	Human HOXB7 varian	Human ovarian canc	Е			Drosophila melanog	Antennapedia-caveo	Internalization se	Beta-catenin deriv	Human nucleic acid	Human colon cancer	Human polypeptide		Amino acid sequenc
AAB80924	AAB80925	AAB13423	AAW11630	AAY79919	AAE31836	ABP53779	AAW45976	AAW82957	AAY78416	AAY58610	AAW11629	AAY27444	ABB83151	ABP58107	AAY42291	AAY27403	AAY04364	ABB84470	AAE00811	AAE32060	ABB99729	AAE10922	ABG96337	AAE32047	ABB72035	ABB57755	ABB58929	AAU79344	AAW91049	AAB27063	AAB21030	AAB53629	AAM41487	AAM39701	AAW48885
22	22	21	18	21	24	23	18	19	21	21	18	20	23	24	20	20	20	23	22	24	24	22	23	24	22	22	22	23	20	21,	21	21	22	22	19
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10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31		33	34	35	36	37	38	39	40	41	42	43	44	45

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28 AA		
peptide,		(first entry)
andard;		
Bt		002
LT 1 3740 ABB08740 standard; peptide;	ABB08740;	14-JUN-2002

RESULT 1 ABB08740

ALIGNMENTS

kinase activation; leukocyte; inflammation; E-selectin; osteoclast; autoimmune disease; transplant rejection; osteoporosis; cancer; Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis; rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; antiinflammatory; immunosuppressive; osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antiasthmatic; antiallergic; dermatological; antibacterial; IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB; IKKbeta NEMO binding domain peptide SEQ ID NO 18.

02-MAY-2001; 2001WO-US40654. 02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260. 08-NOV-2001.

WO200183547-A2 Homo sapiens

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cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; esteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
                                                                         ataxia telangiectasia, allergy, anaphylaxis, arthritis.
                                                                                                                                                                                                                     02-MAY-2001; 2001WO-US14346.
                                                                                                                                                                                                                                                       02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
                                                                                                                                                                                                                                                                                                            (PRAE-) PRAECIS PHARM INC. (UYYA ) UNIV YALE.
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                                                                                                                                                                               08-NOV-2001.
                                                                                                             Synthetic.
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                                                                                                                                                                                                                            The invention relates to modulating NP-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (C (ABB00725-ABB00742) comprising at least one NBMO binding domain (ABB77313). The compound has acts through selective inhibition of C cytokine-mediated NF-kB activation by blocking the interaction of NEMO binding domain. Blockage of IKKbeta-NEMO interaction results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IKKbeta Fre compound may also into sites of acute and chronic inflammation, by down-regulating the expression of E-selectin on leukocytes or by blocking osteoclast conditions, where the condition is an inflammatory disorder, an autoimmune disease, transplant rejection, osteoporosis, cancer, an autoimmune disease, atherosclerosis, a viral infection or ataxia conditions, where the condition is an inflammatory disorder, an autoimmune disease, atherosclerosis, a viral infection or ataxia curticaria, anaphylaxis, cutaneous inflammaton, sepsis, psoriasis, curticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis, cremandidesse, rhenitis, psoriatic arthritis, osteoarthritis, psoriatic arthritis, used arthritis, osteoarthritis, psoriatic arthritis, lupus and boursitis. The inflammatory disorder may also be dermatitis, eczema, psoriatis, osteoarthritis, psoriatic arthritis, lupus and psoriasis, osteoarthritis, soriacis are also dermatitis, conditions applyatic arthritis, drug and food sensitivity, contact dermatitis, cryoglobulinaemia or multiple sclerosis. For chronic viral infections cryoglobulinaemia or multiple sclerosis. For chronic viral infections cryoglobulinaemia or multiple sclerosis. For chronic cryoglobulinaemia or multiple sclerosis. For chronic viral infections creating anaphylaxis, drug and food sensitivity, contact dermatitis, any may any any and inferior cryoglobulinaemia or multiple aclerosis. For chronic viral infections craesing anaphylaxis, drug and chronic and conticosteroids in minhibard and inferior and co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunosuppression in transplants and cancer therapy. Also for identifying antiinflammatory compounds and for diagnosis of an inflammatory disorder. The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of the NEWO binding domain of IKKDeta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antitheumatic; antiatchritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema;
                                                                                                       Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting a cell with an anti-inflammatory compound comprising at least one NEMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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100.0%; Pred. No. 7.9e-15;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 28; Conservative
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                                                                     WPI; 2002-179350/23
(UYYA ) UNIV YALE.
                                   Ghosh S;
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Phillips K;

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                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid residues, fused to a NEMO binding sequence (AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antinheumatic, antiartheumatic, antiartheumatic, antiartheumatic, osciptus antibacterial, immunosuppressive, dermacological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatorid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzhaimer's disease; atherosclerosis; viral infections; and ataxia relangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                    The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AMM48627) or AAM48646-AAM48651) which comprises from 6-15
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100.0%; Pred. No. 7.9e-15;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                Example 5; Fig 5; 88pp; English.
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us-09-643-260-18.rag

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NEWO binding domain (NBD) peptides. The NEWO binding domains are found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-lapha (IKKalpha) proteins. The antiinflammatory compounds of the invention are useful for modulating nuclear factor-kappaB (NF-kappaB) induction in a cell, where the compounds are capable of blocking the interaction between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The antiinflammatory compound further comprises at least one membrane translocation domain. The compounds are useful for treating inflammatory disorders, autoimmune diseases, osteoporosis, cancer, Alzheimer's disease, atherosclerosis, viral infections, Ataxia telanglactasia, and for transplantation detection. The compounds the invention block NF-kappaB induction by IKK but do not inhibit
                                    Human; antiinflammatory compound; NEMO binding domain; NBD; IKKDeta; IKapaB kinase-alpha; IKKalpha; NF-kappaB; nuclear factor-kappaB kinase-alpha; IKKalpha; NF-kappaB; nuclear factor-kappaB induction; inflammatory disorder; atheroism disease; osteoporosis; cancer; Alzheimer's disease; atherosclerosis; viral infection; Ataxia telangiectasia; transplantation detection; immunosuppressive; osteopathic; cytostatic; noorropic; neuroprotective; antiatherosclerotic; virucide; vasotropic; antirheumatic; antiathritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention relates to antiinflammatory compounds comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel antiinflammatory peptide compounds comprising NEMO binding domain, useful for modulating NF-kappaB induction in a cell and for treating NF-kappaB-mediated inflammation disorders e.g., asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the basal activity of NP-kappaB. The present sequence represents an antiinflammatory compound of the invention.
Wild-type human NEMO binding site (NBD) peptide.
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                                                                                                                                                                                                                                                                                                                                                                                            02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.
                                                                                                                                                                                                                                                                                                                                                     02-MAY-2001; 2001US-0847940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    psoriasis, vasculitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-209142/20.
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                                                                                                                                                                                                                               Homo sapiens.
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ö Gaps ö 100.0%; Score 162; DB 24; Length 28; 100.0%; Pred. No. 7.9e-15; ive 0; Mismatches 0; Indels C Best Local Similarity 100.0 Matches 28; Conservative Query Match

Claim 23; Fig 5; 82pp; English.

1 DRQIKIWFQNRRMKWKKTALDWSWLQTE 28 DRQIKIWFQNRRMKWKKTALDWSWLQTE 28

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ABB08741 standard; peptide; 28 AA. 14-JUN-2002 (first entry) ABB08741; RESULT 4 ABB08741 ****

Mutated IXXbeta NEMO binding domain peptide SEQ ID NO 19.

autoimmune disease; transjant rejection; osteoporosis; cancer;
Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;
antiarteriosclerotic; virucide; antishimatic; antiallergic;
dermatological; antibacterial; antishoriatic; antitheumatic;
antiarthritic; osteopathic; antiulcer; mutant; mutein. ø Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting cell with an anti-inflammatory compound comprising at least one NEMO IKKbeat; IKKalpha, NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB; kinase activation; leukocyte; inflammation; E-selectin; osteoclast; /note= "Wildtype Trp substituted by Ala" /note= "Wildtype Trp substituted by Ala" Location/Qualifiers 02-MAY-2001; 2001WO-US40654. 02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260. WPI; 2002-179350/23. Misc-difference 24 Misc-difference 22 (UYYA) UNIV YALE. Ghosh S; binding domain WO200183547-A2 Homo sapiens. 08-NOV-2001 Synthetic. May MJ,

The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB077313). The comprision at least one NEMO binding domain (ABB077313). The compound has acts through selective inhibition of cytokine-mediated NF-kB activation by blocking the interaction of NEMO cytokine-mediated NF-kB activation by blocking the interaction of NEMO binding domain. Blockage of IKKDeta-NEMO interaction results in inhibition of IKCDeta kinase activation and subsequent decreased phosphorylation of IKCDETA kinase activation and subsequent decreased phosphorylation of IKCDETA kinase activation and subsequent decreased phosphorylation of IKCDETA kinase activation and correction conformed in the selection of Eselection on leukocytes or by blocking osteoclast confideration. The compound is useful in treating NF-kB mediated confitient in the compound is useful in treating NF-kB mediated confitient in the inflammatory disorder is an inflammatory disorder. Alzheimer's disease, transplant rejection, osteoporosis, cancer, at the inflammatory disorder is asthma, allergies, uriticaria, anaphylaxis, cutaneous inflammation, sepasis, psoriasis, chematorial confit of the inflammatory disorder is asthma, allergies, uriticaria, anaphylaxis, cutaneous inflammation, sepasis, psoriasis, osteoarthritis, psoriatic arthritis, inflammatory disorder may also be dermatitis, concomposition or psoriasis, osteoarthritis, psoriatic arthritis, lupus and sporial infections of psoriasis, celevathritis, psoriatic arthritis, lupus and sporial sporial sporial arteritis, cryoglobulinaenia or multiple sclerosis, concomposis, temporal arteritis, cryoglobulinaenia or multiple sclerosis. For chronic or infinity or colitis, cryoglobulinaenia or multiple sclerosis. caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral diseases include HIV and influenza. The compound may also be useful for treating anaphylaxis, drug and food sensitivity, contact dermatitis, sunburn or aging. The compound may be used to replace corticosteroids in any application in which corticosteroids are used, including immunosuppression in transplants and cancer therapy. Also for identifying antiinflammatory compounds and for diagnosis of an inflammatory disorder.

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The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of a mutated NEMO binding domain of IKKDeta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid residues, tused to a NEMO binding sequence (AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antibsoriatic, antirheumatic, antiarthritic, osteopathic, antiabacterial, immunosuppressive, dermatclogical, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of Ikkbeta kinase compounds are useful for treating inflammatory disorders, e.g. asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                       Gaps
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                                                                                                                 Length 28;
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                                                                                                               Score 134; DB 23;
Pred. No. 4.3e-11;
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                                                                                                           82.7%;
92.9%;
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                                                                                                       Query Match
Best Local Similarity 92.9
Matches 26; Conservative
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lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatcory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteopoxosis, Alzheimer's disease; atherosclerosis; viral infections; and ataxia relangiectasia. The compounds are also useful for treading pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; antiinflammatory compound; NEMO binding domain; NBD; IKKOeta; IkappaB kinase-alpha; IKKalpha; NF-kappaB; nuclear factor-kappaB kinase-alpha; IKKalpha; NF-kappaB; autoimmune disease; osteoporosis; cancer; Alzheimer's disease; atherosclerosis; viral infection; Ataxia telangiectasia; transplantation detection; immunosuppressive, osteopotahic; cytostatic; nootropic; neuroprotective; antiatherosclerotic; virucide; vasotropic; antirheumatic; antiatherosclerotic; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEMO binding domain (NBD) peptides. The NEMO binding domains are found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha (IKKalpha) proteins. The antiinflammatory compounds of the invention are useful for modulating nuclear factor-kappaB (NF-kappaB) induction in a cell, where the compounds are capable of blocking the interaction between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
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                                                                                                                                                                                                                 Length 28;
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Pred. No. 4.3e-11;
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                                                                                                                                                                                                               82.7%;
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                                                                                                                                                                                                                                      Best Local Similarity
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antinflammatory compound further comprises at least one membrane translocation domain. The compounds are useful for treating inflammatory disorders, autoimmune diseases, osteoporosis, cancer, Alzhaimer, e disease, atherosclerosis, viral infections, Ataxia telangiectasia, and for transplantation detection. The compounds of the invention block NF-kappaB induction by IKK but do not inhibit the basal activity of NF-kappaB. The present sequence represents a human mutant NBD peptide.
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                                                                                                                                                                                                                     82.7%; Score 134; DB 24; Length 28; 92.9%; Pred. No. 4.3e-11; ive 0; Mismatches 2; Indels
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Best Local Similarity 92.9'
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compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEWO binding domain that results in inhibitino of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, pranulomatosis, multiple sclerosis, transplant rejection; osteoporosis, Alzheimer's disease, atherosclerosis, viral infections, and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                   Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                              Length 18;
                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                            64.8%; Score 105; DB 23;
100.0%; Pred. No. 1.9e-07;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phillips
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-inflammatory peptide SEQ ID NO 132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; Page 63; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM48629 standard; Peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Findeis MA,
                                                                                                                                                                                                                                                                                                                                                                                                    28
                                                                                                                                                                                                                                                                                                                                                                                                                                         18
                                                                                                                                                                                                                                                                                                                                                                                                                            1 REMKWKKTALDWSWLQTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAY-2001; 2001WO-US14346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.
                                                                                                                                                                                                                                                                                                                                                                                                      11 RRMKWKKTALDWSWLQTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 18, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PRAE-) PRAECIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-121889/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ghosh S,
                                                                                                                                                                                                                                                                                         18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-NOV-2001.
                                                                                                                                                                                                                                                        arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM48629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               May MJ,
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07-DEC-2000; 2000US-0731023

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mino acid residues, fused to a MEMO binding sequence
(AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
contropic, antiatherosclerotic, virucide and antiallergic activity. The
compounds act as selective inhibitors of cytokine-mediated NFkappaB
activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
the NEMO binding domain that results in inhibition of IKKbeta kinase
activation and subsequent decreased phosphorylation of IkappaB. The
compounds are useful for treating inflammatory disorders, e.g. asthma,
lung inflammation or cancer, psoriasis, rheumatoid arthritis,
osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
cyaranulomatosis, multiple sclerosis, transplant rejection; osteoporosis;
Alzheimer's disease, atherosclerosis, transplant rejection; and ataxia
telangiectasia. The compounds are also useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caveolin, scaffolding domain, endothelial nitric oxide synthase, eNOS, vasodilation inhibitor; inflammation inhibitor; tumour cell angiogenesis; tumour cell proliferation, osteoporosis, arthritis; atherosclerosis; asthms; Alzheimer's disease, allergy, allergy chinitis; uticaria; anaphylaxis; dry sensitivity; food sensitivity; dermatitis; eczema; poriasis; sunburn, aging; osteoarthritis; psoriatic arthritis; lupus; spondylarthritis; chronic obstruction pulmonary disease; cancer; Cav; chronic inflammatory bowel disease; tumour growth; malignant neoplasm; human; fruit fly; antennapedia internalisation signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Control peptide based on a human caveolin-1 scaffolding domain shown in AAU79340 residues 82-101"
                                                                                                                                                                                                                                                                                                                                       pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
(AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.8%; Score 105; DB 23; Length 18; 100.0%; Pred. No. 1.9e-07;
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|Jabel= Antennapedia_internalisation_signal
|note= "Specifically_claimed in claim_9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antennapedia-caveolin-X fusion peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU79345 standard; Peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.5°,
100.08; Fir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 RRMKWKKTALDWSWLQTE 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RRMKWKKTALDWSWLQTE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17..32
/label= Cav-X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-SEP-2000; 2000US-231327P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
tes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200220768-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU79345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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The invention describes an isolated caveolin scaffolding domain peptide (I). A fusion peptide (II) containing (I) and at least a membrane translocation sequence is useful for down regulating endothelial nitric oxide synthase (eNOS) activity in a cell, resulting in blockage of vasodilation. (II) is therefore useful for inhibiting inflammation and crumour cell angiquenesis/proliferation in an animal; and for blocking the interaction of caveolin with a protein in vivo. (II) may be useful in the interaction of caveolin with a protein in vivo. (II) may be useful in transment of inflammatory conditions such as osteoporosis, rheumatoid are also useful for treating pathological processes associated with a pro-inflammatory response including allergies such as allergic rhinitis, are uncorrectly as dermatitis, especially as dermatitis, espendylaxis, dry sensitivity, contaneous inflammation such as dermatitis, such as osteoarthritis, psoriatic arthritis, such as osteoarthritis, psoriatic arthritis, lupus, spondylarthritis, and chronic obstruction pulmonary disease and chronic inflammatory bowel disease. (I) and (II) are useful for replacing corricosteroids useful for immunosuppression in transplant and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 patients. When administered along with one or more antiinflammatory agent (I) and (II) are useful for inhibiting tumour growth or malignant neoplasm including cellular angiogenetics, proliferation, invasiveness, and metastasis in biological systems. This sequence represents a fusion peptide of the invention created from the fruit fly antennapadia internallsation signal and control sequence Cav-X. based on the human caveolin-1 scaffolding domain shown in ANU79340, residues 82-101.
                                                                                                                                                                  modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smad, Cytostatic, vulnerary, cerebroprotective, immunosuppressive, Anti-HIV; antidiabetic, ophthalmological; antiinflammatory, SIM; Smad Interaction Motif; tissue repair; fibrotic condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                  New peptide having caveolin scaffolding domain, useful for mo activity of endothelial nitric oxide synthase and inhibiting inflammation and tumour cell angiogenesis proliferation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 101; DB 23;
Pred. No. 1.4e-06;
3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunosuppression; diabetic nephropathy; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RQIKIWFONRRMKWKKTALDWSWLQT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ROIKIWFONRRMKWKINGIDKAFFTT 26
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                                                                                                                                                                                                                                                     Claim 16; Page 72; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.3%;
69.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 69.2°
Matches 18, Conservative
                                                                                                                         WPI; 2002-329877/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mixer SIM peptide.
                                       (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200114413-A2
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Modified-site
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                                                                                Sessa WC;
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Misc-difference 26
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                         The present invention relates to peptides capable of interacting with a Smad protein, comprising a Smad Interaction Motif (SIM, amino acid sequence PP(T/N)K). The present sequence is one such Smad interacting peptide. Smad proteins are a family of highly conserved, intracellular proteins that signal cellular responses downstream of Transforming Growth Factor-beta (TGF-beta) family serine/threonine kinase receptors. The SIM is thought to be necessary for interaction with the MHZ domain of Smad2. The peptides of the present invention are useful in the manufacture of a medicament for the treatment of a patient in need of modulation of activin or TGF-beta signalling; cancer; a patient in need of reducing extracellular matrix deposition, encouraging tissue repair and/or regeneration, tissue remodelling or healing of a wound, injury or surgery, or reducing scar tissue formation arising from injury or brain; a patient with or at risk of end-stage organ failure, pathologic extracellular matrix accumulation, a fibrotic condition, disease states associated with immunosuppression (such as different forms of malignancy, chronic degenerative diseases, and AIDS), diabetic nephropathy, tumour growth, kidney damage (for e.g. obstructive neuropathy, IgA nephropathy or non-inflammatory renal disease) or renal fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Wild-type Pro replaced by Ala. Wild-type sequence given in AAB80924."
                                                                                                                                                                                                                           Polypeptide capable of interacting with a Smad polypeptide, useful in the treatment of cancer and for tissue remodelling or healing of a wound, injury or surgery, comprises a Smad Interaction Motif and is less than 32 amino acids in length -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smad, Cytostatic, vulnerary, cerebroprotective, immunosuppressive, Anti-HIV, antidiabetic, ophthalmological; antinflammatory, SIM, Smad Interaction Motif; tissue repair; fibrotic condition;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 100; DB 22; Length 41;
Pred. No. 2.2e-06;
3; Mismatches 2; Indels
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                                                                                                             (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LID.
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                                                                                                                                                                                                                                                                                                                           Claim 16; Page 140; 179pp; English
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                                                                                                                                                   Howell MT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.78;
77.38;
                                                                         99GB-0020000.
                                   25-AUG-2000; 2000WO-GB03265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Joury Match
Best Local Similarity 77.33,
Best Local 7; Conservative
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                                                                                                                                                   Germain SE, Hill CS,
                                                                                                                                                                                       WPI; 2001-265836/27.
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                                                                         25-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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The present invention relates to peptides capable of interacting with a smad protein, comprising a Smad Interaction Motif (SIM; amino acid sequence PP(TVN)K). The present sequence is one such Smad interacting peptide. Smad proteins are a family of highly conserved, intracellular peptide. Smad proteins are a family of highly conserved, intracellular proteins that signal cellular responses downstream of Transforming Growth Excor-beta (TGG-beta) family serine/hreonine kinase receptors. The SIM is thought to be necessary for interaction with the MH2 domain of Smad2. The peptides of the present invention are useful in the manufacture of a medicament for the treatment of a patient in need of modulation of activity or TGF-beta signalling; cancer; a patient in need of reducing extracellular matrix deposition, encouraging tissue repair and/or regeneration, tissue remodelling or healing of a wound, injury or segeneration, reducing scar tissue formation arising from injury to the brain; a patient with or at risk of end-stage organ failure, pathologic extracellular matrix accumulation, a fibrotic condition, disease states associated with immunosuppression (such as different forms of malignancy, chronic degenerative diseases, and AIDS), diabetic nephropathy, tumour growth, kidney damage (for e.g. obstructive neuropathy, Igh nephropathy, or non-inflammatory renal disease) or renal fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alpha smooth muscle actin; alpha-SM; wound contraction; hypertrophic scar; fibromatosis; Dupuytren disease; fibrotic condition; lung fibrosis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptide capable of interacting with a Smad polypeptide, useful in the treatment of canner and for tissue remodelling or healing of a wound, injury or surgery, comprises a Smad Interaction Motif and is less than 32 amino acids in length -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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/note= "Wild-type Pro replaced by Ala"
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                                                                                                                                                                                                                                                                                                                                                                                                                       (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 123; 179pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Germain SE, Hill CS, Howell MT;
                                                                                                                                                                                                                                                                                                                                     99GB-0020000.
                                                                                                                                                                                                                                                  25-AUG-2000; 2000WO-GB03265.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-265836/27.
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                                                                                  WO200114413-A2
                                                                                                                                                                                                                                                                                                                                     25-AUG-1999;
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Papillomavirus; PV; infection; cell proliferation; E2; peptidomimetic; E1; antiviral; virucide; cytostatic; antiproliferative; dermatological; preneoplastic lesion; neoplastic lesion; cutaneous lesion; wart; epidermodysplasia verruciformis; anorectal carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of papillomavirus E2 protein peptidomimetics for treating papillomavirus-infected cells and papillomavirus-induced conditions in mammals by inhibiting E1-E2 interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes the use of a small organic compound (A) which competitively inhibits interaction of a papillomavirus (PV) E2 protein with a PV E1 protein for treating a cell infected with PV or a
                                                                                                                                                                                                                                                        The present sequence is a cell permeable anti-apoptotic protein blocking peptide, which can be used to inhibit tumour growth, e.g. by ex vivo purging or (after stabilisation) in vivo administration. The peptide preferably blocks Bcl-2, and comprises a signal peptide mediating cell penetration and a functional sequence corresponding to a Bcl-2 domain.
                                                                                                                                                                   Peptide(s) that block anti-apoptotic proteins - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                               60.5%; Score 98; DB 18; Length 26;
89.5%; Pred. No. 2.5e-06;
iive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human papillomavirus 16 E2 fusion peptide Ant-WP.
                                                                                           Kiehntopf M;
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                                                                                                                                                                                                                         Claim 6; Page 7; 7pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERQIKIWFONRRMKWKKAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 89.5
                                                                                                                                                                                    inhibiting tumour growth
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                                                                                           Herrmann F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus.
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                                                      (KIEH/) KIEHNTOPF M.
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                                                                                                                              WPI; 1997-088160/09
                 BRACH M.
HERRMANN
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                 (BRAC/) I
(HERR/) I
                                                                                         Brach M,
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to novel peptides comprising of a specific tetrapeptide associated with an oligopeptide which allows the introduction of the tetrapeptide into the target cell. The present sequence is one such peptide. Residues 1 to 4 of the present sequence correspond to the oligopeptide. Residues 1 to 4 of the present sequence correspond to the oligopeptide. The specific tetrapeptide of the present sequence interferes with alpha smooth muscle (alpha-SM) actin organisation in stress fibers. The present sequence may be used in the prevention and/or treatment of a disease related to alpha-SM actin prevention, e.g. wound contraction, hypertrophic scars, fibromatosis and fibrotic conditions. The present sequence may also be used to treat bupuytren disease and lung fibrosis.
                                                                                                                                                                                                                                                                                               A peptidic product for prevention and treatment of a disease related to alpha-SM actin expression comprises a tetrapeptide associated with a chemical entity that is able to introduce the tetrapeptide into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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1.9e-06;
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/note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 60.5%; Score 98; Local Similarity 100.0%; Pred. No. es 17; Conservative 0; Mismatch
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/label= sig_peptide
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                                                                                                                                                                                    (UNIO ) UCB-BIOPRODUCTS
                                                                                                                                                                                                                         Scarso A;
                                                                                                                                                                                                                                                          WPI; 2000-452308/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 AA;
                                    WO200038733-A1
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                                                                                                            15-DEC-1999;
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                                                                       06-JUL-2000
                                                                                                                                                                                                                         Gabbiani G,
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Sequence

Query Match

Matches

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Synthetic

Peptide

Key

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to novel peptide modulators of androgen receptor. The peptides of the invention are useful for treating androgen-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptide modulators of androgen receptor, useful for treating androgen-associated disorder, e.g. prostate cancer, particularly hormonally refractive prostate cancer, colon cancer, lung cancer, acne,
            cytostatic, antiproliferative and dermatological activities. Methods from the present invention can be used to treat PV-induced conditions including growth of PV preneoplastic and neoplastic lesions, cutaneous lesions chosen from warts and other benign cutaneous lesions, plantar warts (verruca plantaris), common warts (verruca plans), Butcher's common warts, flat warts, ganital warts (condyloma acuminatum) and epidermodysplasia verruciformis, laryngeal, oral, pharyngeal, oesophageal and other upper airway papilloma or vaginal, cervical, vulvar, penile and anorectal carcinoma. The E2 inhibitors may also be used to treat epithelial and internal fibropapillomas in animals. The present bequence represents a peptide sequence used in the exemplification of the present invention.
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 virucide,
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                                                                                                                                                                                                                                                                          Score 97; DB 21; Length 34; Pred. No. 4.5e-06; 3; Mismatches 5; Indels
(A) has antiviral,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Androgen receptor binding peptide #87.
mammal with a PV-induced condition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oza VB,
                                                                                                                                                                                                                                                                       Match 59.9%;
Local Similarity 64.3%;
es 18; Conservative 3
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28-JAN-2002; 2002US-352399P.
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                                                                                                                                                                                                                                        34 AA;
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                                                                                                                                                                                                                                          Sequence
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associated disorders such as prostate cancer, particularly hormonally refractive prostate cancer, colon cancer, lung cancer, benign prostatic hypertrophy, acne, hirsutism, male pattern baldness, Stein-Leventhal syndrome, androgen insensitivity syndrome, infertility, endometrial cancer and X-linked spinal bulbar muscular atrophy. The present sequence is an androgen receptor binding peptide.
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                                                                                                                                                                                   59.3%; Score 96; DB 24; Length 26; 77.3%; Pred. No. 4.6e-06; ive 2; Mismatches 3; Indels
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Job time : 107.289 secs
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US-09-643-260-18

OM protein - protein search, using sw model

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      ; Search time 32.9737 Seconds (without alignments) 35.929 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Total number of hits satisfying chosen parameters: 162 1 DRQIKIWFQNRRMKWKKTALDWSWLQTE 328717 segs, 42310858 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries BLOSUM62 Gapop 10.0 , Gapext 0.5 Issued_Patents_AA:* Minimum DB seq length: 0 Maximum DB seq length: 200000000 Perfect score: Scoring table: Sequence: Searched: Databaве

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 79, Appl Sequence 34, Appl Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli Sequence 50, Appli Sequence 51, Appli Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 1, Appli Sequence 9, Appli Sequence 1, Appli Sequence 33, Appli Sequence 33, Appli Sequence 33, Appli Sequence 33, Appli Sequence 33, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli
SUMMARIES	US-09-347-504-79 US-09-419-826-34 US-09-419-826-34 US-08-702-044-3 US-08-751-344B-6 US-08-751-344B-6 US-08-751-344B-6 US-08-751-344B-6 US-09-051-334-51 US-09-051-334-51 US-09-051-934-51 US-08-751-344B-6 US-09-051-934-51 US-08-751-344B-6 US-08-751-344B-6 US-08-751-344B-6 US-08-910-540-3 US-08-910-540-3 US-08-910-540-3 US-08-910-540-3 US-08-910-540-3 US-08-910-540-3 US-08-910-540-3 US-09-10-296-099-33 US-09-10-296-099-33
88	
Length	22222222222222222222222222222222222222
% Query Match	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0
Score	
Result No.	

RESULT 1 US-09-347-504-79 Sequence 79, Application US/09347504 Patent No. 6399075 GENERAL INPORMATION: APPLICANT: Howley, Peter M. APPLICANT: Benson, John APPLICANT: Benson, John TITLE OF INVENTION: PAPLILCANT TITLE OF INVENTION: PAPLILCANT TITLE OF INVENTION: PAPLILCANT TITLE OF SECTION WUMBER: US/09/347,504 CURRENT FILING DATE: 1999-07-02 SOFTWARKE: PatentIN Ver. 2.1 SEQ ID NO 79 SEQ ID NO 79 LENGTH: RT TYPE: PRT CORGANISM: Homo sapiens US-09-347-504-79	Query Match 59.9%; Score 97; DB 4; Length 34; Best Local Similarity 64.3%; Pred. No. 1.9e-06; Matches 18; Conservative 3; Mismatches 5; Indels 2; Gaps Matches 1 DRQIKIWFQNRRWKKTALDWSWLQTE 28	TITLE OF INVERTION: MEDILIARE READABLE FORM: MEDILIARE READABLE FORM: MEDILIARE READABLE FORM: MEDILIARE READABLE FORM: MEDILIARE: M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Arpin, Monique
APPLICANT: Crepaldi, Tiziana
APPLICANT: Crepaldi, Tiziana
APPLICANT: Gutreau, Alexis
APPLICANT: Gutvard, Daniel
TITLE OF INVENTION: on tyrosine 353
TITLE OF INVENTION: on tyrosine 353
FILE REPERENCE: 391082000100
CURRENT APPLICATION NUMBER: US/09/040,725A
NUMBER OF SEQ ID MATE: 1998-03-18
SOFTWARE: PatentIn Ver. 2.1
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OTHER INFORMATION: Xaa = tyrosine or a phosphorylated tyrosine
                                                                                                                                                                                                                                                                                                                      Query Match 58.6%; Score 95; DB 4; Length 24; Best Local Similarity 85.0%; Pred. No. 2.4e-06; Matches 17; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.0%; Score 94; DB 4; Length 27;
89.5%; Pred. No. 3.6e-06;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                              ; LOCATION: 19
; OTHER INFORMATION: /note= "X = Phosphotysine"
US-09-419-826-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09040725A
Patent No. 6399584
GENERAL INFORMATION:
APPLICANT: Institut Curie
APPLICANT: CNRS
                                                                                                                                                                                                                                                                                                                                                                                                              2 RQIKIWFQNRRMKWKKTALD 21
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Patent No. 5858973
GENERAL INFORMATION:
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                FILING DATE: 14-APR-1997
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                        NAME/KEY: Modified-site
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Matches 17; Conservative
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                           TOPOLOGY: linear
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LENGTH: 27
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APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
UNDER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/75,344B
FILING DATE: 19-NO. 6210960-1996
PRIOR APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT IRPORMATION:
NAME: Williams Ph.D., Kathleen M.
REFERENCE/DOCKET NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELECOMMUNICATION INFORMATION:
                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202.044
FILING NAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 94.1%; Pred. No. 8.4e-06;
Matches 16; Conservative 1; Mismatches 0;
                                                                                                                                                                                    APPLICALL...
FILING DATE: 23-FEB-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAMME: Williams Ph.D., Kathleen A.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 34,380
REFERENCE/OKCKET NUMBER: 34,380
TELEPHONE: (617) 542-2290
TELEPHONE: (617) 542-2290
TELEFAX: (617) 542-2290
TELEFAX: (617) 542-0313
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                  23-FEB-1994
78: 800
78: 800
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US-08-751-344B-3
; Sequence 3, Application US/08751344B
; Patent No. 6210960
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CITY: Boston
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COUNTRY: US
ZIP: 02109
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Sequence 9, Application US/08751344B
Patent No. 6210960
GENERAL INFORMATION:
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                43 ERQİKİWEQNRRMKWKK 59
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Best Local Similarity 94.19
warches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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Fatent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STREET: One Financial Center
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 94.1%; Pred. No. 8.4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                         Length 61;
                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96,137-A (11274/02148)
                                                                                                                                                                                                                         Score 94; DB 3; 1
Pred. No. 8.4e-06;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: FLORDY disk
COMPUTER: ELODPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/202,044
FILING DATE: 19-NO. 6210960-1996
PRIOR APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 96,137-A (11)
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                  1 DRQIKIWFQNRRMKWKK 17
(617) 345-9100
            TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (617) 345-9100
                                                                                                                                                                                                                         Query Match
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                       ; MOLECULE TYPE: peptide; HYPOTHETICAL: NO; ANTI-SENSE: NO; FRAGMENT TYPE: internal US-08-751-3448-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 61 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
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TELEPHONE:
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Sequence 50, Application US/09057363C
Sequence 50, Application US/09057363C
Patent No. 6551994
GENERAL INFORMATION: Batchuk, Orest W.
GOUT, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE
INTERACTION BETWEEN ALPHA-CATENIN AND BETA-CATENIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.0%; Score 94; DB 3; Length 61; 94.1%; Pred. No. 8.4e-06;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
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COMPUTER IN PC COMPACIBLE
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COMPUTER IN PC COMPACIBLE
COMPACING SYSTEM: PC-DOS/MS-DOS
SOFTWARE WORDMER: US/08/751,344B
FILING DATE: 19-No. 6210960-1996
FILING DATE: 19-No. 6210960-1996
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELEFONE: (617) 345-9110
TELEFONE: (617) 345-9111
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 anning acids
TWOTH: 61 anning acids
TWOTH: 61 anning acids
TWOTH: 61 anning acids
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Application US/09051934C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Van der Geer
TITLE OF INVENTION: Peptide Inhibitors of a Phosphotyrosine-Binding Domain
TITLE OF INVENTION: Containing Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 57.4%; Score 93; DB 4; Length 22; Best Local Similarity 94.1%; Pred. No. 3.9e-06; Matches 16; Conservative 1; Mismatches 0; Indels
                                       ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                   NAME: Christiansen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 100086.406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFRAX: (206) 682-6031
                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION UNMERS: US/09/057,363C
FILING DATE: 08-Ap--1998
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/051,934C
CURRENT PILING DATE: 1998-04-22
EARLIER APPLICATION NUMBER: 60/011,799
EARLIER PILING DATE: 1996-02-20
EARLIER APPLICATION NUMBER: 60/010,384
EARLIER FILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 60/005,944
EARLIER FILING DATE: 1995-10-27
NUMBER: OF SEQ ID NOS: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: phosphotyrosine binding domain US-09-051-934-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 51, Application US/09051934C Patent No. 6028053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RQIKIWFQNRRMKWKKTALD 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DRQIKIWFQNRRMKWKK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 NRQIKIWFQNRRMKWKK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-057-363C-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 51
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
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RESULT 10 US-09-051-934-52

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Patent No. 6028653
GENERAL INFORMATION:
APPLICANT: Van der Geer
TITLE OF INVENTION: Peptide Inhibitors of a Phosphotyrosine-Binding Domain
TITLE OF INVENTION: Containing Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Habener M.D., Joel F.

APPLICANT: Hiller Ph.D., Christopher P.

TITLE OF INVENTION: NOVEL TRANSCRIPTION PACTOR AND USES

TITLE OF INVENTION: THEREFOR

NUMBER OF SUCHENCES: 29

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96,137-A (11274/02148)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3;
                                                                                                             CURRENT APPLICATION NUMBER: US/09/051,934C
CURRENT FILING DATE: 1998-04-22
EARLIER PEDILGATION NUMBER: 60/011,799
EARLIER PILING DATE: 1996-02-20
EARLIER APPLICATION NUMBER: 60/010,384
EARLIER PILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 60/005,944
EARLIER FILING DATE: 1995-10-27
NUMBER: OF SEQ ID NOS: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 57.4%; Score 93; DB Best Local Similarity 80.0%; Pred. No. 4.9e Matches 16; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-No. 6210960-1996
PRIOR APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , LOCATION: (24)
, OTHER INFORMATION: Phosphorylated at Tyr
US-09-051-934-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: phosphotyrosine binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: One Financial Center STATE: MA
STATE: MA
COUNTY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Williams Ph.D., Kathleen M. REGISTRATION NUMBER: 34,380 REFERENCE/DOCKET NUMBER: 96,137-A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08751344B Patent No. 6210960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ROIKIWFONRRMKWKKTALD 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ROIKIWFONRRMKWKKHIIE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (617) 345-9100
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 52
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617) 345-9111
FORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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61 amino acide

LENGTH:

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Sequence 6, Application US/08810540

Patent No. 5929042

GENERAL INFORMATION:

APPLICANT: Troy, Carol M.

TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL

TITLE OF INVENTION: DEATH AND USES THEREOF

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham, LLP
                                                                                                                                APPLICANT: Troy, Carol M.
APPLICANT: Troy, Carol M.
APPLICANT: Shelanski, Michael L.
TITLE OF INVENTION: DEATH AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,540
FILING DATE: 03-MAR-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51247
TELECOMMUTCATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.8%; Score 92; DB 2; L
100.0%; Pred. No. 3.8e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                   ; Sequence 3, Application US/08810540; Patent No. 5929042; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 RQIKIWFQNRRMKWKK 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-810-540-6
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-810-540-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NADLER, STEVEN G.
APPLICANT: NADLER, STEVEN G.
APPLICANT: CLEAVELAND, JEFFREY S.
APPLICANT: BLAKE, JAMES
APPLICANT: HAFFAR, OWAR K.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
CORRESPONDENCE ADDRESS: 24
CORRESPONDENCE ADDRESS: 24
CORRESPONDENCE ADDRESS: 24
CORRESPONDENCE ADDRESS: 24
COTTY: MENLO PARK
STATE: CA
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                                                                                                                                                                                    Length 61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: EC-LUSS/MS-LUSS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,958
FILING DATE: 12-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026978
FILING DATE: 20-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
RAGISTRATION NUMBER: 5998-0019
FILECOMMUNICATION NUMBER: 5998-0019
TELECOMMUNICATION NUMBER: 5998-0019
TELECOMMUNICATION INFORMATION:
TELEPAX: (650) 325-7812
TELEPAX: (650) 325-7812
TELEPAX: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 92; DB 2; Ler
Pred. No. 3.8e-06;
                                                                                                                                                                             Query Match 57.4%; Score 93; DB 3; 18est Local Similarity 88.2%; Pred. No. 1.1e-05; Matches 15; Conservative 2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08928958
Patent No. 5877282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pi
Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                 1 DRQIKIWFONRRMKWKK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ROIKIWFONRRMKWKK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                             FRAGMENT TYPE: internal
                                   MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                         unknown
  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: Bi
                                                                                        õ
                                                               HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                US-08-751-344B-7
TYPE: am.
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-928-958-7
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Length 16;

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Sequence 7, Application US/09072429
Sequence 7, Application US/09072429
Patent No. 5962415
GENERAL INFORMATION:
APPLICANT: Nadler, Steven G.
TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE
TITLE OF INVENTION: INHIBITOR OF NUCLEAR PROTEIN TRANSLOCATION AND TITLE OF INVENTION: INMUNOSUPPRESSANT AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Bristol-Myers Squibb Company
STREET: P.O. Box 4000
CITY: Princeton
CITY: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,540
FILING DATE: 03-MAR-1997
CLASSIFICATION: 514
ATTONNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 0575/51247
TELECOMMUNICATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURSITENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,429
FILING DATE: 04-MAY-1998
CLASSIFICATION: S14
ATTORNEY/AGENT INFORMATION:
NAME: Klein, Christopher A.
REGISTRATION NUMBER: 34,363
REFERENCE/DOCKET NUMBER: ON0141b
TELLEPHONE: (609) 252-3714
                                                                                                                                                                                                                                                                     TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RQIKIWFQNRRMKWKK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 RQIKIWFQNRRMKWKK 17
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide US-09-072-429-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-810-540-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-09-072-429-7
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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.	Title: US-09-643-260-17 Perfect score: 41 Sequence: 1 LDWEWL 6	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 1107863 seqs, 158726573 residues	Total number of hits satisfying chosen parameters: 1107863	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	A_Geneseq_19Jun03:* SiDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:* SiDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:* SiDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:* SiDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:* SiDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:* SiDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:* SiDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:* SiDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:* SiDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:* SiDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:* SiDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:* SiDS1/gcgdata/geneseq/geneseqp-emb
	Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds (without alignments) 41.814 Million cell updates/sec	: February 18, 2004, 13:37:19 ; Search time 22.77	: February 18, 2004, 13:37:19; Search time 22.77 (without alignments) 41.814 Million cell US-09-643-260-17 ce: 1 LDWEWL 6 g table: BLOSUM62 Gapop 10.0, Gapext 0.5	February 18, 2004, 13:37:19; Search time 22.77 (without alignments)	February 18, 2004, 13:37:19; Search time 22.77 (without alignments)	February 18, 2004, 13:37:19; Search time 22.77 (without alignments)	February 18, 2004, 13:37:19; Search time 22.77 (without alignments) 10S-09-643-260-17 ce: 1 LDWEWL 6 g table: BLOSUM62 Gapop 10.0 , Gapext 0.5 dapop 10.0 , Gapext 0.5 mubber of hits satisfying chosen parameters: 1107863 m DB seq length: 0 m DB seq length: 2000000000 m DB seq length: 20000000000 m DB seq length: 20000000000 m DB seq length: 20000000000 m DB seq length: 2000000000000000000000000000000000000
OM protein - protein search, using sw model		t score: ce:	US-09-643-260-17 ce: 1 LDWEWL 6 g table: BLOSUM62 Gapop 10.0 , Gapext 0.	US-09-643-260-17 t score: 41 ce: 1 LDWEWL 6 g table: BLOSUM62 Gapop 10.0 , Gapext 0.5 ed: 1107863 seq8, 158726573	US-09-643-260-17 ce: 1 LDWEWL 6 g table: BLOSUM62 ed: 1107863 segs, 158726573 residues number of hits satisfying chosen parameters:	US-09-643-260-17 t score: 41 ce: 1 LDWEWL 6 g table: BLOSUM62 ed: 1107863 seqs, 158726573 residues number of hits satisfying chosen parameters: m DB seq length: 0 m DB seq length: 2000000000	US-09-643-260-17 t score: 41 Ce: 1 LDWEWL 6 g table: BLOSUM62 ed: 1107863 seqs, 158726573 residues number of hits satisfying chosen parameters: m DB seq length: 0 m DB seq length: 0 m DB seq length: 2000000000 rocessing: Minimum Match 0% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		Mutated IXXbeta NE	NBD mutant peptide	Anti-inflammatory	Anti-inflammatory	Human NEMO binding	Anti-inflammatory	Anti-inflammatory	Anti-inflammatory	Anti-inflammatory
SUMMAKIES			ID		ABB08739	AAM48522	AAM48542	AAM48614	ABU08432	AAM48618	AAM48611	AAM48619	AAM48610
			80	-	23	23	23	23	24	23	23	23	23
			e Match Length DB I		9	9	9	9	9	7	80	80	6
	de	Query	Match	1	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
			Score		41	41	41	41	41	41	41	41	41
		Result	No.		-	7	m	4	S	ø	7	æ	6

	Human peptide enco Schizosaccharomyce Benzodiazepines bi Hutative P. abyssi Witative P. abyssi Putative P. abyssi Micromonospora eve Drosophila melanog IKKDeta NEMO bindi Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory IKK-alpha polypept Anti-inflammatory Anti-inflammatory IKK-alpha polypept Anti-inflammatory	#LIGNMENTS #LIGNMENTS #ABB08739 standard; peptide; 6 AA. #ABB08739; 14-JUN-2002 (first entry) Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 17. IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB; kinase activation; lenkocyte; inflammation; Belectin; osteoporosis; cancer; autoimmune disease; transplant rejection; asthma; anaphylaxis; psoriasis; rheumatorid arthritis; crohn's disease; multiple sclerosis; munosuppression; antinflammatory; immunosuppression; antinflammatory; immunosuppression; antinflammatory; immunosuppression; antiatreriosclerotic; virucide; antiathmatic; antiallergic; dermatological; antibacterial; antibacterial; antibacterial; antibacterial; antialcer; mutant; mutein. Homo sapiens. Key iccation/Qualifiers Misc-difference 4 //note= "Wildtype Ser substituted by Glu" WO200183547-A2.
AAM4861 AAM4861 AAM4861 AAM4861 AAM4861 AAM4860 AAM5705 AAM5746 AAM6748	ABG3 7095 ABA2 3 765 ABA2 3 745 AAB9 6114 AAB9 6410 AAB0 68725 AAB0 852 AAM4 8535 AAM4 8533	tide; 6 AA. tide; 6 AA. inding domain p inding dowling kocyte; inflamm ansplant reject tral; inflamm anspression; an crontroid; antia trerial; antips trerial; antips thic; antiulcer "Wildtype Ser
555555555555555555555555555555555555555	202222222222222222222222222222222222222	de; 6 ding c ding c object splant splant splant splant spress rucide erial; ic; ar
243 243 260 270 270 270 270	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	ALIG rd, peptide; 6 AA. Irst entry) NEMO binding domain a; NEMO; NEMO bindi nn; leukocyte; infla ase; transplant reje ase; transplant reje ase; transplant reje ase; transplant reje ase; transplant reje ase; transplant reje ase; transplant reje antionoursuppression; costatic; noctropic; antibacterial; anti antibacterial; antiulc antibacterial; antiulc antibacterial; antiulc becopathic; antiulc Afroce "Wildtype Se /note = "Wildtype Se
		(first (first eta NEM alpha; acion; isease; disease rthriti id; imm clyroti al; ant clyroti al; ant clyroti clyroti al; ant
	00000000000000000000000000000000000000	standard;); (1002 (firs IKKalpha; ictivation; ine disease ir's disease ir's disease ir's disease ir's disease ir's disease ir's disease ir's disease ir's disease ir's disease ir's disease iriosclerot ogical; an iritic; ost iritic; ost iritic; ost iritic; ost iritic; ost iritic; ost iritic; ost iritic; ost iritic; ost iritic; ost iritic; ost iritic; ost iritic; ost
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100 00 00 00 00 00 00 00 00 00 00 00 00	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	RESULT AND SERVICE

antiasthmatic; cytostatic; antipsoriatic; nootropic;

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antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Page 48; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                          02-MAY-2001; 2001WO-US14346.
                                                                                                                                                                                                                                                                                                                                                                                                                       22-AUG-2000; 2000US-0643260.
                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-2000; 2000US-201261P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PRAE-) PRAECIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-121889/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                          WO200183554-A2.
                                                                                                                                                                                                                                                                                                                 08-NOV-2001.
                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               May MJ,
    The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB08725) comprising at least one NEWO binding domain (ABB77313). The compound has acts through selective inhibition of (ABB08725) comprising the acts through selective inhibition of twick at the NEWO binding domain. Blocking the interaction of NEWO interaction results in inhibition of IKAGpa Kinase activation and subsequent decreased phosphorylation of IKAGpa Kinase activation and subsequent decreased phosphorylation of IKAGpa Kinase activation and subsequent decreased phosphorylation of IKAGpaB. The compound may also act (directly or indirectly) by blocking the recruitment of leukocytes into sites of acute and chronic inflammation, by down-regulating the expression of E-selectin on leukocytes or by blocking osceoclast differentiation. The compound is useful in treating NF-kB mediated conditions, where the condition is an inflammatory disorder and conditions, where the condition is an inflammatory disorder is asthma, allergies, urticaria, anaphylaxis, cutaneous inflammatory disorder is asthma, allergies, urticaria, anaphylaxis, cutaneous inflammation, seppis, psoriasis, chemacoid arthritis, osteoarthritis, psoriatic arthritis, lupus and bursitis. The inflammatory disorder may also be dermatitis, cromany associatic arthritis, lupus and spondylarthritis. Also for Crohu's giraniomary disease, ulcerative colitis, polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis, suppolylarianis, or multiple sclerosis. For chronic viral infections croyoglobulinaemia or multiple sclerosis. For chronic viral infections croyoglobulinaemia or multiple sclerosis. For chronic viral infections crosused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral and food sensitivity, contact dermatitis, and application in which corticosteroids are used, included in multiple and contact persections and influence. The infection or active and persection or repease include HIV and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiinflammatory compounds and for diagnosis of an inflammatory disorder. The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of a mutated NEWO binding domain of IKKOeta.
                                                                                                                                                                                                                          Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting a cell with an anti-inflammatory compound comprising at least one NEMO
                                                                                                                                                                                                                                                                                                                                    Claim 23; Page 45; 82pp; English.
                                      02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
02-MAY-2001; 2001WO-US40654
                                                                                                                                                                                        WPI; 2002-179350/23
                                                                                                   (UYYA ) UNIV YALE.
                                                                                                                                              Ghosh S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 AA;
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                                                                                                                                            May MJ,
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Phillips K;

Findeis MA,

Ghosh S,

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(AAM48620-AAM4864). To AAM48864-AAM48651) WALCH COUNTERED LICH.

(AAM48525-AAM48619). The antinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, contropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFKappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta kinase activation by blocking interaction of IkappaB kinase beta (IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammatory bowel disease, sepsis, vasculitis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, arangimenters disease, atherosclerosis, viral infections; and ataxia telangiectasia. The compounds are also useful for treating paphilay.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pro-inflammatory responses such as allergies, urticaria, anaphylldrug or food sensitivity, eczema, dermatitis, sunburn, aging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 41; DB 23;
100.0%; Pred. No. 9.3e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
AAM48542
ID AAM48542 standard, Peptide, 6 AA.
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Best Local Similarity
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9 1 LDWEWL RESULT 2 ò

100.0%; Score 41; DB 23; Length 6; 100.0%; Pred. No. 9.3e+05; ive 0; Mismatches 0; Indels

6; Conservative

Query Match Best Local Similarity

Best Loc Matches

20-MAR-2002 (first entry) AAM48522;

AAM48522 standard; Peptide; 6 AA.

AAM48522

NBD mutant peptide SEQ ID NO 17.

Anti-inflammatory peptide SEQ ID NO 117.

(first entry)

20-MAR-2002

AAM48614;

AAM48614 standard; Peptide; 6 AA.

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WO200183554-A2.
                   08-NOV-2001
               Synthetic.
                                                           arthritis.
 AAM48542;
                             May MJ,
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AAM48614
ID AAM
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(AAM48620-AAM48645), comprising a membrane translocation domain

(AAM48620-AAM48645), comprising a membrane translocation domain

(AAM48620-AAM48619). The antiinflammatory compounds have antiathmatic, antipactatic, antipactatic, antiinflammatory compounds have antiathmatic, antipactatic,                                                                                                                                                                                                                                                Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; derivatedogical; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEWO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autolmmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to an antiinflammatory compound (especially
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                                                                                                                           Anti-inflammatory peptide SEQ ID NO 45.
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22-AUG-2000; 2000US-0643260.
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20-MAR-2002 (first entry)
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The invention relates to an antiinflammatory compound (especially AMM48629-AMM48645), comprising a membrane translocation domain (AAM48620-AMM4862), comprising a membrane translocation domain characteristic and residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antisathmatic, orticatatic, antipacontatic, antiheumatic, antiathriac, osteopathic, corpounds act as selective inhibitors of cytokine-mediated NFRappas compounds act as selective inhibitors of cytokine-mediated NFRappas compounds act as selective inhibitors of cytokine-mediated NFRappas cortivation by blocking interaction of Ikappas kinase beta (IKKbeta kinase cutivation by blocking interaction of Ikappas kinase beta (IKKbeta kinase cutivation by blocking interaction of Ikappas kinase beta (IKKbeta kinase compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteopacenthatitis, inflammatory bowel disease, sepsie, vasculitis, costeopacentis, costeopacenthatics, antiple sclerosis; transplant rejection; osteoporosis; caranulomatosis, multiple sclerosis; transplant rejection; osteoporosis; callammatory responses such as lupus, polymyalgia, scleroderma, callammatory responses such as allergies, urticaria, anaphylaxis, arthritis; arthritis; anticallammatory responses such as allergies, urticaria, anaphylaxis, arthritis; arthritis; anticallammatory responses such as allergies, urticaria, anaphylaxis, arthritis; arthritis; anticallammatory responses such as allergies, urticaria, anaphylaxis, arthritis; arthritis; anticallammatory responses such as allergies, urticaria, anaphylaxis, arthritis; arthritis; anticallammatory dermatiiis, and ataxia arthritis; arthritis; anticallammatory dermatiiis, and ataxia arthritis; arthritis; and ataxia and ataxia arthritis; arthritis; and ataxia and ataxia arthritis; arthritis; and ataxia and ataxia arthritis; arthritis; and ataxia and ataxia arthritis; arthritis; and ataxia and ataxia arthritis; arthri
                                                                                                                                                                                     Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; antirheumatic; antiarthricis; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neurological; neurocatic, membrane translocation domain; NEWO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Findeis MA, Phillips K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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Gaps

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100.0%; Score 41; DB 23; Length 6; llarity 100.0%; Pred. No. 9.3e+05; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 6; Conserv

6 AA;

LDWEWL 6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta; IkappaB kinase-alpha; IKKalpha; NF-kappaB; nuclear factor-kappaB kinase-alpha; IKKalpha; NF-kappaB; nuclear factor-kappaB induction; inflammatory disorder; atheroscierosis; osteoporosis; cancer; Alzheimer's disease; atherosclerosis; viral infection; Ataxia telangiectasia; transplantation detection; immunosuppressive, osteopathic; cytostatic; nootropic; neuroprotective; antiatherosclerotic; virucide; vasotropic; antirheumatic; antiatheritic; mutant; mutein.
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                                                                   ö
   Length 6;
                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human NEMO binding site (NBD) mutant peptide #15.
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   Score 41; DB 23;
Pred. No. 9.3e+05;
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   100.0%;
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22-AUG-2000; 2000US-0643260.
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Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                1 LDWEWL 6
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GHOSH S.
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100.0%; Score 41; DB 24; Length 6;

Query Match

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AMM48628-AAM48645), comprising a membrane translocation domain (APM48620-AMM48645), comprising a membrane translocation domain (AAM48620-AMM48645), comprising a membrane translocation domain amino acid residues, fused to a NEWO binding sequence and of AAM48620-AAM48650). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antitheumatic, antiarthritic, osteopathic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEWO binding domain that results in inhibition of IKRbeta kinase activation and subsequent decreased phosphorylation of IKRpeBB. The compounds are useful for treating inflammatory disorders, e.g. asthma, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, creating inflections; and ataxia telangiectasia. The compounds are also useful for treating the treating infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
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                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation.
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                                 Indels
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              Pred. No. 9.3e+05; 
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                      Anti-inflammatory peptide SEQ ID NO 121
100.08; Pr
                                                                                                                                                                                                                 AAM48618 standard; Peptide; 7 AA.
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                                   6; Conservative
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AAM48618
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20-MAR-2002
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                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AM48651), comprising a membrane translocation domain (AAM48620-AM48621) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiaethmatic, cytostatic, antipsoriatic, antiinflammatory compounds have antiaethmatic, antibacterial, immunosuppressive, dermatological, neuroprotective, anotropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFKAAppaB activation by blocking interaction of IkAppaB kinase beta (IKAbeta) at the NEWO binding domain that results in inhibition of IKAbeta kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis,
                                                                                         Gaps
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drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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                                                              100.0%; Score 41; DB 23; Length 7; 100.0%; Pred. No. 9.3e+05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                      Anti-inflammatory peptide SEQ ID NO 114.
                                                                                                                                                                                                           AAM48611 standard; Peptide; 8 AA.
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22-AUG-2000; 2000US-0643260.
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                                      7 AA;
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             arthritis.
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                                   bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granullomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosels; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis.
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inflammatory bowel disease, sepsis, vasculitis,
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                                                                                                                                                                                                                                                                                                                                              8 AA;
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compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEWO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IKKbeta kinase compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatory disorders, e.g. asthma, osteoarhritis, inflammatory bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, pranulomatosis, multiple sclerosis; transplant rejection; osteoporosis, granulomatosis, multiple sclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-inflammatory peptide SEQ ID NO 113.
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Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKWbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple soletosis; transplant rejection; osteoprosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                          amino acid residues, fused to a NEWO binding sequence (AAW48525-AAW48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antiinflammatory compounds have antiasthmatic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEWO binding domain that results in inhibition of IKKbeta kinase
                                                                                                                                                                                                                                                                                                             activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammatchion or cancer, psoriasis, rheumatchid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease, atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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                                                                AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AWM48627 or AAM48646-AAM48651) which comprises from 6-15
                                                     invention relates to an antiinflammatory compound (especially
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                          Claim 6; Page 62; 88pp; English.
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22-AUG-2000; 2000US-0643260.
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CAMAMABASS-AAMABG19). The antinflammatory compounds have antiasthmatic, cytostatic, antipoentatic, antihemmatory compounds have antiasthmatic, cytostatic, antipoentatic, antihemmatory compounds have antiasthmatic, antiboentatic, antihemmatory dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NikappaB compounds act as selective inhibitors of cytokine-mediated NikappaB compounds are useful for treating inflammatory disorders, e.g. asthma, compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation of IkappaB. The activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, burstitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, coranulomatosis, multiple sclerosis, transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis, viral infections, and ataxia telangiectasia. The compounds are also useful for treating
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Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 41; DB 23;
100.0%; Pred. No. 9.3e+05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                        Claim 6; Page 62; 88pp; English.
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Best Local Similarity
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Findeis MA, Phillips K;

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anino acid residues, fused to a NEMO binding sequence
(AAM4825-AAM48619). The antiinflammatory compounds have antiasthmatic,
cytostatic, antipostiatic, antirheumatory compounds have antiasthmatic,
antibacterial, immunosupressive, dermatological, neuroprotective,
compounds act as selective inhibitors of cytokine-mediated NFkappaB
compounds act as selective inhibitors of cytokine-mediated NFkappaB
activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
the NEMO binding domain that results in inhibition of IKKbeta kinase
activation and subsequent decreased phosphorylation of IKKappaB. The
compounds are useful for treating inflammatory disorders, e.g. asthma,
lung inflammation or cancer, psoriasis, rheumatoid arthritis,
compounds are useful for treating inflammatory disorders, e.g. asthma,
lung inflammation diseases such as lupus, polymyalgia, scleroderma,
bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
cranulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
Alzheiner's disease, atherosoflerosis; viral infections; and ataxia
telangiectasia. The compounds are also useful for treating
pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
arthritis, anticultivity, eczema, dermatitis, sunburn, aging and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 62; 88pp; English.
                                                                                                                                             02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
                                                                                       02-MAY-2001; 2001WO-US14346.
                                                                                                                                                                                                                                 (PRAE-) PRAECIS PHARM INC. (UYYA ) UNIV YALE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 AA;
                                 08-NOV-2001.
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                                                                                                                                                                                                                                                                                                                           May MJ,
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AAM48615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Inventor relates to an autonometry Compound of AMM48620-AMM48645), comprising a membrane translocation domain (AMM48620-AMM48645), comprising a membrane translocation domain (AMM48620-AMM48627) or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatcry compounds have antiasthmatic, ortostatic, antiathrematic, antiathrematic, antiathrematic, antiathrematic, ortospic, antiathrematic, virtude and antiallergic cactivity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKAppaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoprosis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis, transplant rejection; osteoporosis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; chung inflammatory responses such as lupus, polymyalgia, scleroderma, prelangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, arthritis, includent of screems, dermatitis, sunburn, aging and
                                                                                                                                                                                                                                                                                          domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
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                                                                                                                                                                                                                                                               Novel antiinflammatory compound comprising membrane translocation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to an antiinflammatory compound (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,
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                                                                                                                                                Ghosh S, Findeis MA, Phillips K;
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                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 62; 88pp; English.
22-AUG-2000; 2000US-0643260.
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                                                            (PRAE-) PRAECIS PHARM INC.
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Best Local Similarity luv...
6; Conservative
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                                                                                    (UYYA)
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                                                                                                                                                                                                                                                                                                                                                                        Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
                                        Gaps
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100.0%; Score 41; DB 23; Length 10; 100.0%; Pred. No. 4.4;
                                0; Indels
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                                                                                                                                                                                                                 AAM48615 standard; Peptide; 10 AA.
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                                        6; Conservative
                      Local Similarity
                                                                               1 LDWEWL 6
                                                                                                                    LDWEWL
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Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEWO binding domain; eczema; cytokine; NPkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.

RESULT 13 AAM48612

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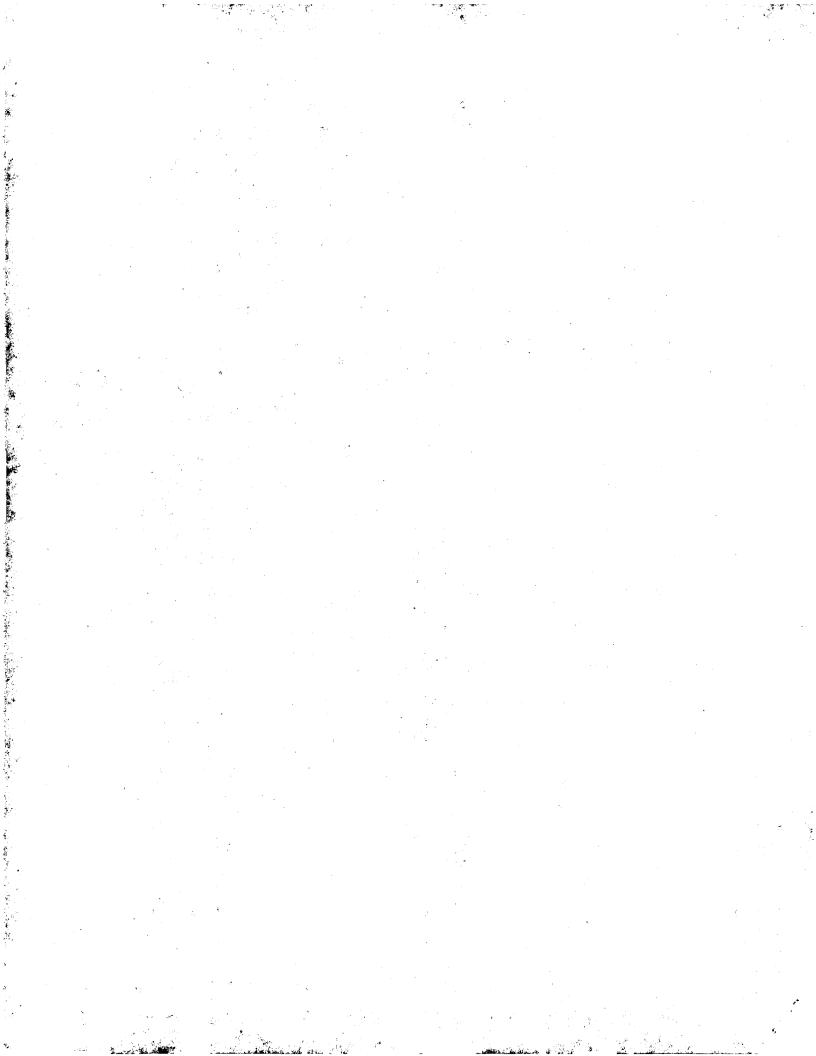
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antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
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                                                                                                                                                                                                                                                                                                                                                           The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48625), comprising a membrane translocation domain (AAM48620-AAM48625) which comprises from 6-15 mino acid residues, fused to a NEWO binding sequence (AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, notropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKOpeta kinase activation and subsequent decreased phosphorylation of IkAOpeta kinase activation and subsequent decreased phosphorylation of IkAOpeta kinase activation or cancer, psoriasis, rheumatoid arthritis, ung inflammatory discorders, e.g. asthma, ung inflammatorial inflammatory discorders, e.g. asthma, contominated diseases such as lugus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis, transplant rejection; osteoporosis; chalmagiscreasia. The compounds are also useful for treating and ataxia continuation.
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drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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                                                                                                                                                                                                                                                                                     domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
 osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                         Novel antiinflammatory compound comprising membrane translocation
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                                                                                                                                                                                                                       Phillips K;
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                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 62; 88pp; English.
                                                                                                                                                                                                                       Ghosh S, Findeis MA,
                                                                                                                 02-MAY-2001; 2001WO-US14346.
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22-AUG-2000; 2000US-0643260.
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Best Local Similarity
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                                                               WO200183554-A2.
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                                       Synthetic.
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The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM4862), comprising a membrane translocation domain (AAM48620-AAM48619). The AAM48661 which comprises from 6-15 anino acid residues, fused to a NEMO binding sequence (AAM48519). The antiinflammatory compounds have antiasthmatic, cytostatic, antipscriatio, antiheumatic, antiarthrile, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFKappaB compounds act as selective inhibitors of cytokine-mediated NFKappaB compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psorfiasis, rheumatoid arthritis, compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammatonis, unflammatory bowel disease, sepsis, vasculitis, osteoparosis, unsitials, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; viral infections, and ataxia pro-inflammatory responses such as allevasis, urbating, anaphylaxis, crug or food sensitivity, eczema, dermatitis, sunburn, aging and
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immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antialtegic; membrane translocation domain; NEWO binding domain; eczema; cytokine; NFkappaB, IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple aclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
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Job time : 22.7763 secs
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Q96mel oryza sativ
Q90wes oncorhynchu
Q80wg9 oncorhynchu
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Q90wg15 oryzias lat
Q9bx70 pseudomonas
Q84304 lysobacter:
Q53756 mycobacter:
Q53756 mycobacter:
Q9xt14 pseudomonas
Q8vt24 pseudomonas
Q8vt24 pseudomonas
Q8vt28 acetobacter
Q92mu7 rhizobium m
Q8vuq6 pseudomonas
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Q8xvb4 ralatcnia s
Q91427 pseudomonas
Q91424 agrobacteri
Q8g3a8 brucella su
Q8yeh7 brucella me
Q97f0 caulobacter
Q92u27 rhizobium n
Q987z1 rhizobium n
Q9448 arabidopsis
Q9m0y4 arabidopsis
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STRAIN=NEM316 / Serotype III;
STRAIN=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot
Kunst F.;
"Genome sequence of Streptococcus agalactiae, a pathogen causing
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
Streptococcus.
MCBI_TaxID=216495;
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Hypothetical protein; Complete proteome.
SEQUENCE 173 AA; 20135 MW; FSF34044F0224CD1 CRC64;
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100.0%; Pred. No. 48;
iive 0; Mismatches 0;
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Q92MU7
Q8VUQ6
Q8ZC58
Q8XVB4
Q91427
Q8UB44
Q8G3A8
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Q9KER2
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Mol. Microbiol. 45:1499-1513(2002).
EMBL; AL766847; CAD46531.1; -.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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PubMed=11572479;
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Sulfolobus tokodaii
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                                                                                                                                                  STRAIN=2603 V/R / Serotype V;
MEDLINE=22222988; PubMed=12200547;
Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S., Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madfelt L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daudherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarealli M., Mora M., Rinaudo D., Rappuoli E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=IT1360;
MEDLINE=99402735; PubMed=10473401;
Fridjonsson O., Watzlawick H., Gehweiler A., Rohrhirsch T., Mattes R.;
"Cloning of the gene encoding a novel thermostable alpha-galactosidase from Thermus brockianus IT1360.";
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                     "Complete genome sequence and comparative genomic analysis of ar emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
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"The structure of the alpha-galactosidase gene loci in Thermus brockianus IT1360 and Thermus thermophilus TH125.";
Extremophiles 4:23-33(2000).
EMBL, AP138398, AAD3467.1; --
InterPro; IPR001554; Glyco hydro 14.
InterPro; IPR001554; Glyco hydro 14.
                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 40; DB 16; Length 173; 100.0%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                    Streptococcus agalactiae (serotype V).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                    Transferase, Complete proteome.
SEQUENCE 173 AA; 20135 MW; 0081677125975921 CRC64;
                                                  Last annotation update)
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Last annotation update)
                                      Last sequence update)
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  173 AA
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                          Created)
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           01-MAR-2003 (TrEMBLrel. 23, Cre
01-MAR-2003 (TrEMBLrel. 23, Last
01-MAR-2003 (TrEMBLrel. 23, Last
Acetyltransferase, GNAT family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
 PRELIMINARY;
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Best Local Similarity
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                                                                                                                           NCBI_TaxID=216466;
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                                                                                                                 Streptococcus.
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Putative anaerobic glycerol-3-phosphate dehydrogenase subunit C.
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                                                                                                          Length 645;
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DNA Res. 8:123-140(2001).
BMBL; AP000989; BAB67479:1; -.
InterPro; IPR004017; DUF224.
InterPro; IPR004017; DUF224.
Prim; PF02754; DUF224.
PROSITE; PS00198; AFE4S_FERREDOXIN; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 396 AA; 45359 MW; 15301A2AF22DDC9F CRC64;
                                                                100.0%; Score 40; DB 2; Length bw. 1.7e+02; Pred. No. 1.7e+02; Indels
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Pfam; PF01373; Glyco hydro 14; 1.
Pfam; PF02449; Glyco hydro 42; 1.
SEQUENCE 645 AA; 73420 WW; C79A9E1C0020EC40 CRC64;
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SEQUENCE FROM N.A.
Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;
                                                                                                                                                                                                                                                                                                                                                                                                         396 AA
                                                                                                                        100.0%; Prec. No.
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737 LDWSWL 742
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Q9QRU7
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Q9QRU6
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STRAIN-C57BL/6J; TISSUE-Urinary bladder;
STRAIN-C57BL/6J; TISSUE-Urinary bladder;
MEDLINE-22354683; PubMed=12466851;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
Malysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK035326; BAC29034.1;
SEQUENCE 745 AA; 84770 MW; 48C9E01C17A61184 CRC64;
         alpha, beta and gamma.";
L Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-1-SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; AJ414555; CAC93686.1; -..
R InterPro; IPR000219; Prot, kinase.
R InterPro; IPR000219; Ser_Thr_pkinase.
R ProDom; P000601; Prot_kinase; 1.
R PROSITE; S00010; Prot_Kinase; 1.
R PROSITE; PS00101; PROTEIN KINASE ATP; 1.
R PROSITE; PS001019; PROTEIN KINASE DOM; 1.
R PROSITE; PS001019; PROTEIN KINASE DOM; 1.
R PROSITE; PS00109; PROTEIN KINASE ST; 1.
W ATP-binding; Kinase; Seriac(threonine-protein kinase; Transferase.)
O SEQUENCE 740 AA; 84343 MW; 01903BE11F44D176 CRC64;
                                                                                                                                                                                                                           Gaps
"Identification and characterisation of the bovine IkB kinases (IKKs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;

Mammalia; Butheria, Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                  Length 740;
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83.3%; Pred. No. 5.6e+02;
tive 1; Mismatches 0; Indels
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Query Match
Beet Local Similarity 83.3%;
Berhan 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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"Pyrococcus abyssi genome sequence: insights into archaeal chromosome
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MEDLINE=98295987; PubMed=9634230;
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Best Local Similarity 66.7%;
Matches 4; Conservative
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                                                       STRAIN=GE5 / Orsay;
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141 IDWAWI 146
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                                                                               Heilig R.;
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007806
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                                                       Yeb C.-T.;
"Replication of hepatitis C virus in the ascitic mononuclear cells and development of distinct quasispecies in the ascitic fluid.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF109743; AAD51574.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cathepsin B-like protease (Fragment).
Trypanosoma rangeli.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
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Pyrococcus.
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Nobrega O.T., Teixeira A.R.L., Campbell D.A., Santana J.M.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF400046; AAK85411.1; -.
                                                                                                                                                                                                                                                                                      90.0%; Score 36; DB 12; Length 27; 100.0%; Pred. No. 33; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.0%; Score 36; DB 5; Length 207; 100.0%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 AA; 22968 MW; 7AF0D959D5F81C5B CRC64;
                                                                                                                                                                                                                                       27 AA; 2964 MW; 8A68DCDC25CE4FAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Purine phosphoribosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SMO0645; Pept Cl; 1.—
ROSGIE; PS00139; THIOL_PROTEASE CYS; 1.
PROSITE; PS00639; THIOL_PROTEASE HIS; 1.
Hydrolase; Protease; Thiol protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000668; Peptidase_C1.
InterPro; IPR000169; SHprot_acsite.
Pfam; PF00112; Peptidase_C1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS, PR00705; PAPAIN.
ProDom, PD000158; Peptidase_C1; 1.
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.00
--hes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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|DWAWL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DWAWL 75
                                                                                                                                                                                                                                                                                                                                                                                                 2 DWAWL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 DWAWL 6
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NON TER
SEQUENCE
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Q962U3
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Q9V227

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STRAIN=CDC 1551 / Oshkosh,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann B.D., Dodgon R., Gwinn M.L., Haft D., Hickey B.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagels K., Krogh A., Mclean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Sulton J.E., Seeger K., Skelton S., Squares S., Squares B., Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence."; Mature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                             Score 36; DB 17; Length 215;
Pred. No. 2.4e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
hosphotransferase (Aminoglycoside 3'-phosphotransferase).
RV3817 OR MTCY409.13C OR MT3925.1.
Mycobacterium tuberculosis.
structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ1482831; CAB49171.1; --
HSSP; Q26997; 1QK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; 297188; CAB10016.1; -.
                                                                                                                                            InterPro, 17, PR000836; PRIransferase.
Pfam, PF00156; Pribosyltran; 1.
Glycosyltransferase; Transferase; Complete proteome.
SEQUENCE 215 AA; 24832 WW; ASSB71EBED5FD723 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THEORPEO, 1P. 0.025.5; APH.
Pfam; PF01636; APH; 1.
Transferase; Complete proteome.
SEQUENCE 251 AA; 27241 MW; 52E07FDA006A21B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.0%; Score 36; DB 16; 100.0%; Pred. No. 2.8e+02;
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RESULT 13

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STRAIN=A3(2);
Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                   90.0%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                           EMBL; AE009235; AAL43864.1; -.
EMBL; AE008379; AAK90334.1; -.
InterPro; IPR000515; BPD transp.
Pfam; PP00528; BPD transp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  316 AA; 35079 MW;
                                                                                                          Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9XBD4;
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amycolatopsis orientalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome. SEQUENCE 316 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LDWAW 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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            Gaps
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                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN=ATCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043;

MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABC transporter, membrane spanning protein.
ATU3048 OR AGR L 3514.
ATU3048 OR PORTED (STRAIN CS8 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiane.
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.0%; Score 36; DB 16; Length 304; 100.0%; Pred. No. 3.4e+02; ive 0; Mismatches 0; Indele
          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 AA; 33430 MW; DC278071764B671C CRC64;
                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Probable cytochrome c oxidase assembly factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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                                                                                                                                                            304 AA
        0; Mismatches
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PROSITE; PS00943; UBIA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE004449; AAG03503.1; -. InterPro; IPR006369; CyoE_CtaB. InterPro; IPR000537; UbiA.
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   opportunistic pathogen."
Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 LDWAW 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                       86 DWAWL 90
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SEQUENCE 304 AA
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                                         2 DWAWL 6
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=287;
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        Matches
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MEDLINE=21608551; PubMed=11743194; Miller N., Blanchard M., Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurchlo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Qurchlo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Holmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Holmagan C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.; He plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; "The genome of the natural genetic engineer Agrobacterium tumefaciens Gaps Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-P., Gordon M.P., Olson M.V., Nester E.W., ö Score 36; DB 16; Length 316; Pred. No. 3.5e+02; 7137741D79029267 CRC64;

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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Beeudonocardineae; Pseudonocardiaceae; Amycolatopsis. STRAIN=A3(2); Lennard N., Harris B.; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Putative integral membrane sugar transporter.

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van Wageningen A., Kirkpatrick P., Williams D., Harris B., Kershaw J., Van Wageningen A., Jones M., Jones S., Solemberg P., Iennard N., Jones M., Jones S., Solemberg P., Sequencing and analysis of genes involved in the biosynthesis of a vancomycin group antibiotic.", Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

-I. SUBCELLUIAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY). EMBL, ALO78635, CAB45038 1.

InterPro; IPRO07114; MFS.

InterPro; IPRO07114; MFS.

InterPro; IPRO08528; Sub_transporter.

PROSITE; PS50850; MFS; 1.

SQ SEQUENCE 444 AA; 48039 MW; 51ACE2D9EB121EDA CRC64;

Query Match

90.0%; Score 36; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels

1 LDWAW 5

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||||| 194 LDWAW 198

Search completed: February 18, 2004, 14:35:58 Job time : 18.3684 secs

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

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Sequence 16, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
    APPLICANT: May, Michael J.
    APPLICANT: May, Michael J.
    APPLICANT: Ghosh, Sankar
    TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
    FILE REPERENCE: PPI-117CP
    CURRENT APPLICATION NUMBER: US/09/847,940B
    CURRENT FILING DATE: 2001-05-02
    PRIOR APPLICATION NUMBER: 09/643,260
    PRIOR FILING DATE: 2000-08-22
    NUMBER OF SEQ ID NOS: 27
    SOFTWARE: PatentIn Ver. 2.0
    SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
                                                              US-09-847-946A-30
US-09-847-946A-38
US-09-847-946A-32
US-09-847-946A-35
US-09-847-946A-35
US-09-847-946A-36
US-09-847-946A-36
US-09-847-946A-136
US-09-847-946A-143
US-09-847-946A-143
US-09-847-946A-143
US-09-847-946A-143
US-09-847-946A-143
US-09-847-946A-143
US-09-847-946A-143
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US-09-847-946A-143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 -09-847-946A-146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-847-946A-131
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US-09-847-946A-16
Sequence 16, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
    Similarity
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Sequence
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1: \( cgn2 = 6/ptodata/1/pubpaa/USO7 \) PUBCOMB.pep:*

2: \( cgn2 = 6/ptodata/1/pubpaa/USO7 \) PUBCOMB.pep:*

3: \( cgn2 = 6/ptodata/1/pubpaa/USO6 \) NEW PUB.pep:*

4: \( cgn2 = 6/ptodata/1/pubpaa/USO6 \) NEW PUB.pep:*

5: \( cgn2 = 6/ptodata/1/pubpaa/USO7 \) NEW PUB.pep:*

6: \( cgn2 = 6/ptodata/1/pubpaa/USO7 \) NEW PUB.pep:*

7: \( cgn2 = 6/ptodata/1/pubpaa/USO8 \) NEW PUB.pep:*

8: \( cgn2 = 6/ptodata/1/pubpaa/USO8 \) PUBCOMB.pep:*

9: \( cgn2 = 6/ptodata/1/pubpaa/USO8 \) PUBCOMB.pep:*

10: \( cgn2 = 6/ptodata/1/pubpaa/USO8 \) PUBCOMB.pep:*

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12: \( cgn2 = 6/ptodata/1/pubpaa/USO8 \) PUBCOMB.pep:*

13: \( cgn2 = 6/ptodata/1/pubpaa/USO8 \) PUBCOMB.pep:*
                  GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-847-946A-16
US-09-847-946A-10
US-09-847-946A-110
US-09-847-946A-111
US-09-847-946A-111
US-09-847-946A-111
US-09-847-946A-109
US-09-847-946A-109
US-09-847-946A-109
US-09-847-946A-104
US-09-847-946A-101
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US-09-847-946A-101
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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US-09-847-946A-110

| Sequence 110, Application US/09847946A |
| Publication No. US2003005499A1 |
| GENERAL INFORMATION: |
| APPLICANT: May, Michael J |
| APPLICANT: Ghosh, Sankar |
| APPLICANT: Findeis, Mark A |
| APPLICANT: Findeis, Mark A |
| APPLICANT: Phillips, Kathryn |
| APPLICANT: Phillips, Kathryn |
| APPLICANT: Phillips, Sankar |
| APPLICANT: Phillips, Mark A |
| APPLICANT: Phillips, Sankar |
| APPLICANT: Phillips, Sankar |
| CURRENT PHILLON: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF |
| FILE REFERENCE: PPI-119 |
| CURRENT PLILNG DATE: 2001-05-02 |
| PRIOR PILING DATE: 2000-05-02 |
| PRIOR PLILING DATE: 2000-05-05 |
| PRIOR PLILING DATE: 2000-05-05 |
| PRIOR P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence:NEMO binding OTHER INFORMATION: sequence US-09-847-946A-106
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US-09-847-946A-110
                                                                                                 APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REPERENCE: PDI-119
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-05-02
PRIOR PLING DATE: 2000-05-100
PRIOR PLING DATE: 2000-05-100
PRIOR PRIOR DATE: 2000-05-100
PRIOR PLING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PATENTIN Ver. 2.0
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                         Ghosh, Sankar
Findeis, Mark A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 110
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Best Local Similarity 100.
Matches 6; Conservative
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APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Findels, Mark A
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Cerhard
ITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR PILING DATE: 2000-06-02
PRIOR PILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
                             APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
LENGTH. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide US-09-847-946A-16
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TYPE: PRT ORGANISM: Artificial Sequence '
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 105
LENGTH: 9
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Best Local Similarity 100.
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                                                               APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Ghosh, Sankar
APPLICANT: Pindeis, Mark A
APPLICANT: Pindeis, Mark A
APPLICANT: Pindlips, Kathryn
APPLICANT: Hannig, Gerhard
TITE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
PRIOR APPLICATION NUMBER: 09/647,261
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Ghosh, Sankar
APPLICANT: Ghosh, Sankar
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
FILE REPERENCE: PLING DATE: 2001-05-02
PRIOR PPLICATION NUMBER: 09/643,260
PRIOR PLING DATE: 2000-06-02
PRIOR PLING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PATENTIN VEY: 2.0
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OTHER INFORMATION: Description of Artificial Sequence: NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-111
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Sequence 103, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 6; Conservative
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Sequence 102, Application US/09847946A

PUBLICATION NO. US20030054999A1

GENERAL INFORMATION:
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Hannig Gerharyn
APPLICANT: Hannig Gerharyn
APPLICANT: Hannig Gerharyn
APPLICANT: NUMBER: US/09/847,946A
CURRENT APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-06-22
NUMBER: OS/09/43,260
PRIOR FILING DATE: 2000-08-22
NUMBER: OS/09/43,260
SEQ ID NOS: 160
SEQ ID NO 102
LENGTH: 9
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APPLICANT: May, Michael J
APPLICANT: Apolicant: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT APPLICATION NUMBER: G0/201,261
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
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US-09-847-946A-102
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100.0%; Pred. No. 7e+05;
iive 0; Mismatches 0;
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Pred. No. 7e+05;
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100.08; FL
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                Best Local Similarity 100.
Matches 6; Conservative
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US-09-847-946A-107
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APPLICANT: May, Markat J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
ITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/99/847,946A
CURRENT APPLICATION NUMBER: 60/201,261
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR PILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SSQ ID NO 108
LENGTH: 9
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Bublication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Phillips, Kathryn

APPLICANT: Hannig, Gerhard

TITLE OF INNENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REFERENCE: PPI-119

CURRENT FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 05/201,261

PRIOR APPLICATION NUMBER: 06/201,261

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR PLING DATE: 2000-08-22

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: PATENTIN VET: 2.00
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US-09-847-946A-109
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i. Sequence 108, Application US/09847946A
i. Publication No. US20030054999A1
i. GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 6; Conservative
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LDWAWL 6
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LENGTH: 9
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Sequence 107, Application US/09847946A

Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Hannig, Gerhard

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REFERENCE: PPL-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR FILING DATE: 2000-06-02

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO! 107
                                                                                                                                                                                                                                                                                                                                                APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
ITILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR PILING DATE: 2000-05-02
PRIOR PLILING DATE: 2000-05-02
PRIOR PLILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 160
SEQ ID NO 104
LENGTH: 10
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SEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
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US-09-847-946A-101

US-09-847-946A-101

Sequence 101, Application US/09847946A

Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Findels, Mark A

APPLICANT: Findels, Mark A

APPLICANT: Philips, Kathryn

APPLICANT: Philips, Kathryn

APPLICANT: Philips, Carhard

TITLE OF INVENTION NUMBER: US/09/847,946A

CURRENT APPLICATION NUMBER: 60/201,261

PRIOR APPLICATION NUMBER: 60/201,261

PRIOR PILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-08-22

NUMBER: OF SEQ ID NOS: 160

SOFTWARE: Patentin Ver. 2.0

LENGTH: 11
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Facent No. US20020156000A1
GENERAL INFORMATION:
APPLICANT: MAY, Michael J.
APPLICANT: MAYOR, Sankar
ITILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
ITILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/847,940B
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR PLILNG DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 6
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; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-9408-2
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                     Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
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3 LDWAWL 8
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US-09-847-946A-107
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US-09-847-940B-2
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Query Match

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Best Local Similarity 83.3%; Pred. No. 7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps Qy 1 LDWAWL 6

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMERIES	
Result No.	Score	Query	Query Match Length DB	08	ΙD	Description
-	40	100.0	9	23	ABB08738	Mutated IKKbeta NE
~	40	100.0	9	23	AAM48521	NBD mutant peptide
m	40	100.0	9	23	AAM48541	Anti-inflammatory
4	40	100.0	9	23	AAM48603	Anti-inflammatory
ហ	40	100.0	9	24	ABU08431	Human NEMO binding
9	40	100.0	7	23	AAM48607	Anti-inflammatory
7	40	100.0	80	23	AAM48600	Anti-inflammatory
80	40	100.0	80	23	AAM48608	Anti-inflammatory
σι	40	100.0	6	23	AAM48599	Anti-inflammatory

/note= "Wildtype Ser substituted by Ala"

WO200183547-A2

08-NOV-2001

Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory	Streptococcus poly Streptococcus poly Human IKKbeta muta Human polypeptide Human polypeptide	IKKOeta NEMO bindi Anti-inflammatory NBD mutant peptide Human NEMO binding Anti-inflammatory	Anti-inflammatory Anti-inflammatory IXK-alpha polypept Anti-inflammatory Anti-inflammatory Anti-inflammatory	Anti-inflammatory IXKbeta NEMO bindi Anti-inflammatory Anti-inflammatory Human NBD peptide Human IKKbeta pept	Anti-inflammatory NBD peptide. Synt Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory
AAM48602 AAM48605 AAM48606 AAM48601 AAM48604 AAM48604	ABP30297 ABP27565 ABB77306 AAM40149 AAM41935	ABB08725 AAM48530 AAM48655 ABU08418 AAM48534	AAM48527 AAW48535 AAW96182 AAM48526 AAM48529 AAM48532	AAM48533 ABB77313 AAM48528 AAM48531 ABB77311 AAM48506	AAM48525 AAM48640 AAM48641 AAM48642 AAM48645 AAM48639 AAM48639
232333	22333	2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	3333333	333333	3333333
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ALIGNMENTS

RESULT 1 ABB08738

kinase activation; leukocyte; inflammation; B-selectin; offeoclast; autoimmune disease; transplant rejection; osteoporosis; cancer; Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis; rheumatoid arthritis; crohi's disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; antiinflammatory; immunosuppression; osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antiashmatic; antiallergic; dermatological; antibacterial; antibsoriatic; antirheumatic; antichematic; antiallergic; antiarthritic; osteopathic; antiulcer; mutant; mutein. IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB; Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 16. Location/Qualifiers ABB08738 standard; peptide; 6 AA (first entry) Misc-difference Homo sapiens. 14-JUN-2002 Synthetic. ABB08738; N

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Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB70312). The compound as acts through selective inhibition of (ABB70313). The compound has acts through selective inhibition of cytokine-mediated NF-kB activation by blocking the interaction of NEMO interaction results in inhibition of IKKDeta kinase activation and subsequent decreased phosphorylation of IKADeta kinase activation and chronic inflammation, by down-regulating the expression of E-selectin on leukocytes or by blocking obsecolast differentiation. The compound is useful in treating NF-kB mediated autoimmune disease, transplant rejection, osteoporosis, cancer, Alzheimer's disease, atherosclerosis, a viral infection or ataxia telangiectasia. The inflammatory disorder is asthma, allergies, uricaria, anaphylaxis, cutaneous inflammatory disorder is asthma, allergies, cheumatoria arthritis, osteoarthritis, psoriatic arthritis, lupus and bursitis. The inflammatory disorder may also be dermatitis, erzema, psoriatic arthritis, lupus and cursianis, osteoarthritis, psoriatic arthritis, lupus and cursianis, osteoarthritis, psoriatic arthritis, lupus and cursianis, osteoarthritis, sporiatic arthritis, lupus and colymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis, caused by Epstein-barr, cytomegalovirus or herpes simplex. Other caused by Epstein-barr, cytomegalovirus context dermatitis, and anaphylaxis, drug and food sensitivity, contact dermatitis, and influenza. The compound may be used to replace corricosteroids in minionsuppression in which corricosteroids are used, including invisorion and influenza and encer therapy. Also for disorder immunosuppression in which corricosteroids are used, include life and encer therapy. Also for disorder and influen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiinflammatory compounds and for diagnosis of an inflammatory disorder. The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of a mutated NEWO binding domain of IKKOeta.
                                                                                                                                                                           Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting a cell with an anti-inflammatory compound comprising at least one NEMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                            Claim 23; Page 45; 82pp; English.
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02-MAY-2001; 2001WO-US40654.
                            02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
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                                                                                                                                             WPI; 2002-179350/23
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Best Local Similarity
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                                                                                                             May MJ, Ghosh S;
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antirheumatic; antiarthritic; oeteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NBMO binding domain; eczema; cytokine; NRkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48646-AAAM48651) which comprises from 6-15 amino acid residues, fused a NEWO binding sequence (AAM48619). The antiinflammatory compounds have antiasthmatic, Cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallargic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB compounds act as selective inhibitors of cytokine-mediated NFkappaB the NEWO binding domain that results in inhibition of IKKDeta is activation and subsequent decreased phosphorylation of IKKDeta kinase activation and subsequent decreased phosphorylation of IKRDeta kinase compounds are useful for treating inflammatory disorders, e.g. asthma,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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100.0%; Pred. No. 9.3e+05;
ive 0; Mismatches 0;
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Anti-inflammatory peptide SEQ ID NO 106

(first entry)

20-MAR-2002

AAM48603;

AAM48603 standard; Peptide; 6 AA

AAM48603 ID AAM

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20-MAR-2002
               08-NOV-2001
            Synthetic.
                                               arthritis.
                       мау мЈ,
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AMM48620-AMM48645), comprising a membrane translocation domain.

(AAM48620-AMM48645), comprising a membrane translocation domain.

(AAM48620-AMM48619). The antiinflammatory compounds have antiathmatic, antipacterial, immunosuppressive, dermatological, neuroprotective, notropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB corprotion by blocking interaction of IkappaB kinase beta (IKKObeta) at the NEWO binding domain that results in inhibition of IKKOpeta at the NEWO binding domain that results in inhibition of IkappaB. The activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatoin of IkappaB. The activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatoid arthritis, osteoarthitis, inflammatory bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, bursitis; autoimmune diseases such as lupus, polymyalgia, and ataxia telandiscial. The compounds are also useful for treating contains and ataxia.
                                                                                                                                                                                                                                                                                                                             antificumatic; antiarchritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NRkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                               Antlinflammatory, antiasthmatic, cytostatic, antipsoriatic, nootropic,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phillips K;
                                                                                                                                                                                        Anti-inflammatory peptide SEQ ID NO 44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 61; 88pp; English.
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AAM48541;
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The invention relates to an antiinflammatory compound (especially AMM48629-AMM48645), comprising a membrane translocation domain (AAM48620-AAM48645), comprising a membrane translocation domain acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, ortostatic, antipocriatic, antirheumatic, antiarthritic, descepathic, corpounds act as selective, inhibitors of cytokine-mediated NFRappas compounds act as selective inhibitors of cytokine-mediated NFRappas compounds act as selective inhibitors of cytokine-mediated NFRappas compounds are as selective inhibitors of cytokine-mediated NFRappas cortivation by blocking interaction of Ikappas kinase beta (IKKbeta kinase the NEMO binding domain that results in inhibition of IKKpeta kinase compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, compounds are useful for treating inflammatory disorders, e.g. asthma, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; clangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxie, corpounds are also useful for treating and ataxia are bettive in the compounds are also useful for treating and pro-inflammatory responses such as allergies, urticaria, anaphylaxie, compounds are also useful for treating and ataxia and proper and as allergies, urticaria, anaphylaxie, archemical and anaphylaxie, and allergies and as allergies, urticaria, anaphylaxie, and allergies.
                                                                                                                                                        Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; derivation in neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 62; 88pp; English.
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22-AUG-2000; 2000US-0643260.
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                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
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   100.0%; Score 40; DB 23; Length 6; 100.0%; Pred. No. 9.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                      ABU08431 standard; peptide; 6 AA.
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22-AUG-2000; 2000US-0643260.
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                                                                                                                                                                                                                                                                                                                                           antificumatic, di antiarchitic, deteopachic; antibacterial, virucide, immunosuppressive, dermatological, neuroprotective, antiatherosclerotic, antialegic, membrane translocation domain; NEWO binding domain, eczema, cytokine, NekappaB; KappaB kinase beta; IKKDeta, cancer, psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; rransplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
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drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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                                                                100.0%; Score 40; DB 23;
100.0%; Pred. No. 9.3e+05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                       AAM48600 standard; Peptide; 8 AA.
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22-AUG-2000; 2000US-0643260.
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osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, burstitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sumburn, aging and arthritis.
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which comprises from 6-15

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RESULT 10
AAM48602
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compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkKpeta kinase compounds are useful for teating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatory disorders, e.g. asthma, osteoarthritis, inflammatory bowel disease, sepsis, vasculities, bursitis, autoimmune diseases such as lupus, polymyalgia, soleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis, Alzheimer's disease; atherosclerosis, viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, utricaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
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                                                                                                                                                                                                                                                                                  100.0%; Score 40; DB 23; Length 8; 100.0%; Pred. No. 9.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-inflammatory peptide SEQ ID NO 102.
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(AAM48525-AAM48619). The antinflammatory compounds have antiasthmatic, amino acid residues, fused to a NEWO binding sequence
(AAM48525-AAM48619). The antinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiasthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, cartisaterial, immunosuppressive, dermatological, neuroprotective, corpounds act as selective inhibitors of cytokine-mediated NRRappaB activation by blocking interaction of IkappaB insee beta (IKKbeta) at the NEWO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IKKbeta kinase activation and subsequent decreased phosphorylation of IKKbeta kinase compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoparthritis, inflammatory bowel disease, sepsis, vasculitis, osteoporosis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, caranlomatosis, multiple sclerosis; transplant rejection; osteoporosis, clanapiectasia. The compounds are also useful for treating telangicctasia. The compounds as allergies, urticaria, anaphylaxis, chikisis, criticaliamatory responses such as allergies, urticaria, anaphylaxis, chikisis, the compounds are also useful for treating and critis; are compounds are also useful for treating and critis; and compounds are also useful for treating and critis; and compounds are also useful for treating and critis; and compounds are also useful for treating and critis; and compounds are also useful for treating and critis; and compounds are also useful for treating and critis; and critis and critis and critis and critis are also useful for treating and critis.
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100.0%; Pred. No. 9.3e+05;
live 0; Mismatches 0;
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The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48645), comprising a membrane translocation domain card residues, tused to a NEMO binding sequence (AAM48625-AAM48619). The antiinflammatory compounds have antisathmatic, cytosteric, antipacriatic, antirheumatic, antiarthatic, osteogethic, corpounds act as selective, inhibitors of cytokine-mediated NFkappaB compounds act as selective inhibitors of cytokine-mediated NFkappaB compounds act as selective inhibitors of cytokine-mediated NFkappaB cativation by blocking interaction of IrappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoathritis, inflammatory bowel disease, sepsis, vasculitis, osteoathritis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatomis, multiple sclerosis, transplant rejection; osteoporoals, all antimer's disease; atherosclerosis, viral infections; and ataxia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
                                                                                 Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
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                                                                                                                                                                                                                            Claim 6; Page 62; 88pp; English.
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(AAM48525-AAM48619) The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antisheumatic, antiarthitic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, corpounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKkappaB The compounds are useful for treating inflammatory disorders, e.g. asthma, compounds are useful for treating inflammatory disorders, e.g. asthma, compounds are useful for treating inflammatory disorders, e.g. asthma, compounds are useful for treating inflammatory disorders, e.g. asthma, compounds are useful for treating inflammatory disorders, e.g. asthma, compounds are useful for treating inflammatory disorders, e.g. asthma, consecutivitis, nuttingle sclerosis, transplant rejection; osteoporosis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; viral infections; and ataxia telammatory responses such as allergies urricaria, anaphylaxis, cuthylity, eczema, dermatitis, sunburn, aging and
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                                                                                                                                     AAM48620-AAM48645), comprising a membrane translocation domain
(AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
                                                                                                           invention relates to an antiinflammatory compound (especially
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-inflammatory peptide SEQ ID NO 108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM48605 standard; Peptide; 9 AA.
                                                    Claim 6; Page 62; 88pp; English.
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22-AUG-2000; 2000US-0643260.
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psoriasis
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Length 9; Indels Phillips K;

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AMM48620-AMM48645), comprising a membrane translocation domain (AAM48620-AMM48645), comprising a membrane translocation domain (AAM48620-AMM48619). The antinical parameters from 6-15 amino acid residues, fused to a NEWO binding sequence (AAM48619). The antinicheumatic, antiarthritic, osteopathic, antipacterial, immunosuppressive, dermatological, neuroprotective, notropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB contropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB cativation by blocking interaction of IkappaB kinase beta (IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammation of IkappaB. The compounds are useful for treating inflammatory discorders, e.g. asthma, ung inflammation or cancer pooriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, all planeimer's disease, attensederosis, viral infections; and ataxia consideration; and ataxia consideration; and ataxia consideration; and ataxia consideration.
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                                                                                                                  02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.
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                                                                                                                                                                                                                                       domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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                                                                                                                    May MJ, Ghosh S, Findeis MA, Phillips K;
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22-AUG-2000; 2000US-0643260.
                                               (PRAE-) PRAECIS PHARM INC.
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                                                                     UNIV YALE.
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RESULT 13 AAM48601

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Synthetic

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antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
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drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
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                  ataxia telangiectasia; allergy; anaphylaxis; arthritis
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                                                                                                                                                                                             02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.
                                                                                                                                                          02-MAY-2001; 2001WO-US14346.
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The invention relates to an antiinflammatory compound (especially AAM48629-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48620) comprising a membrane translocation domain characteristic actions of a mino acid residues, fused to a NEMO binding sequence (AAM48625-AAM48619). The antiinflammatory compounds have antisthmatic, cytostatic, antipheratic, antitheumatic, antiartherize, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds are as selective inhibitors of cytokine-mediated NFRappaB activation by blocking interaction of InappaB kinase beta (IKKbeta kinase the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IKKbeta kinase activation and subsequent decreased phosphorylation of IKKbeta kinase activation and subsequent decreased phosphorylation of IKKpeta kinase activation or cancer, psoriasis, rheumatory disorders, e.g. asthma, lung inflammaton or cancer, psoriasis, rheumatoid arthritis, orsteoarthritis, antiphe sclerosis, sepsis, vasculitis, orsteoarthritis, antiphe sclerosis; viral infection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; osteoporosis; clangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allorgies, unticaria, anaphylaxis, arrection; or food sensitivity, eczema, dermatitis, sunburn, aging and
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immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain, NEWO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; csteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
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Copyright in - protein search, February 18, Score: 36 1 LDWSYL 6 1 LDWSYL 6 1 LDWSYL 6 1 ABJ0525 seqs, mber of hits satisfy DB seq length: 20000 Cessing: Minimum Mat Maximum Mat Listing fir	se : Pred. No. score gree and 1s dee	Result Query Query Description 1 36 100.0 939 16 987QR3 Q89qr3 anabaena sp 2 36 100.0 106.0 1039 10 00 3 34 94.4 38.9 17 16 08FWV 08fmv4 corynabacte 4 34 94.4 38.9 17 16 08FWV 08fmv4 corynabacte 4 34 94.4 38.9 17 16 08FWV 08fmv4 corynabacte 058160 pyrcocccus 058160 pyrcocccus 058160 pyrcocccus 058160 pyrcocccus 058160 pyrcocccus 059160 pyrcocccus 059160 059160 059160 059160 059160 059160 059160 059160 059160 05916 05916 05916 05916 05916 05916 05916 05916 05916 05916 05916 05916 05916 05916 05916 05916 05916 059

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Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.; Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                   Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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Pred. No. 2.6e+02;
1; Mismatches 0; Indels
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Lyne M., Rajandream M.A., Barrell B.G., Xiang Z., Aves S.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AL023290; CAA18895.1; -
GeneDB SPombe; SPBC15G4.04c; -
InterPro; IPR002493; AA/rel_permease.
InterPro; IPR004919, AAc_permease.
InterPro; IPR004915; AA_permease.
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83.3%; Pred. No. 5.4e+02;
ive 1; Mismatches 0; Indels
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EMBL; AP000002; BAA29509.1; -.

InterPro; IPR002934; NTP transf.

Pfam; PF01909; NTP transf 2; 1.

Hypochetical protein; Complete proteome.

SEQUENCE 389 AA; 46335 MW; 81F32C817B1A53D4 CRC64;
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TIGRERMS; TIGR00907; 2A0304; 1.
PROSITE; PS00218; AMINO ACID PERMEASE 1; 1.
SEQUENCE 542 AA; 59726 WW; 17D9B15C04299468 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
01-AUG-1998 (TrEMBLrel. 07, Created) (1-AUG-1998 (TrEMBLrel. 07, Last sequence update) (1-UNG-1202 (TrEMBLrel. 21, Last annotation update) Hypothetical protein PH0423.
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83.3%;
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Best Local Similarity 83.3%,
5; Conservative
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                                                                                                     Pyrococcus horikoshii.
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SPBC15C4.04C.
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Best Local Similarity
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                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                          Pyrococcus.
NCBI_TaxID=53953;
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SEQUENCE FROM N.A.
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
Usuda Y., Sugimoto S.;
"The entire genomic sequence of Corynebacterium efficiens YS-314.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AP00522; BAC19205.1; -
EMBL, AP005222; BAC19205.1; -
SEQUENCE 317 AA; 33135 MW; 3805EDE05030A81C CRC64;
                                          01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative membrane glycoprotein, possible vacuolar protein sorting
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83.3%; Pred. No. 2.1e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                      STRAIN=972h-;
Purnelle B., Goffeau A., Wood V., Lyne M., Barrell B.G.,
Rajandream M.A.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO21767; CAA16914.1;
GeneDB_SPombe; SPBC16C6.06;
InterPro; IPR002860; GH BNR.
InterPro; IPR005881; VPSIO.
Pfam; PRO2212; BNR; 12.
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SEQUENCE 1466 AA: 165061 MW; CEB315E0F768BD79 CRC64;
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NCBI_TaxID=152794;
                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).

Bukaryota; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetales; Schizosaccharomyces.

Schizosaccharomyces.
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                    01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2003 (TrEMBLrel. 23,
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114 MDWSYL 119
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RESULT 4 058160 ID 05 AC 05

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SEQUENCE FROM N.A. te Pas M.F., Leanhouwers J.I., Knol E.F., Booij M., Priem J., van der Lende T.; "Marker polymorphism in the porcine muscle glycogen synthase (glycogen
                                                                                                                                         Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                      88.9%; Score 32; DB 6; Length 142; 83.3%; Pred. No. 2.1e+02; ive 0; Mismatches 1; Indels
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Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AJS07152; CAD47844.1; -.
                                                                                                                                                                                                                                                                                                                                           142 AA; 15951 MW; C02BAD285FBF8A7E CRC64;
                                                                                                    Glycogen synthase (Fragment).
                                                       01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 83.3%;
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nes 5; Conservative
                              PRELIMINARY;
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                                                                                                                                                                                                                                                STRAIN-cv. Columbia;
Town Co., Haas B.J., Wu D., Maiti R., Hannick L.I., Chan A.P.,
Town C.D., Haas B.J., Wu D., Maiti R., Hannick L.I., Chan A.P.,
Tallon L.J., Rooney T., Utterback T.R., Vanaken S.E., Feldblyum T.V.,
White O., Framer C.M.;
"Arabidopsis thaliana chromosome 1 BAC T4M14 genomic sequence.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC027036; AAK62781.1;
Hypothetical protein.
SEQUENCE 75 AA; 8834 MW; B34EB2BBSC41EBBS CRC64;
                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                  88.9%; Score 32; DB 10; Length 75; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 8.8 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2002 (TEMBLrel. 22, Last annotation update)
Hypothetical protein slr1082.
                                           75 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 AA
                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 LDWSFL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LDWSYL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LDWSY 5
                                                                                                                                                                                           eurosids II; Brae
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                     Q94HW4;
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                                         094HW4
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             RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence analysis of the genome of the unicallular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).

EMBL; D90908; BAA17745.1; -. InterPro; IPR002636; DUP29.

Pfam, PF01724; DUF29; 1.

Hypotherical protein; Complete proteome.

SEQUENCE 153 AA; 18387 MW; 6E54EB36EDCB9AF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
Tabata S.;
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                                                                                                                                                                                                                           Synechocystis sp. (strain PCC 6803).
Bacteria, Cyanobacteria, Chroococcales, Synechocystis.
                                                          01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein s1r1813.
153 AA.
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Best Local Similarity 100.
Matches 5; Conservative
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Pfam; PF02597; This; 1.
STRAIN=cv. Columbia;
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                                                                                                                                                                                                                                                                208 LDWSY 212
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                                                                                                                                                                                                                       1 LDWSY 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=13773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LDWSY 5
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                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                              Q8ZYL1
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Matches
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Q8ZYL1
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Q9FNJ0
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MEDLINE=20083487; PubMed=10617197;

Lin X., Kaull S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carrear A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;

"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae;
Suromatobit, Brassicales, Brassicaces, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Azavind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.9%; Score 32; DB 16; Length 172; 100.0%; Pred. No. 2.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein, Complete proteome.
SEQUENCE 172 AA; 19874 MW; CCF8D41A4DCF7DC0 CRC64;
                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein DRA0366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last annotation update)
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                                                                                      PRT;
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MEDLINE=20036896; PubMed=10567266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 286:1571-1577(1999).
EMBL; AE001863; AAF12501.1; -.
TIGR; DRA0366; -.
                                                                                                                                                                                                                                                                                       Deinococcaceae; Deinococcus.
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 5; Conservative
                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                              Deinococcus radiodurans.
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AT2G36550.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1299;
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                                                                                                                                                                                                                    DRA0366.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Genomic DNA, chromosome 5, Pl clone:MDJ22.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyra; Eudaryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI TaxID=3702;
                                                                                                                                                                                          Gaps
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Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
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                                                                                                                                   Length 221;
                                                                                                                                88.9%; Score 32; DB 10; Length 22 100.0%; Pred. No. 3.3e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
Lin X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                   EMBL; AC006919; AAD24637.1; -.
SEQUENCE 221 AA; 25043 MW; D3037BC4CC103990 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea, Crenarchaeota, Thermoprotei, Thermoproteales, Thermoproteaceae; Pyrobaculum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 AA; 25544 MW; 111B06C8F85982EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Molybdenum cofactor biosynthesis protein D/E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.9%; Score 32; DB 17; L 100.0%; Pred. No. 3.4e+02; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aerophilum.";
Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002)
EMBL; AAE097922.1; -.
EMBL; PRO03448; Mb biosynth_MoaE.
InterPro; IPR003749; ThIS.
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STRAIN=IM2 / ATCC 51768 / DSM 7523;
PubMed=11792869;
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Erassicales; Brassicaceae; Arabidopsis.
"Structural analysis of Arabidopsis thaliana chromosome 5. II. Sequence features of the regions of 1,044,062 bp covered by thirteen physically assigned P1 clones.";
DNA Res. 4:291-300(1997).
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Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S., Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A.
Zumstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
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88.9%; Score 32; DB 10; Length 278;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                           Length 262;
                                                                                                                                                                                                                                                  Query Match

88.9%; Score 32; DB 10; Length 26
Best Local Similarity 100.0%; Pred. No. 3.98+02;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clones.";
DNA Res. 7:131-135(2000).
EMBL; AB022216; BAB02739.1; -.
SEQUENCE 278 AA; 31217 MW; A16AE1E0910484B2 CRC64;
                                                                                                                                                                                                262 AA; 30706 MW; CE15DD9E2CD3C6B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Chromosome XV reading frame ORF YOL092W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 AA
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MEDLINE-20277480; PubMed-10819329;
                                                                                                          EMBL; AB006699; BAB11677.1; -.
InterPro; IPR06566; FBD.
SWART; SM0679; FBD; 1.
SEQUENCE 262 AA; 30706 MW;
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"A 29.425 kb segment on the left arm of yeast chromosome XV contains
more than twice as many unknown as known open reading frames.";
EMBL, 274834, CAA99104.1;
EMBL, X83121; CAA58187.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                 88.9%; Score 32; DB 3; Length 308; 83.3%; Pred. No. 4.6e+02; ive 0; Mismatches 1; Indels
                                           Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                     308 AA; 34872 MW; 38EB1645FA034812 CRC64;
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                                                                                                                                    MEDLINE=96021609; PubMed=8533473;
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.33,
                                                                                                                                                                                                                                                                                               SGD; SO005452; YOL092W.
InterPro; IPR006603; CTNS.
SMART; SM00679; CTNS; 2.
SEQUENCE 308 AA; 34872 M
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SEQUENCE FROM N.A.
                                                                                       SEQUENCE FROM N.A.
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

February 18, 2004, 14:12:09; Search time 6.5921 Seconds (without alignments) 87.531 Million cell updates/sec Run on:

US-09-643-260-15 36

1 LDWSYL 6 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

Result No.	Score	* Query Match	Length	80	SUMMARIES	Deacritica
				3		TOTAL TOTAL
	36	100.0	7 939	7	AE2275	hypothetical prote
	36	100.0	フ'	•	T39557	vacuolar protein s
	34	94.4	86/		H64885	ydaS protein - Esc
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	32	88.9	136	~	\$74785	hypothetical prote
	32	œ		~	S77187	hypothetical prote
	32	88.9		~	A75592	
	32	88.9		N	H84781	
	32	88.9		~	T40878	probable FAD synth
	32	88.9		~	S57377	memb
	32			~	T32669	hypothetical prote
	32			~	T45032	hypothetical prote
	32			~	B71857	8
	32	88.9		~	S27492	hypothetical prote
	32			~	D90047	hypothetical prote
	32	88.9		~	T43863	Ø
	32			N	B70446 .	
	32			~	T48367	cal
	32	88.9	542	~	A69261	ס
	32			N	B82975	choline dehydrogen
	32			~	AC0143	choline dehydrogen
	32			~	AE1969	sulfate permease f
	32	88.9	7	~	T40070	origin recognition
	32	88.9		N	A33369	glycogen(starch) s
	32	88.9	_	~	A32156	glycogen(starch) s
	32	٠.	8	~	F85334	myosin heavy chain
	32	88.9	1446	~	T04528	myosin heavy chain

hypothetical prote	myosin heavy chain	probable myosin he	myosin heavy chain	hypothetical prote	myosin heavy chain	protein T23G18.2 [hypothetical prote	inositol monophosp	5-amino-6-(5-phosp	hypothetical prote	WD-repeat protein	glycogen(starch) s	glycogen(starch) s	conserved helix-lo	gamma-glutamyl car
F96587	T00727	A84743	T07961	F86178	T18278	A86216	T24188	G81026	B82644	D81971	T50211	S45686	A35362	149101	A39283
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1556	1583	1611	1643	1736	2245	2658	223	231	237	264	206	703	703	745	757
88.9	88.9	6.88	88.9	88.9	88.9	88.9	86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1
32	32	32	32	32	32	32	31	31	31	31	31	31	31	31	31

ALIGNMENTS

AE2275
hypothetical protein alr3756 [imported] - Nostoc sp. (strain PCC 7120)
Cypecies Nostoc sp. PCC 7120
A;Note: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AE275
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE275
A;Accession: AE275
A;Accession: Declaininary
A;Molecule type: DNA
A;Residues: 1-939 «KUR>
A;Cross-references: GB:BA000019; PIDN:BAB75455.1; PID:g17132890; GSPDB:GN00179
A;Cross-references: strain PCC 7120
C;Genetics:
A;Gene: alr3756

Gape ö 100.0%; Score 36; DB 2; Length 939; 100.0%; Pred. No. 80; 0; Indela 0; Mismatches Query Match
Best Local Similarity 100.
Matches 6; Conservative

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|||||| 648 LDWSYL 653 9 1 LDWSYL

ò 8 RESULT 2

vacuolar protein sorting - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T39557
R;Purnelle, B.; Goffeau, A.; Wood, V.; Lyne, M.; Barrell, B.G.; Rajandream, M.A. aubmitted to the EMBL Data Library, February 1998
A;Reference number: 221863
A;Accession: T39557
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1466 <PUR>
A;Cross-references: EMBL:AL021767; PIDN:CAA16914.1; GSPDB:GN00067; SPDB:SPBC16C6.06
A;Experimental source: strain 972h-; cosmid c16C6
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Antrons: 58/3

100.0%; Score 36; DB 2; Length 1466; 100.0%; Pred. No. 1.3e+02; Query Match Best Local Similarity

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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc. A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B. Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Lerine, A.; Liu, H.; Masuda, S.; Mauselly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetellf, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanhon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekjquchi, J.; Sekowska, A.; Sero, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Tarpstrap, P.; Tognoni, A.; Tosato, V.; Uchiyama, A;Tille: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Accession: H69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: S74785
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-330 «KUN» A;Residues: 1-330 «KUN» A;Residues: 1-330 «KUN» A;Cross-references: GB:Z99107; GB:AL009126; NID:g2632866; PIDN:CAB12540.1; PID:g2633034 A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reaidues: 1-542 <LYN>
A;Cross-references: EMBL:AL023290; PIDN:CAA18895.1; GSPDB:GN00067; SPDB:SPBC15C4.04c
A;Experimental source: strain 972h-; cosmid c15C4
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C;Accession: T39474
R;LyTuc, M; Rajandream, M.A.; Barrell, B.G.; Xiang, Z.; Aves, S.
aubmitted to the EMBL Date Library, May 1998
A;Reference number: 221857
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 1.6e+02;
1; Mismatches 0; Indels
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A,Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
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Pred. No.
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C,Superfamily: hypothetical protein ydeD
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83.3%;
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Similarity 83.3%;
5; Conservative
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LDWSYV 441
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Best Local Similarity
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                                                                                                                                                                                                                                                                                 C;Species: Escherichia coii (Bitalin N-14)
C;Species: Escherichia coii (Bitalin N-14)
C;Bate: 12-Sep-1997 #Bequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Bates 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Bates 200: H64885
A; Blunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A; Ittle: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MuID:97426617; PMID:9278503
A;Reference number: A64720; MuID:97426617; PMID:9278503
A;Reference type: DRA
A;References: GB:AE000233; GB:U00096; NID:91787613; PIDN:AAC74439.1; PID:91787620; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin M.; Offichu, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: H71152
A;Status; preliminary; nucleic acid sequence not shown; translation not shown
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A,Residues: 1-389 «KAM»
A;Cross-references: GB:AP000002; NID:g3236129; PIDN:BAA29509.1; PID:g3256826
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
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C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: H71152
E;Kawarabayasi, Y:; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamot
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: H69798
               Gaps
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C;Superfamily: Pyrococcus horikoshii hypothetical protein PH0423
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               Indels
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1; Mismatches
               Mismatches
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Best Local Similarity 83.3
Matches 5; Conservative
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Matches 5; Conservative
               Conservative
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               Matches
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Pred. No.
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Best Local Similarity 100..
                                               Best_Local Similarity 100.
Matches 5, Conservative
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A,Molecule type: DNA
A,Residues: 1-221 <STO>
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A; Introns: 46/2; 182/3
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A;Gene: At2g36550
A;Map position: 2
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Best Local &
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R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
R;Kaneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Residues: 1-153 «KAN»
A, Cross-references: EMBL:D90908; GB:AB001339; NID:g1652725; PIDN:BAA17745.1; PID:g165282
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: hypothetical protein slr1203
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A,Experimental source: strain R1
                                                                                              A;Accession: S74785
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Roseule type: 1-136 cKAN>
A;Crose-references: EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAA16936.1; PID:g165201
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein slr0489
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Bacte: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C;Bacte: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.,
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.
S.; Smith, H.O.; Veneer, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Fitle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
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C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
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C;Superfamily: Deinococcus radiodurans hypothetical protein DRA0366
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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Pred. No. 59;
1; Mismatches 0; Indels
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                                                                         A; Reference number: S74322; MUID: 97061201; PMID: 8905231
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Pred. No. 67;
0; Mismatches
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3%;
Matches 5; Conservative
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A;Molecule type: DNA
A;Residues: 1-172 <WHI>
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LDWSFL 47
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hypothetical protein At235550 [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 0.2Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: H84781
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
euss, D.; Nieffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-265 <WOO>
A;Cross-references: EMBL:AL031764; PIDN:CAA21108.1; GSPDB:GN00068; SPDB:SPCC1235.04c
A;Experimental source: strain 972h-; cosmid c1235
                                                                                                                                                                                                                                                   A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thalians. A,Reference number: A84420; MUID:20083487; PMID:10617197
A,Accession: H84781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40879
R;Wood, v., Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
aubmitted to the EMBL Data Library, September 1998
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100.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 0;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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100.0%; Pred. No. >..
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5; Conservative
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C;Species: Saccharomyces cerevisiae
C;Acession: S57377; S66786; S50413
R;Zumetesion: S57377; S66786; S50413
R;Zumetesion: S57377; S66786; S50413
R;Zumetesion: S57377; S66786; S50413
R;Zumetesion: B; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.
A;Title: A 29.425 kb segment on the left arm of yeast chromosome XV contains more than the A;Title: A 29.425 kb segment on the left arm of yeast chromosome XV contains more than A;Reference number: S57377
A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence Database, July 1996
A;Cross-references: EMBL:X83121; NID:G600461; PIDN:CAA58187.1; PID:g600466
R;Zumetein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.
A;Residues: 1-308 cZUW>
A;Residues: 1-308 cZUW>
A;Residues: 1-308 cZUW>
A;Residues: 1-308 cZUW>
A;Residues: 1-308 cZUW>
A;Residues: BMBL:Z74834; NID:g1419937; PID:g1419938; MIPS:YOL092w
A;Cross-references: EMBL:Z74834; NID:g1419937; PID:g1419938; MIPS:YOL092w
C;Genetics:
A;Cross-references: SGD:S0005452
A;Map posttion: 15L
C;Superfamily: Saccharomyces probable membrane protein YBR147w
C;Keywords: transmembrane protein
F;14-10/Domain: transmembrane #status predicted cTMI>
F;14-10/Domain: transmembrane
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C. Species: Caenorhabditis elegans
C. Species: Caenorhabditis elegans
C. Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C. Accession: T3269
R. Davidson, S.; Wohldmann, P.; Bauer, C.; O'Neal, D.
Submitted to the EMBL Data Library, December 1997
A. Description: The sequence of C. elegans cosmid F16B4.
A. Reference number: Z21208
A. Accession: T3269
A. Accession: T3269
A. Reference type: DNA
A. Molecule type: DNA
A. Molecule type: DNA
A. Residues: 1-362 CDAV>
A. Residues: 1-362 CDAV>
A. Cross-references: EMBL:AF039048; PIDN:AAB94233.1; GSPDB:GN00023; CESP:F16B4.2
A. Experimental source: strain Bristol N2; clone F16B4
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A;Introns: 48/2; 112/2; 160/3; 255/3; 291/2; 333/3
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Best Local Similarity
Matches 5; Conserv
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26 LDWSFL 31
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RESULT 14 T45032

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hypothetical protein Y39B6B.f [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000 C;Accession: T4503.
C;Accession: T4503.
R;Milson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burton, raser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Johns B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D. Nature 368, 32-38, 1994
A;Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, E.; E. Cock, L.; Wilkinson-Sproat, J.; Wohldman, P. A;Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans. A;Reference number: 843531; MUID:94150718; PMID:7906398
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A;Variety: strain J99
C;Date: 12-Feb-1999 #text_change 08-Oct-1999
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Accession: B71857
C;Accession: B71857
S;Alm, K.J. Mang L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R., Ives, C.; Gibson, R.; Marberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999 #text of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
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AjMolecule type: DNA
AjResidues: 1-393 «ARN»
AjCross-references: GB:AE001531; GB:AE001439; NID:g4155617; PIDN:AAD06611.1; PID:g415562
AjExperimental source: strain J99
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A;Experimental source: clone Y39B6B
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 3
A;Introns: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3; 370/3
A;Note: Y39B6B.f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: February 18, 2004, 14:38:51 Job time: 7.5921 secs
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28 31 86.1 756 2 US-09-099-124A- 29 31 86.1 756 3 US-09-032-476-5 30 31 86.1 756 3 US-09-854-5 31 31 86.1 756 3 US-09-854-5 33 31 86.1 756 3 US-09-168-629-1 34 31 86.1 756 3 US-09-910-820-820-820-820-820-820-820-820-820-82	31 86.1 996 4 31 86.1 997 4 30 83.3 122 4 30 83.3 363 1 30 83.3 417 3 30 83.3 417 3 30 83.3 417 4	ALIGNMENTS RESULT 1 US-09-252-991A-27150 ; Sequence 27150, Application US/09252991A ; Patent No. 6551795	GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield et al. TITLE OF INVENTION: NUCLEIC ACID AND AMINO J. TITLE OF INVENTION: AERUGINOSA FOR DIAGNOST: FILE REFERENCE: 107196.136 CURRENT APPLICATION NUMBER: US/02/252,991A CURRENT FILING DATE: (1999-02-18) PRIOR FPLICATION NUMBER: US 60/074,788	; PRIOR APPLICATION NUMBER: US 60/094,190 ; PRIOR FLING DATE: 1998-07-27 ; SEQ ID NO 27150 ; LENGTH: 829 ; TYPE: RRI ; TYPE: RRI ; GGANISM: Pseudomonas aeruginosa US-09-252-991A-27150	Query Match Best Local Similarity 100.0%; Pred. No. 1.1 Matches 6; Conservative 0; Mismatches Oy 1 LDWSYL 6 Db 486 LDWSYL 491	RESULT 2 US-09-134-001C-4300 ; Sequence 4300, Application US/09134001C ; Patent No. 6380370 ; GENERAL INFORMATION: ; APPLICANT: Lynn Doucette-Stamm et al ; TITLE OF INVENTION: BPIDERMIDIS POR DIAGNOSY; ; TITLE OF INVENTION: BPIDERMIDIS POR DIAGNOSY; ; PILE REFERENCE: GTC-007 ; CURRENT APPLICATION NUMBER: US/09/134,001C ; CURRENT FILING DATE: 1998-08-13 ; PRIOR FILING DATE: 1997-11-08 ; PRIOR APPLICATION NUMBER: US 60/055,779 ; PRIOR FILING DATE: 1997-08-14 ; NUMBER OF SEQ ID NOS: 5674 ; SEQ ID NO 4300 ; TYPE: PRT
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM protein - protein search, using sw model Run on: February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds (without alignments)		Total number of hits satisfying chosen parameters: 328717 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 00% Maximum Match 100%	first atents -6/ptc -6/ptc -6/ptc -6/ptc	o. is the number of results predicted by chanceater than or equal to the score of the resulderived by analysis of the total score distribs SUMMARIES Query	Score Match Length DB ID 36 100.0	8 31 86.1 745 2 UG-08-887-518-3 Sequence 3, Appli 19 31 86.1 745 2 UG-08-023-321-3 Sequence 3, Appli 10 31 86.1 745 2 UG-08-023-321-3 Sequence 4, Appli 11 31 86.1 745 2 UG-09-032-475-3 Sequence 4, Appli 11 31 86.1 745 2 UG-09-099-125A-4 Sequence 4, Appli 14 31 86.1 745 2 UG-09-099-125A-4 Sequence 4, Appli 14 31 86.1 745 3 UG-09-099-124A-4 Sequence 4, Appli 16 31 86.1 745 3 UG-09-099-124A-4 Sequence 4, Appli 17 31 86.1 745 3 UG-09-093-324-4 Sequence 6, Appli 17 31 86.1 745 3 UG-09-093-324-4 Sequence 2, Appli 18 31 86.1 745 3 UG-09-093-124A-4 Sequence 2, Appli 18 31 86.1 745 3 UG-09-093-124-4 Sequence 10, Appli 19 31 86.1 745 4 UG-09-109-84-9 Sequence 10, Appli 19 31 86.1 745 4 UG-09-109-98-4 Sequence 10, Appli 19 31 86.1 745 4 UG-09-109-98-4 Sequence 10, Appli 19 756 2 UG-09-88-758-3 Sequence 2, Appli 24 31 86.1 756 2 UG-09-083-321-4 Sequence 4, Appli 25 3 UG-09-083-321-4 Sequence 2, Appli 26 UG-09-083-321-4 Sequence 2, Appli 26 UG-09-083-321-4 Sequence 2, Appli 27 UG-09-083-321-4 Sequence 2, Appli 27 UG-09-083-321-4 Sequence 3, Appli 27 UG-09-083-321-4 Sequence 6, Appli 27 UG-09-083-321-4 Sequence 6, Appli 27 UG-09-083-321-4 Sequence 6, Appli 27 UG-09-083-321-4 Sequence 6, Appli 27 UG-09-083-321-4 Sequence 6, Appli 27 UG-09-083-321-4 Sequence 7, Appli 27 UG-09-083-321-4 Sequence 7, Appli 27 UG-09-083-321-4 Sequence 7, Appli 27 UG-09-083-321-4 Sequence 7, Appli 27 UG-09-083-321-4 Sequence 7, Appli 27 UG-09-083-321-4 Sequence 7, Appli 27 UG-09-09-09-09-09-09-09-09-09-09-09-09-09-

, Appli	, Appli	, Appli	, Appli	5, Appl	, Appli		', Appli	, Appli	6, Appl	123, App	121, App	397, App	, Appli	, Appli	8, Appl	, Appli	8, Appl
Sequence 2	Seguence 2	Sequence 2	Sequence 2	Sequence 1	Seguence 9	Sequence 2	Seguence 9	Seguence 4	Sequence 1	Sequence 1	Sequence 1	Sequence 3	Sequence 2	Sequence 4	Sequence 1	Sequence 4	Sequence 1
US-09-099-124A-2	US-09-032-476-2	US-08-890-854-2	US-09-023-324-2	US-09-168-629-15	US-08-910-820-9	US-09-109-986-2	US-09-844-908-9	US-09-868-758-4	US-07-756-250-16	US-09-417-197-123	US-09-417-197-121	US-08-936-165A-397	US-07-681-704A-2	US-08-640-906-4	US-08-640-906-18	US-09-395-936-4	US-09-395-936-18
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86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1	86.1	83.3	83.3	83.3	83.3	83.3	83.3
31	31	31	31	31	31	31	31	31	31	31	31	30	30	30	30	30	30
28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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NO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS GNOSTICS AND THERAPEUTICS
INO ACID SEQUENCES RELATING TO PSEUDOMONAS NOSTICS AND THERAPEUTICS
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0
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.. 1.1e+02;
ches 0; Indels
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 651;
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Pred. No. 4.3e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LI, Joachim J
APPLICANT: GAVIN, Kimberly
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...651
SEQUENCE DESCRIPTION: SEQ ID NO: 4902:
                                                                                                                                                                                                                                                                                                           ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STALL
COUNTY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"MUTTER: IBM PC compatible
""""" PC - DOS/MS - DOS
               REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN Ph. D., Richard Aron
RECISTRATION NUMBER: 36,627
                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.9%; Scor.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/08484105 Patent No. 5589341
                                                                                                  TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4902:
SEQUENCE CHARACTERISTICS:
LENGTH: 651 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STILLMAN, Bruce
BELL, Stephen P
KOBAVASHI, Ryuji
RINE, Jasper
FOSS, Margin
MCNALLY, Francis J
LAURENSON, Patricia
                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HERSKOWITZ, Ira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (415) 494-8771
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Best Local Similarity 100.
Matches 5; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 LDWSY 364
                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-107-532A-4902
                                                                                                                                                                                                                                                                                                                                  FEATURE:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                           Sequence 17139 Application US/09252991A
Sequence 17139 Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFREENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17139
LENGTH: 597
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                               Length 462;
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100.0%; Pred. No. 4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                      .1e+02;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                           Mismatches
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FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                               Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 100.(
Matches 5; Conservative
                                                           Query Match
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                             159 LDWSY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 DWSYL 157
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RESULT 7
US-08-596-985-2
; Sequence 2, Application US/08596985
; Patent No. 5736374
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TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein US-08-596-985-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: STILLMAN, Bruce
APPLICANT: STILLMAN, Bruce
APPLICANT: STILLMAN, Bruce
APPLICANT: ROBAYASHI, Ryuji
APPLICANT: ROBAYASHI, Ryuji
APPLICANT: ROBAYASHI, Ryuji
APPLICANT: ROBAYASHI, Ryuji
APPLICANT: HENSKOWITZ, Ira
APPLICANT: LAURENSON, Parricia
APPLICANT: LAURENSON, Parricia
APPLICANT: GAVIN, Kimberly
ITILE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES
MUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 9411-4191
COMPUTER FRANADIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.9%; Score 32; DB 1; Length 706; llarity 100.0%; Pred. No. 4.7e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                88.9%; Score 32; DB 1; Length 706; 100.0%; Pred. No. 4.7e+02; tive 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/08484106
Patent No. 5614618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
LENGTH: 706 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    706 amino acids
706 amino acida
                                                                                                                                Query Match 88.9
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-484-106-16
                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                          US-08-484-105-16
LENGTH:
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GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Berka, Randy M.
APPLICANT: Ward, Michael
APPLICANT: Ward, Michael
TITLE OF INVENTION: Increased Production of
TITLE OF INVENTION: Beta-galactosidase in Aspergillus oryzae
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc
STREET: 180 Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 911;
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SEGTWARE: PatentIn Release #1.0, Version #1.25
SCOTWARE: OS-FEB-1996
CLASSIFICATION NUMBER: US/08/596,985
FILING DATE: OS-FEB-1996
CLASSIFICATION NUMBER: 08/267,631
FILING DATE: 39-401.1994
ATTORNEY/AGENT INFORMATION:
NAME: HOFN, MATGARET A
REGISTRATION NUMBER: 33-401
REFERENCE/DOCKET NUMBER: 33-401
REFERENCE/DOCKET NUMBER: GC250
TELEPHONE: (415) 12-7536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 1; I
Pred. No. 6.1e+02;
0; Mismatches 1;
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Gaps
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Patent No. 5851812
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: ADDRESS: ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
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Patent No. 5854033
PAPLICANT: No. 5854033
APPLICANT: Rothe, Mike
APPLICANT: Nu, Lin
TITLE OF INVENTION:
NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
                                                                                                                        Query Match 86.1%; Score 31; DB 2; Length 745; Best Local Similarity 83.3%; Pred. No. 7.4e+02; Matches 5; Conservative 1; Mismatches 0; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NATA:

APPLICATION NUMBER: US/08/890,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 86.1%; Score 31; DB 2; Le
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 5; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-"
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 745 amino acids
            STRANDEDNESS: single
                                  TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                    738 LDWSWL 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||:|
738 LDWSWL 743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                           US-09-023-321-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-09-032-475-3
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APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSHS STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 31; DB 2; Length 745; Pred. No. 7.4e+02; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
ANAME: ATTORNEY/AGENT INFORMATION:
ANAME: ATTORNEY/AGENT INFORMATION:
ANAME: ATTORNEY/AGENT INFORMATION:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNET/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4341
TELEFAX: (415) 343-4341
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELEPHONE: (415) 343-4341
TELEPHONE: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-023-321-3
; Sequence 3, Application US/09023321
; Patent No. 5844073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 745 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             738 LDWSWL 743
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Sequence 4, Application US/09099124A

Patent No. 5939302

GENERAL INFORMATION:

APPLICANT: Goeddel, David V.

APPLICANT: Woronicz, John

TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

CITY: SAN FRANCISCO

STATE: 74104

COUNTRY: USA

ZIP: 94104

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/099,124A
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                                                                                                                                                                                                                                                                                                                                                         Length 745;
                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 2; Pred. No. 7.4e+02;

    Mismatches

NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 197-006-1
TELECAMUNICATION INFORMATION:
TELEPHONE: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
RICR APPLICATION DATA:
RAPPLICATION NUMBER: US/08/890,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: OSMAN, RICHARD A
RECISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 745 amino acids
amino acid
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Best Local Similarity 83.3°
                                                                                                                                                                                                                                                                                                                                                         Query Match 86.1
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   738 LDWSWL 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LDWSYL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LDWSYL 6
                                                                                                                                                                                                                                                                                                              US-09-099-125A-4
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| Patent No. 5916760
| GENERAL INFORMATION:
| APPLICANT: Goeddel, David V. |
| APPLICANT: Woronicz, John | TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods | NUMBER OF SEQUENCES: 4 |
| CORRESPONDENCE ADDRESS: | ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP | STREET: 268 BUSH STREET; SUITE 3200 | CITY: SAN FRANCISCO | STATE: CALIFORNIA | COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31; DB 2; Length 745;
Pred. No. 7.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.30
                          ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: USA ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,518
FILING DATE:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 797-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4341
TELEFAX: (415) 343-4341
TELEFAX: (415) 343-4341
TELEFAX: (415) 343-4341
TELEFAX: (415) 343-4341
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APPLICATION NUMBER: US/09/099,125A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.1%;
83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: peptide US-09-032-475-3
         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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738 LDWSWL 743
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                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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US-09-099-125A-4
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| Patent No. 6235512
| GENERAL INFORMATION:
| APPLICANT: Rothe, Mike
| APPLICANT: Rothe, Mike
| TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
| TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
| TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
| TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
| TITLE OF INVENTION: IKK- PROTEINS |
| ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
| STREET: 268 BUSH STREET, SUITE 3200
| CITY: SAN FRANCISCO
| STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                            APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
APPLICANT: Cao, Zhaodan
APPLICANT: Cao, Zhaodan
APPLICANT: Cacherine
TITLE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: SAB BUGH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALLFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB 3; Length 745
Pred. No. 7.48+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIPTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                             Sequence 4, Application US/09032476
Patent No. 6235492
GENERAL INFORMATION:
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TELEFAX: (415) 343-4342
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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MOLECULE TYPE: peptide
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738 LDWSWL 743
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738 LDWSWL 743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-08-890-854-4
                                                                                                             US-09-032-476-4
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Gaps
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Pred. No. 7.4e+02;
1; Mismatches 0; Indels
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/890,854
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: February 18, 2004, 14:41:51 Job time : 8.06579 secs
                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.1%;
                                                                                                                                                                                                                                                                                                (415) 343-4341
                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 343-4341
TELERAX: (415) 343-4341
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
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94104
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Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence Sequence

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OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
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APPLICANT: May, Michael J.
APPLICANT: Ghosh, Sankar
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-11TOP
CURRENT PPILICATION NUMBER: US/09/847,940B
CURRENT FILING DATE: (2001-05-02)
PRIOR: FILING DATE: (2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VOEY: 2.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 36; DB 10; Length 100.0%; Pred. No. 7e+05;
US-10-032-585-7639

US-10-369-493-15366

US-10-369-493-2523

US-10-213-990-30

US-10-080-943-2

US-09-847-9468-2

US-09-847-946A-33

US-09-847-946A-33

US-09-847-946A-38

US-09-847-946A-38

US-09-847-946A-35

US-09-847-946A-35

US-09-847-946A-35

US-09-847-946A-34

US-09-847-946A-34

US-09-847-946A-132

US-09-847-946A-132

US-09-847-946A-132

US-09-847-946A-132

US-09-847-946A-144

US-09-847-946A-144

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US-09-847-946A-144

US-09-847-946A-144

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US-09-847-946A-144

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US-09-847-946A-144

US-09-847-946A-145

US-09-847-946A-145
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US-09-847-946A-15
Sequence 15, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/09847940B Patent No. US20020156000A1 GENERAL INFORMATION:
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        Query Match
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Sequence 14, Appl
Sequence 14, Appl
Sequence 385, App
Sequence 385, App
Sequence 385, App
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed; and is derived by analysis of the total score distribution.
                                                                                                                                           February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds (without alignments) 75.239 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1
Sequence 4
Sequence 1
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(cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.ppp:*
(cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.ppp:*
(cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.ppp:*
(cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.ppp:*
(cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp:*
(cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp:*
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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. US-10-847-946A-14

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. US-09-974-879-385

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. US-09-918-683-385

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. US-09-918-683-385

. US-10-364-493-1378

. US-10-369-493-267

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. US-10-369-493-388
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published_Applications_AA:*
                                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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36
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Perfect score:
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Sequence 135,

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APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
TITLE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR PILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
                                                                                                                                                                                                                                                            , OTHER INFORMATION: Description of Artificial Sequence:NBD mutants US-09-847-940B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: NBD peptide
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Pred. No. 7e+05;
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; Publication No. US20030028003A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: 125 Human Secreted Proteins
; TILE REFRENCE: PS020P2
; CURRENT APPLICATION NUMBER: US/09/974,879
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/239,893
; PRIOR APPLICATION NUMBER: US 60/239,893
; PRIOR APPLICATION NUMBER: US 60/239,893
                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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CURRENT APPLICATION NUMBER: US/09/847,940B CURRENT FILING DATE: 2001-05-02 PRIOR APPLICATION NUMBER: 09/643,260 PRIOR FILING DATE: 2000-08-22 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.9%;
                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                 88.9%;
83.3%;
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
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Best Local Similarity
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US-09-974-879-385
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Sequence 432, Application US/10287274

Sequence 432, Application US/2030181408A1

Sequence 432, Application No. US20030181408A1

Sequence ADELICANT: FOREXATION:

APPLICANT: Oblien, Kari

APPLICANT: Oblien, Kari

TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETC

FILE REFERENCE: ELITRA.008DV1

CURRENT FILING DATE: 2002-10-31

PRIOR FILING DATE: 1999-11-09

PRIOR FILING DATE: 2000-11-09

PRIOR FILING DATE: 2000-11-09

PRIOR FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 469

SEQ ID NO 432

LENGTH: 98
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                       APPLICANT: Finder, Mark A
APPLICANT: Finder, Mark A
APPLICANT: Finder, Kathryn
APPLICANT: Hannig, Gerhard
ITILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
ITILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
ITILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide US-09-847-946A-15
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PEPLICANT: Ghosh, Sankar
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REPERENCE: PPI-117CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels
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Pred. No. 1.3e+02;
1; Mismatches 0; Indels
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Patent No. US20020156000A1
GENERAL INFORMATION:
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Best Local Similarity 83.3
Matches 5; Conservative
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67 IDWSYL 72
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US-10-287-274-432
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.9%; Score 32; DB 12; Length 27;
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TITLE OF INVENTION: 125 Human Secreted Proteins
FILE REFERENCE: PZ020P1
CURRENT APPLICATION UNMER: US/09/818,683
CURRENT FILING DATE: 2001-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Prec. ...
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                 EARLIER APPLICATION NUMBER: 60/064,908
EARLIER PILING DATE: 1997-11-07
EARLIER PILING DATE: 1997-11-07
EARLIER PILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,985
EARLIER APPLICATION NUMBER: 60/066,094
EARLIER APPLICATION NUMBER: 60/066,094
EARLIER APPLICATION NUMBER: 60/066,094
EARLIER APPLICATION NUMBER: 60/066,099
EARLIER PILING DATE: 1997-11-17
EARLIER APPLICATION NUMBER: 60/066,099
EARLIER APPLICATION NUMBER: 60/066,099
EARLIER APPLICATION NUMBER: 60/066,099
EARLIER APPLICATION NUMBER: 60/066,099
EARLIER PILING DATE: 1997-11-17
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EARLIER FILING DATE: 1997-11-17
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; Sequence 12565, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-305-736-385
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: 125 Human Secreted Proteins
FILE REFERENCE: P2020P1
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CURRENT PELING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: US/09/305,736
EARLIER APPLICATION NUMBER: PCT/US98/23435
EARLIER FILING DATE: 1998-11-04
EARLIER APPLICATION NUMBER: 60/064,911
EARLIER APPLICATION NUMBER: 60/064,912
EARLIER APPLICATION NUMBER: 60/064,903
EARLIER PILING DATE: 1997-11-07
EARLIER PELLING DATE: 1997-11-07
EARLIER PELLING DATE: 1997-11-07
EARLIER PELLING DATE: 1997-11-07
EARLIER PELLING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,908
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              PRIOR APPLICATION NUMBER: US 09/305,736
PRIOR APPLICATION NUMBER: US 06/064,911
PRIOR PILING DATE: 1999-05-05
PRIOR PLING DATE: 1999-11-04
PRIOR PILING DATE: 1997-11-07
PRIOR PPLICATION NUMBER: US 60/064,912
PRIOR PELING DATE: 1997-11-07
PRIOR PELING DATE: 1997-11-07
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PRIOR PELING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,984
PRIOR PELING DATE: 1997-11-07
PRIOR PELING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/066,094
PRIOR PELING DATE: 1997-11-17
PRIOR PELING DATE: 1997-11-17
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2001-03-28
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Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Homo sapiens
US-09-974-879-385
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Sequence 267, Application US/10369493

Sequence 267, Application Wo. 10320030233675A1

GENERAL INFORMATION:
APPLICANT: Goo, Yongei
APPLICANT: Glodman, Barry S.
APPLICANT: Glodman, Barry S.
APPLICANT: Glodman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: BARRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: BARRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: BARRESSION OF MICROBIAL PROPERTIES
CURRENT APPLICATION NUMBER: US 40/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PRILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 267
LEMANT. F.
                                                                                                                                                                                      Gaps
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                                                                                                                                Length 412;
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                                                                                                                             88.9%; Score 32; DB 12; Length 41 100.0%; Pred. No. 9.7e+02; tive 0; Mismatches 0; Indels
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APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OP INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
SPRIOR FILING DATE: 2001-06-3
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8567
                                                  ; OTHER INFORMATION: Orthologous to G1062
US-10-374-780A-1378
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8567, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Xenorhabdus nematophilus
US-10-369-493-267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                     Query Match
Best Local Similarity 100.vv
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ORGANISM: Oryza sativa
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Best Local Similarity
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US-10-156-761-8567
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APPLICANT: Dubell III, Arnold T
APPLICANT: Pineda, Omaira
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 12; Length 376; 9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
  TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure

: LOCATION: (1)..(376)

: OTHER INFORMATION: unsure at all Xaa locations

US-10-399-493-12565
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CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US/10/374,780A
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR PILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-11-19
PRIOR PPLICATION NUMBER: 60/336,049
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-12-11
PRIOR PPLICATION NUMBER: 60/336,692
PRIOR PILING DATE: 2001-12-11
PRIOR PPLICATION NUMBER: 10/171,468
PRIOR PPLICATION NUMBER: 10/171,468
PRIOR PPLING DATE: 2002-06-14
PRIOR PPLING DATE: 2002-06-09
PRIOR PPLING DATE: 2002-08-09
PRIOR PFLING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                  FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
FRICK APPLICATION NUMBER: US 60/360,039
FRICK FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12565
TENGTH: 376
TYPE: PRT
ORGANISM: Aspergillus nidulans
                                                                                                                                                                                                                                                                                                                                                                                                                                            88.9%; Score 32; 100.0%; Pred. No.
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GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
APPLICANT: Ricchmann, Jose Luis
APPLICANT: Hack, Jacqueline B
APPLICANT: Heard, Jacqueline B
APPLICANT: Heard, Jacqueline B
APPLICANT: Heard, Jacqueline B
APPLICANT: Ratcliffe, Oliver
APPLICANT: Ratcliffe, Oliver
APPLICANT: Reuber, T. Lynne
APPLICANT: Reuber, T. Lynne
APPLICANT: Reddie, James
APPLICANT: Reddie, James
APPLICANT: Reddie, James
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Best Local Similarity 100.
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117 DWSYL 121

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APPLICANT: CALSACTORY (ALCAL)
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramimoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Brokaryotes
TITLE OF INVENTION: BLITRA.011A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/291,078
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
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PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-12
PRIOR SPELING DATE: 2001-12-12
PRIOR SPELING DATE: 2001-12-14
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2001-12-14
PRIOR PELING DATE: 2001-12-14
PRIOR PERSON PRIOR PERSON FOR PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PERSON PRIOR PER
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                                                                                                                                                                                                                                                              Sequence 12101, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Obleen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yumamoto, Robert T.
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ORGANISM: Pseudomonas aeruginosa
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US-09-815-242-12101
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US.10-369-493-13768

Sequence 13768, Application US/10369493

Sequence 13768, Application US/10369493

Sequence 13768, Application US/10369493

Sequence 13768, Application No. US.2030233675A1

SEQUENCE INFORMATION:

APPLICANT: Gare, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Applicant S.

APPLICANT: Barry S.

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APPLICANT
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                                                 88.9%; Score 32; DB 12; Length 525; 100.0%; Pred. No. 1.2e+03; ive 0; Mismatches 0; Indels
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Query Match
Best Local Similarity 100.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Mutated IXKbeta NE	NBD mutant peptide	Human NEMO binding	Human IKKbeta muta	E. coli growth and	Micromonospora eve	Mutated IXKbeta NE	NBD mutant peptide	Human NEMO binding
SUMMARIES	ID	ABB08737	AAM48520	ABU08430	ABB77301	AAG98962	AAU04899	ABB08736	AAM48519	ABU08429
	DB	23	23	24	23	22	22	23	23	24
	Query Match Length DB	9	9	9	756	96	193	9	Q	9
de	Query Match	100.0	100.0	100.0	100.0	94.4	91.7	88.9	88.9	88.9
	Score	36	36	36	36	34	33	32	32	32
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08-NOV-2001

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ALIGNMENTS

ABB08737 standard; peptide; 6 AA.

RESULT 1 ABB08737 ABB08737;

Kinase activation; leukocyte; inflammation; B-selectin; osteoclast; autoimmune disease; transplant rejection; osteoporosis; cancer; autoimmune disease; transplant rejection; osteoporosis; cancer; statatistical infection; asthma; anaphylaxis; psoriasis; rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; antiinflammatory; immunosuppressive; osteopathic; cytostatic; noctropic; neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antiasthmatic; antiallergic; dermacological; antibacterial; antibactatic; antitheumatic; antiathritic; osteopathic; antiulcer; mutant; mutein. IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB; Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 15. /note= "Wildtype Trp substituted by Tyr" Location/Qualifiers (first entry) Misc-difference Homo sapiens 14-JUN-2002 Synthetic. N

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antirheumatic; antiarthritic; oeteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NRkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriaals; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                       Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Page 48; 88pp; English.
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                                                                                                                                                                                                                                                                                                                              02-MAY-2001; 2001WO-US14346.
                                                                                                                                                                                                                                                                                                                                                                                                                           (PRAE-) PRAECIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-121889/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ghosh S,
                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                     WO200183554-A2.
                                                                                                                                                                                                                                                                                        08-NOV-2001.
                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    May MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU08430
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                                                                                                                                                                                                                                                                                                                                  The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB08725-ABB08725) comprising at least one NEWO binding domain (ABB77313). The compound has acts through selective inhibition of cytokine-mediated NF-kB activation by blocking the interaction of NEMO interaction results in inhibition of IKCheta kinase activation and subsequent decreased phosphorylation of IKCheta kinase activation and subsequent decreased phosphorylation of IKCheta kinase activation and subsequent decreased phosphorylation of IKCheta kinase activation and cat (directly or indirectly) by blocking the recruitment of leukocytes into sites of acute and chronic inflammation, by down-regulating the expression of E-selectin on leukocytes or by blocking osteoclast differentiation. The compound is useful in treating NF-kB mediated conditions, where the condition is an inflammatory disorder, an autoimmune disease, transplant rejection, osteoporosis, cancer, Alzheiner's disease, atherosoclerosis, a viral infection or ataxia telanglectasia. The inflammatory disorder is asthma, allergies, urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis, changementials, osteoarthritis, psoriatic arthritis, lupus and bursitis. The inflammatory disorder may also be dermatitis, esteroatrhitis, psoriatic arthritis, lupus and spondylarthritis Also for Crohn's disease, ulcerative colitis, polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis, cryolobulinamenia or multiple sclerosis. For chronic viral infections caused by Epstein-barr, cytomegalovirus or herpes simplex. Other diseases include HIV and influenza. The compound may also be useful for sunburn or aging. The compound way be used to replace corticosteroids in which corticosteroids are used, including inflammatory compounds and food sensitivity. Also for identifying any application in which corticosteroids are used, included in which corticosteroids are used, included in which corticosteroids are used.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiinflammatory compounds and for diagnosis of an inflammatory disorder. The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of a mutated NEMO binding domain of IKKOeta.
                                                                                                                                                                                                           Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting a cell with an anti-inflammatory compound comprising at least one NEMO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                          Claim 23; Page 45; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM48520 standard; Peptide; 6 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NBD mutant peptide SEQ ID NO 15.
02-MAY-2001; 2001WO-US40654.
                                     02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
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                                                                                                                                                                        WPI; 2002-179350/23.
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Best Local Similarity
Matches 6; Conserv
                                                                                             (UYYA ) UNIV YALE.
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                                                                                                                                    May MJ, Ghosh S;
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AMM48620-AMM48645), comprising a membrane translocation domain (AAM48620-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627) or AAM48651 which comprises from 6-15 amino acid residues, fueed to a NEWO binding sequence correction, antiposoriatic, antitheumatic, antiarthritic, osteopathic, cartiposoriatic, antirheumatic, antiarthritic, osteopathic, cartiposoriatic, antirheumatic, antiarthritic, osteopathic, noctropic, antiatherosoleroric, virucide and antiallergic activity. The compounds act as selective inhibitors of Cytokine-mediated NFkappaB comparation by blocking interaction of IkappaB kinase beta (IKKObeta) at the NEWO binding domain that results in inhibition of IKKOpeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory discretery discretery, seteoarthritis, inflammatory bowel disease, sepsis, vasculitis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, caranulomatosis, authorosclerosis, transplant rejection; osteoporosis; telangiectasia. The compounds are also useful for treating
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The invention relates to an antiinflammatory compound (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pro-inflammatory responees such as allergies, urticaria, anaphylidrug or food sensitivity, eczema, dermatitis, sunburn, aging and
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100.0%; Pred. No. 9.3e+05;
ive 0; Mismatches 0;
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Best Local Similarity
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Human IKKbeta mutant W741Y. 14-JUN-2002 (first entry)

ABB77301;

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NEWO binding domain (NBD) peptides. The NEWO binding domains are found on IkappaB kinase-beta (IKKDeta) and IkappaB kinase-alpha found on IkappaB kinase-beta (IKKDeta) and IkappaB kinase-alpha are useful for modularing nuclear factor-kappaB (NF-kappaB) induction in a cell, where the compounds are capable of blocking the interaction between one or more IKKs such as IKKapha or IKKDeta, and NEMO. The antiinflammatory compound further comprises at least one membrane translocation domain. The compounds are useful for treating hiflammatory disorders, autoimmune diseases, osteoporosis, cancer, Alzheimer's disease, atterosclerosis, viral infections. Attain telangiectasia, and for transplantation detection. The compounds of the invention block NF-kappaB induction by IKK but do not inhibit the basel activity of NF-kappaB. ABU08418-ABU08432 represent human
                                                                                                                         Human; antinfiammatory compound; NEMO binding domain; NBD; IKKbeta; IkappaB kinase-alpha; IKKalpha; NF-kappaB; IkkappaB kinase-alpha; IKKalpha; NF-kappaB; nuclear factor-kappaB induction; inflammatory disorder; autoimmune disease; osteoporosis; cancer; Alzheimer's disease; atherosclerosis; viral infection; Ataxia telangiectasia; transplantation detecrion; immunosuppressive, osteopabhic; cytostatic; nootropic; neuroprotective; antiatherosclerotic; virucide; vasotropic; antirheumatic; antiatheritic; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to antiinflammatory compounds comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel antiinflammatory peptide compounds comprising NEMO binding domain, useful for modulating NF-kappaB induction in a cell and for treating NF-kappaB-mediated inflammation disorders e.g., asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 36; DB 24; Length 6; 100.0%; Pred. No. 9.3e+05;
                                                                                         Human NEMO binding site (NBD) mutant peptide #13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 22; Page 17; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAY-2001; 2001US-0847940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-209142/20.
N-PSDB; ABX94271, ABX94272.
                                                     12-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   psoriasis, vasculitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NBD mutant peptides.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ghosh S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MAYM/) MAY M J. (GHOS/) GHOSH S.
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                                                                                                                                                                                                                                                                                                                                                               US2002156000-A1
                                                                                                                                                                                                                                                                                                        sapiens.
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                                                                                                                                                                                                                                                                                                                           Synthetic
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                 ABU08430;
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The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound comprises contacting a cell with an anti-inflammatory compound (ABB077313). The compound has acts through selective inhibition of KAB077313). The compound has acts through selective inhibition of KAB077313. The compound has acts through selective inhibition of NEMO interaction results in inhibition of IKKDeta kinase activation and subsequent decreased phosphorylation of IKRDeta kinase activation and subsequent decreased phosphorylation of IKRDeta kinase activation and subsequent decreased phosphorylation of IKRDeta kinase activation and chronic inflammation, by down-regulating the expression of E-selection on leukocytes or by blocking osteoclast differentiation. The compound is useful in treating NF-kB mediated conditions, where the condition is an inflammatory disorder, and autoimmune disease, transplant rejection, osteoporosis, cancer, although architis, osteoarthritis, psoriatic arthritis, psoriatis, and arthritis, psoriatis, and arteritis, inflammatory disease, ulcerative colitis, psoriatis, and arteritis, psoriatis, and sporylation arteritis, psoriatis, and sporylation arteritis, psoriatis are propound and perges almplex. Other viral infections caused by Epstein-barr, cytomegalovirus or herpes aimplex. Other viral diseases include HIV and influenza. The compound may also be useful for
                                                                                                                                                                       kinase activation; leukocyte; inflammation; B-selectin; osteoclast; autoimmune disease; transplant rejection; osteoporosis; cancer; Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis; rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; antiinflammatory; immunosuppression; osteopathic; cytostatic; noctropic; neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antiasthmatic; antiallergic; dermatological; antibacterial; antisoxiatic; antirheumatic; antialtarthritic; osteopathic; antiulcer; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modulating NP-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting cell with an anti-inflammatory compound comprising at least one NEMO
                                                                                                                                                    IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Wildtype Trp substituted by Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 11; Page -; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-2001; 2001WO-US40654.
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22-AUG-2000; 2000US-0643260.
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Synthetic.
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Gaps

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Indels

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Mismatches

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6; Conservative

Matches

1 LDWSYL

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ABB77301 standard; protein; 756 AA.

ABB77301 ID ABB7 RESULT 4

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AAH84373 to AAH84499 represent Escherichia coli growth and proliferation related DNA sequences (I). AAH84500 to AAH84670 encode the E. coli growth and proliferation related proteins given in AAG9908 and AAG98830 to AAG98999. (I) can be used as potential targets for the generation of interact with the gene products of (I). In addition the expression of interact with the gene products of (I). In addition the expression of (I) and the purification of the proteins, the purified proteins can be used to generate reagents and screen small molecule libraries or other candidate compound libraries for compounds that can be further developed to yield novel antimicrobial compounds. In addition, nucleic acid probes complementary to (I) that are specific for particular species of microorganisms can be used to identify particular microorganism species (in clinical speciens), therefore, providing a rapid and dependable method by which to identify the causative agents of a bacterial infection. Also, antibodies generated against proteins translated from
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treating anaphylaxis, drug and food sensitivity, contact dermatitis, sunburn or aging. The compound may be used to replace corticosteroids in any application in which corticosteroids are used, including immunosuppression in transplants and cancer therapy. Also for identifying antiinflammatory compounds and for diagnosis of an inflammatory disorder. The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of an IKKbeta mutant, useful in examples of the invention.

Note: The present sequence is not given in the specification but is derived from GenBank Accession No. 014920 (ABB77294).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E. coli growth and proliferation related protein sequence SEQ ID NO:432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids that inhibit Escherichia coli proliferation, useful for screening for homologous genes and for designing expression vectors
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli, growth, proliferation, microbial, antimicrobial, bacterial infection, microorganism.
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                                                                                                                                                                                                                                                                            100.0%; Score 36; DB 23; Length 756; 100.0%; Pred. No. 2.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG98962 standard; Protein; 98 AA
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                                                                                                                                                                                                                                                                                                                       6; Conservative
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N-PSDB; AAH84633.
                                                                                                                                                                                                                                                                                                                                                                                                     737 LDWSYL 742
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                     756 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli
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mRNA transcribed from proliferation-required sequences can also be use to screen for specific microorganisms that produce such proteins in a species specific manner. AAH84371 and AAH84670 represent sequencing primers used in the isolation of B. coli growth and proliferation related sequence, which are used in an example from the present
                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                              22; Length 98;
                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Micromonospora everninomicin biosynthetic enzyme evrMR2.
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                                                                                                                                                                                                                                                              Score 34; DB
Pred. No. 67;
                                                                                                                                                                                                                                                                                                                  1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU04899 standard; Protein; 193 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is a protein, evrMR2,
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                                                                                                                                                                                                                                                              94.4%;
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                                                                                                                                                                                                                                                                                     Best Local Similarity
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67 IDWSYL 72
                                                                                                                                                                                                                                                                                                                                                                             1 LDWSYL 6
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                                                                                                                                                       invention
                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                 Query Match
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AAU04899
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integrative vector can be used to permanently integrate copies of a heterologous game of choice into chromosomes of different hosts and to integrate genes which increase the yield of known products or to generate novel products such as hybrid antibiotics or other novel secondary metabolites. The vector can also be used to integrate antibiotic resistance genes in order to carry out biconversions with compounds to which the strain is normally sensitive and is thus useful in fermentation processes involving e.g. Streptomyces antibioticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB08725-ABB08742) comprising at least one NEMO binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB; kinase activation; leukocyte; inflammation; E-selectin; osteoclast; autoimmune disease; transplant rejection; osteoprosas; cancer; Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis; rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; antiinflammatory; immunosuppressive; osteopathic; cytosteatic; nootropic, neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antiasthmatic; antiallergic; dermatological; antibacterial; antiboriatic; antiallergic; antialregic; antialregic; antiatrhritic; osteopathic; antiulcer; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting cell with an anti-inflammatory compound comprising at least one NEMO
                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                 DB 22; Length 193;
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-haa 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Wildtype Trp substituted by Phe"
                                                                                                                                                                                                Score 33; DB 2
Pred. No. 2e+02
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                          ABB08736 standard; peptide; 6 AA.
                                                                                                                                                                                              91.7%;
83.3%;
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                                                                                                                                                                                                                                5; Conservative
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                                                                                                                                                                                                                                                                                                    139 LDWAYL 144
                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                           193 AA;
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Synthetic.
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                                                                                                                                                             Sequence
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CC (ABB77113). The compound has acts through selective inhibition of cytokine-mediated NF-kB activation by blocking the interaction of NEMO with INKROEta at the NEMO binding domain. Blockage of INKROETA-NEMO interaction results in inhibition of INKAGETA kinase activation and subsequent decreased phosphorylation of INKAGETA kinase activation and cube (directly or indirectly) by blocking the recruitment of leukocytes are into sites of acute and chronic inflammation, by down-regulating the expression of E-selectin on leukocytes or by blocking osteoclast differentiation. The compound is useful in treating NF-kB mediated conditions, where the condition is an inflammatory disorder, an autoimmune disease, transplant rejection, osteoporosis, cancer, allocimacio atthritis, conditions, an inflammatory disorder, and autoimmune disease, atherosclerosis, a viral infection or ataxia telangiectasia. The inflammatory disorder is asthma, allergies, conditional anaphylaxis, cuteneous inflammatory disease, rethritis, osteoarthritis, osteoarthritis, posteoarthritis, posteoarthritis, posteoarthritis, posteoarthritis, inflammatory disorder may also be dermatitie, eczema, posteoarthritis, socieoarthritis, posteoarthritis, posteoarthritis, undisorder may also be dermatitie, eczema, posteoarthritis, socieoarthritis, posteoarthritis, posteoarthritis, socieoarthritis, so
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.9%; Score 32; DB 23; Length 6; 83.3%; Pred. No. 9.3e+05; ive 1; Mismatches 0; Indels
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2000US-0643260.
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Best Local Similarity 83.33,
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22-AUG-2000;
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The present invention relates to antiinflammatory compounds comprising NEMO binding domain (NBD) peptides. The NEMO binding domains are found on IkappaB kinase-beta (IKKDeta) and IkappaB kinase-alpha (IKKAlpha) proteins. The antiinflammatory compounds of the invention are useful for modulating nuclear factor-kappaB (NF-kappaB) induction in a cell, where the compounds are capable of blocking the interaction between one or more IKKS such as IKKalpha or IKKDeta, and NEMO. The
                                                                                                                                                                                                                                                                                                        Novel antiinflammatory peptide compounds comprising NEMO binding domain, useful for modulating NF-kappaB induction in a cell and for treating NF-kappaB-mediated inflammation disorders e.g., asthma, psoriasis, vasculitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiinflammatory compound further comprises at least one membrane translocation domain. The compounds are useful for treating inflammatory disorders, autoimmune diseases, osteoporosis, cancer, Alzheimer's disease, atherosclerosis, viral infections, Ataxia telangiectasis, and for transplantation detection. The compounds of the invention block NF-kappaB induction by IKK but do not inhibit the basal activity of NF-kappaB. ABU08418-ABU08432 represent human NBD mutant peptides.
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Pred. No. 9.3e+05;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 22; Page 17; 47pp; English.
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23-AUG-2000; 2000US-0649167.
                                            02-MAY-2001; 2001US-0847940.
                                                                                        02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
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                                                                                                                                                                                                                                   Ghosh S;
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                                                                                                                                                            (MAYM/) MAY M J. (GHOS/) GHOSH S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 AA;
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24-OCT-2002.
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                                                                                                                                                                                Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; antiinflammatory compound; NEMO binding domain; NBD; IXXbeta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              irug or food sensitivity, eczema, dermatītis, sunburn, aging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32, DB 23, Length 6;
Pred. No. 9.3e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human NEMO binding site (NBD) mutant peptide #12
                                                                                        Phillips K;
                                                                                                                                                                                                                                                                                                     Example 6; Page 48; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU08429 standard; peptide; 6 AA.
                                                                                        Findeis MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 88.9%;
Similarity 83.3%;
5; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                   (PRAE-) PRAECIS PHARM INC
                                                                                                                                    WPI; 2002-121889/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                        Ghosh S,
                                            (UYYA ) UNIV YALE.
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LDWSFL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2002156000-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arthritis.
                                                                                                                                                                                                                                                            psoriasis
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Matches

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Length 6; 0; Indels

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320 AA;
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                       N-PSDB; AAS91841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9824475-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY11025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and gene mapping, and in recombinant production of (II). The careful as also used in diagnostics as expressed sequence tags to restore normal activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of stress expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences or other invention.

Cand to produce other types of the invention can be be printed diagnostic amino acid sequences of the invention but was obtained in electronic format directly from WIPO can every second or sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.9%; Score 32; DB 22; Length 320;
100.0%; Pred. No. 5.1e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                  Claim 20; SEQ ID No 43875; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human diagnostic protein #27645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG27654 standard; Protein; 320 AA.
           Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT, Liu C,
          Drmanac RT, Liu C,
                                  WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 DWSYL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                     320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 DWSYL 6
                                               N-PSDB; AAS77703
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                                                                                                          biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaccino (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving a polymetric for in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in disorders of generate disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human can appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                      New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.9%; Score 32; DB 22; Length 320; 100.0%; Pred. No. 5.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccine, probe, diagnostic, ORF, cell envelope protein, secreted protein, cytoplasmic protein, cellular protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 58013; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kabok
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY11025 standard; Protein; 393 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Doig PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US22104.
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97US-0823745.
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Query Match
Best Local Similarity 100.00
Them 5; Conservative
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WPI; 2001-639362/73
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                                                                                                                                          Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 97 ORFs are shown. The proteins are variously cell envelope proteins, cytoplasmic proteins, secreted proteins or other cellular proteins, vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a new Helicobacter pylori bacterium having a mutation that affects lipopolysaccharide (LPS) biosynthesis, where either LPS is not expressed or LPS which is expressed does not induce antibodies which cross-react with human self epitopes. The invention is useful for treating or preventing, and in the manufacture of a vaccine for treatment or prophylaxis of Helicobacter pylori
                                products for the diagnosis, prevention and treatment of infection by H. pylori and other Helicobacter species
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori LPS biosynthesis enzyme HP1031 from strain J99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel Helicobacter pylori useful for prophylaxis and treatment of Helicobacter pylori infection, comprises mutation that prevents synthesis of auto-reactive lipopolysaccharide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPS; lipopolysaccharide; biosynthesis enzyme; HP1031; strain J99; antibiotic; vaccine; human self epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                    Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                    88.9%; Score 32; DB 19; I 100.0%; Pred. No. 6.4e+02;
                                                                                                                Claims 37, 41; Page 187-188; 339pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU76667 standard; Protein; 393 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                    Larity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Del Giudice G, Rappuoli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-217026/27.
WPI; 1998-333051/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 DWSYL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 DWSYL 288
                                                                                                                                                                                                                                                                                                                                                   393 AA;
               N-PSDB; AAX30554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200207763-A2
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                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches
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(II) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the s. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides (II) (and/or nucleic acids) may then be polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent objectide sequences from the present invention. AAH55091 to AAH55091 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4472,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
infection. The vaccine does not induce antibodies which cross-react with human self epitopes. The present amino acid sequence repersents the Helicobacter pylori LPS biosynthesis enzyme HP1031 that was isolated from strain J99 and was used in the methods of the invention.
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -

    S. epidermidis open reading frame protein sequence SEQ ID NO:2648.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis SR1 strain; infection; diagnosis;
                                                                                                                                                 Ouery Match 88.9%; Score 32; DB 23; Length 393; Best Local Similarity 100.0%; Pred. No. 6.4e+02; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 18; Page 694-695; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             AAG82777 standard; Protein; 455 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-SEP-2001 (first entry)
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                                                                                                                                                                                                                                                                                   DWSYL 288
                                                                                                             393 AA;
                                                                                                                                                                                                                                         2 DWSYL 6
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                                                                                                                                                                                                                                                                                   284
                                                                                                                Sequence
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NB. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.
                                                                                                                                                                                                                                                                                                Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                  Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4300.
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   Length 455;
                                Indels
 DB 22; L
Query Match 88.9%; Score 32; DB Best Local Similarity 100.0%; Pred. No. 7.4 Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID 4300; 267pp; English.
                                                                                                                                                                        ABP39455 standard; Protein; 462 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0134001.
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97US-064964P.
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                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis.
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Best Local Similarity 10v..
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N-PSDB; ABN92000.
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08-NOV-1997;
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Search completed: February 18, 2004, 14:26:25 Job time : 22.7763 secs

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	23	32	91.4	927	16	Q8Y4S2	
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(without alignments)	25	. 35	91.4	1466	m	042930	
89.145 Million cell updates/sec	56	31	88.6	124	11	090247	
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Scoring table: BLOSUM62	32	31	98.6	134	12	072708	
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	34	31	98.6	134	12	Q99DR2	
Searched: 830525 segs, 258052604 residues	35	31	98.6	134	12	08V019	
	36	31	98.6	134	12	Q993Y9	
Total number of hits satisfying chosen parameters: 830525	37	31	98.6	134	12	098742	
	38	31	98.6	134	12	087216	
Minimum DB seq length: 0	39	31	98.6	134	12	QBJLLO	
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	41	31	98.6	134		Q91BQ2	
Post-processing: Minimum Match 0%	42	31	98.6	134	12	Q8V012	
Maximum Match 100%	43	31	98.6	134		Q91GX4	
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ALIGNMENTS

Database :

SPTREMBL 23:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_lungi:*
4: sp_lunman:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_lunc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_lunclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P72919 synechocyst	O44634 caenorhabdi	Q8yxb1 anabaena sp	Q91mz3 arabidopsis	Q9sge4 arabidopsis	Q8e014 streptococc	Q8e659 streptococc	Q8dc15 vibrio vuln	Q9vxs9 drosophila	O61565 crassostrea	Q9svs7 arabidopsis	O44486 caenorhabdi	Q98ga7 rhizobium l	Q8udw9 agrobacteri	O86850 streptomyce	Q9rks7 streptomyce
SUMMARIES	ID	; P72919	044634	G9YXB1	O9LMZ3	09SGE4	GBE014	. Q8E659	; Q8DC15	65XA6O	061565	09SVS7			6MQD8Q :	086850	G9RKS7
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Description	P72919 synechocyst	044634 caenorhabdi	Q8yxb1 anabaena sp	Q9Imz3 arabidopsis	Q9sge4 arabidopsis	Q8e0i4 streptococc			Q9vxs9 drosophila	O61565 crassostrea	Q9svs7 arabidopsis	044486 caenorhabdi	Q98ga7 rhizobium l	Q8udw9 agrobacteri	O86850 streptomyce	Q9rks7 streptomyce	
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RESULT 044634

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Pfam; PF01740; STAS; 1.
Pfam; PF00916; Sulfate_transp; 1.
PROSITE; PS50801; STAS; 1.
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Best Local Similarity 10v...
6; Conservative
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                                                                             573 AA;
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                                                         Complete proteome. SEQUENCE 573 AA;
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SEQUENCE FROM N.A.
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Q9LMZ3;
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                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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MEDLINE=21595285; PubMed=11759840;

Anneko T., Nakamura Y., Wollk C.P., Kuritz T., Sasamoto S.,

Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,

Makazaki N., Shimpo S., Sugimoto M., Matsumo A., Muraki A.,

Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

Yasuda M., Tabata S.; Sugimoto M., Takazawa M., Yamada M.,

"Complere genomic sequence of the filamentous nitrogen-fixing

"Tomplere genomic sequence of the filamentous nitrogen nitrogen nitrogen nitrogen nitrogen nitrogen nitrogen nitrogen nitrogen nitrogen nitrogen nitrogen nitrogen nitrogen nitrogen nitrogen nitrogen nitrogen nitrogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
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                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Bristol N2;
Davidson S., Wohldmann P., Bauer C., O'Neal D.;
"The sequence of C. elegans cosmid F16B4.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF039048; AAB94233.1; -.
WormPep; F16B4.2; CE17012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 362 AA; 42255 MW; 33D99EF0FD114006 CRC64;
                                01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 42.3 kDa protein.
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Last annotation update)
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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MEDLINE=99069613; PubMed=9851916;
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Ol-MAR-2002 (TrEMBLrel. 20, Last
01-MAR-2003 (TrEMBLrel. 23, Last
Sulfate permease family protein.
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Pfam; PF00646; F-box; 1.
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 PRELIMINARY;
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                                                                                                                               Caenorhabditis elegans.
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"Direct Submission.";
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                     044634;
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Matches
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EMBL, ACO260315, ARPT9832.1; -.

InterPro; IRR006153; Na H. Dorter.

Pfam; PF00999; Na H. Exchanger; 1.

SEQUENCE 2621 AA; 297067 WW; E3534E176F2370A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
Kkim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
Lenz C., Li J., Liu R., Liu K., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., K., Southwick A., Thaveri A.,
Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                               Gaps
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                                                                       Length 573;
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
60239 MW; F2D1C2F66A8E36CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                100.0%; Score 35; DB 16;
100.0%; Pred. No. 2.1e+02;
vative 0; Mismatches 0;
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100.0%; Pred. No. 9.3e+02;
rative 0; Mismatches 0;
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Gaps

Q9SGE4;

O9SGE4

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STRAIN-NEW316 / Serotype III;
MEDLINE=22245168; WibMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Maadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of Streptococcus agalactiae, a pathogen causing invasive neonatal disease.";
MOI. Microbiol. 45:1499-1513(2002).

EMBL; AL766847; CAD46412.1; --
SagaList; gbs0768; --
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Vibrionaceae; Vibrio.
NCBL_TaxID=672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.3%; Score 33; DB 16; Length 216;
83.3%; Pred. No. 1.8e+02;
ive 1; Mismatches 0; Indels
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                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus agalactiae (serotype III).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein, Complete proteome.
SEQUENCE 216 AA; 23587 MW; E55556D5F751CEEF CRC64;
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Last sequence update)
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Last annotation update)
Pred. No. 1.8e+02;
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                                      1; Mismatches
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                  83.3%;
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                                        5; Conservative
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Matches 5; Conservative
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198 MDWSFL 203
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                  Best Local Similarity
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SEQUENCE 556 AA;
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MEDLINE-22222989; PubMed=12200547;

MEDLINE-22222989; PubMed=12200547;

MedSels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,

MedOff L.C., Wolf A.M., Beanan M.O., Brinkac L.M., Daugherty S.C.,

DeBOY R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,

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Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,

Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,

Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Shinn P., Brooks S., Buehler B., Chao Q., Johnson-Hopson C., Khan S.,
Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genomic sequence for Arabidopsis thaliana BAC T23G18 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 35; DB 10; Length 2658; 100.0%; Pred. No. 9.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC011438; AAF18257.1; -.
InterPror; IFR006153; Na H.porter.
Pfam; PF00999; Na H.Exchanger; 1.
SEQUENCE 2658 AA; 301830 MW; 77ECF93667B4293F CRC64;
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Bacteria, Firmicutes, Lactobacillales; Streptococcaceae;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Riboflavin synthase, alpha subunit.
RIBE OR SAG0747.
                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
T23G18.2
                                      PRT; 2658 AA
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                                      PRELIMINARY;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Radams M.D., Celniker S.E., Holt R.A., Fabburner M., Henderson S.N.,

Radams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutcon G.G., Worten J.K., Yandell M.D., Zhang Q., Chen L.X.,

Radion R.G., Morgers Y.-H.C., Blazej R.G., Chang C.R., Miklos G.L.G.,

Radilaw R.M., Basu A., Baxendale J., Bayraktargolu L., Beasley B.M.,

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Radilaw R.W., Banos P.V., Berman B.P., Bhandari D., Bolahakov S.,

Radilaw R.M., Cawley S., Dallike C., Davenport L.B., Davies P.,

Burtis K.C., Busam D.A., Butler H., Cadleu B., Center A., Chandra I.,

Radion R.J., Cawley S., Dallike C., Davenport L.B., Davies P.,

A berloss B., Delcher A., Deng Z., Mays A.D., Dev I.D., Dietz S.M.,

Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Pleischmann W.,

RAD Belbloss B., Delcher A., Howland T.J., Mernahdez J.R., Houck J.,

A dock A., Gong F., Gorrell J.H., Gu Z., Gebart W.M., Glasser K.,

A doldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RAD Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

Jalali M., Kalush F., Kalpen G.H., Ke Z., Kunison J.A., Ketchum K.A.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., Dri V., Rese M.G.,

RAD Mount S.M., Moy W., Murphy B., Murphy L., Murny D.M., Nelson D.L.,

Rad Reinert K., Remington K., Sunger R.D.C., Scheeler F., Shen H.,

Shue B.C., Siden-Kamos I., Simpson M., Stupski M.P., Shu E.,

RAD Spier E., Sparadling A.C., Stapleton M., Strong R., Wing X.,

Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RAD Spier E., Sparadling A.C., Stapleton M., Strong R., Sin H. H.,

Radibs R.M., Woodage T., Worley K.C., Wu D., Yang S., Zho Q.A.,

Radibs R.M., Wedager T., Worley K.C., Wu D., Yang S., Zho Q.A.,

Radibs R.M., Weden E.W., Shops M., Zhong W., Zhong W., Shun E.,

Radibs R.M., Weden R.W., Woodage T., Wu D., Stro
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                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI TaxID=7227;
                                                                                                                                                                                  Last annotation update)
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                                                                                                                   608 AA.
                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                 PRELIMINARY;
                             356 LDWSFI 361
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1 LDWSFL 6
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Gaps Gaps SEQUENCE FROM N.A.
Mistra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
Mistra S., Crosby M.A., Matthews B.B., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. ATP-binding, Kinase, Serine/threonine-protein kinase, Transferase. SEQUENCE 732 AA, 84215 MW, 971EE8D1CA3E39AF CRC64; Crassostrea gigas (Pacific oyster). Eukaryota, Metazoa, Mollusca, Bivalvia, Pteriomorphia, Ostreoida, Ostreoidea, Ostreidae, Crassostrea. Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F. Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; "Sequencing of Drosophila melanogaster genome."; Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases. Rubin G.M., Venter C.J.; ö ; 0 Score 33; DB 5; Length 608; Pred. No. 5.1e+02; 1; Mismatches 0; Indels Length 732; Query Match 94.3%; Score 33; DB 5; Length 732 Best Local Similarity 83.3%; Pred. No. 6.1e+02; Matches 5; Conservative 1; Mismatches 0; Indels Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Vente Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases EMBL; AE003499; AAR48479.2; -. FlyBase; FBGN0030662; CG9220. SEQUENCE 608 AA; 70423 MW; 9278ADD4A34745CA CRC64; (TrEMBLrel. 07, Last sequence update) (TrEMBLrel. 23, Last annotation update) 732 AA. 1; Mismatches PERMYS; PROD069; pkinase; 1.
PRINTS; PRO0109; TYRKINASE.
PRODOM; PD000001; Proc kinase; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1. 01-AUG-1998 (TrEMBLrel. 07, Created) h 94.3%; Similarity 83.3%; 5; Conservative PRELIMINARY; 151 LDWSFI 156 Query Match Best Local Similarity [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. 1 LDWSFL 6 NCBI_TaxID=29159; I-kappa-B kinase. 01-AUG-1998 01-MAR-2003 FlyBase; 061565;

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Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium
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    The C. elegans Sequencing Consortium.";
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
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                                                                                                                                                                                                          Waterston R.;
"Direct Submission.";
"Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF038613, AAB92050.1;
WormPep; F42A6.5; CE17057.
InterPro; IPR001357; BRCT.
Ffam; PR00532; BRCT:
SMART; SM00292; BRCT: 1.
PROSITE; ES50172; BRCT; 1.
PROSITE; ES50172; BRCT; 1.
PHYPOChhetical procein.
SEQUENCE 176 AA; 20612 MW; IF8E5E23AF3E25BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 176;
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                                                                          STRAIN-Bristol N2;
Du Z., Scheet P., Andrews S.;
"The sequence of C. elegans cosmid F42A6.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA RES. 7:331-338(2000).

EMBL; AP003001; BAB50309.1; -.

InterPro; IPR000534; Semialdh dh.

Pfam; PF01118; Semialdhyde dh.

Hypotherical protein; Complete proteome.

SEQUENCE 203 AA; 21716 MW; FC61A9883F2E3EEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein mll3416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
investigating biology. The C
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 83.3°,
Thes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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LDWTFL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mesorhizobium loti.
                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||:||
LDWNFL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37
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                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    098GA7;
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Matches
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                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Bevan M., Van Der Schueren J., Chuang Y-J., Voet M., Robben J.,
Volckaert G., Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C.,
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Van Der Schueren J., Vandenbussche F., Chuang Y.J., Braeken M., Robben J., Volckaert G., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.3%; Score 33; DB 10; Length 962; 83.3%; Pred. No. 8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL035527, CAB36814.1; -.
EMBL, AL03555, CAB361277.1; -.
InterPro; IPR000269; CuNH oxidase.
PROSITE; PS01164; COPPER_AMINE_OXID_1; 1.
Hypotherical protein.
SEQUENCE 962 AA; 108894 MW; 5F48A946474B8927 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (2)
SEQUENCE FROM N.A.
BU Arabidopsis sequencing project;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
11-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 108.9 kDa protein.
F17L22.160 OR AT4G21700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                      962 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 83.5.
S; Conservative
                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Caenorhabditis elegans.
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719 MDWSFL 724
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889 LDWSFI 894
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                    1 LDWSFL 6
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Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Gurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Gelo C., Slater S.;
"Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58";
Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                   Gordon D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                              MEDLINE-2160855), PubMed=11743193;
MEDLINE-2160855), PubMed=11743193;
MOOD D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Mood D.W., Stubal J.C., Kaul R., Mood G.E., Almeida N.F. Jr., Woo L.,
Chara V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., ii, M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Kreepan W., Perry M.,
Channley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
Nester E.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=M145, rakaraburtty R., Nihira T., Yamada Y., Bibb M., rakano E., Chakration of scbR, and scbA genes involved in gamma-butyrolactone binding and synthesis in Streptomyces coelicolor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                         Hypothetical protein Atu1999.
ATU1999 OR AGR C 3633.
Agrobacterium Fumefaciens (strain CS8 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Complete proteome.
SEQUENCE 203 AA; 21846 MW; D5BF6AC4E3C6B7CB CRC64;
                                                               (TrEMBLrel. 21, Last sequence update) (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.4%; Score 32; DB 16; Le
83.3%; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomycineae; Streptomycetaceae; Streptomyces
                  203 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
Hypothetical 31.0 kDa protein.
                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE009151; AAL42992.1;
EMBL; AE008117; AAK87755.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.5
5, Conservative
                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LDWSFL
                                                01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   086850
                                  6MQD80
                 Q8UDW9
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Q8UDW9
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RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AJ007731; CAA07626.1; -...

KW Hypothetical protein.

SQ SEQUENCE 284 AA; 30959 MW; 38DE00712A09BE7D CRC64;

Query Match 91.4%; Score 32; DB 2; Length 284;

Best Local Similarity 83.3%; Pred. No. 3.6e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps
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Qy 1 LDWSFL 6

|||:|| 125 LDWTFL 130 Search completed: February 18, 2004, 14:35:55 Job time : 18.3684 secs

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5.1.6	Compugen Ltd.	
version	(c) 1993 - 2004 Compug	
encore	1993	
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	Copyright	

OM protein - protein search, using sw model

February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds Run on:

(without alignments) 87.531 Million cell updates/sec

US-09-643-260-14 35 1 LDWSFL 6 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMMARIES

	SUMMARIES	Description.	785	hymothetica	Sulfate nerme	brotein	hypothetical p	8	conserved hyp		C86874 ABC transporter pe	probable glycole					hypothetical p	vacuolar prot		S59886 C2 protein - tomat			phosphoribo		hypothetical	alpha-amylase	B84848 hypothetical prote	980 dibenzothiophene	302 thermophilic desul	867 endo-1,4-beta-xyla	
		DB	٤	2		_																									
# aaaaaaaaaaaaaaaaaaaaaaaa		Length	1	362	573	2658	2	176	203	203	339	377	404	556	927	927	939	1466	21	134	135	135	204	225	242	264	266	350	350	355	
it t		Query Match	100.0	100	100.0	100.0	94.3	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4													
1950 1950 1950 1950 1950 1950 1950 1950		Score	35	3.0	32	35	33	32	32	32				32	32	32	32	32	31	31		31	31	31	31	31	31	31	31	31	
25 1000 0 1362 1000 0 3629 1000 0 3629 1000 0 3629 1000 0 3629 1000 0 3629 1000 0 1000 0 1000 0 1000 1000 1000 1		Result No.	-	~	ım	4	ហ	9	7	80	O	10	11	12	13		15			18	19	50	21	22	23	24	25	56	27	28	

connexin40 - dog	connexing - human	endo-1,4-beta-xyla	protein phosphatas	NADH2 dehydrogenas	connexin 45.6 - ch	connexin44 - bovin	connexin 46 - rat	intrinsic membrane	gap junction prote	connexin-56 - chic	probable potassium	copper-binding pro	hypothetical prote
A49024	138429	E97644	T38772	T11921	150219	146053	S25764	139176	149624	A45338	T43531	H87368	D84668
00	N (V	~ (N (4	~	~	~	7	7	~	~	~	~	03
357	328	365	383	400	400	402	416	432	440	510	569	570	575
88.6	98.0	988.6	98.6	88.6	98.6	98.6	98.6	98.6	98.6	98.6	88.6	98.6	88.6
31	31	31	31	31	31	31	31	31	31	31	31	31	31
30	35	33	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

C; Species: Synechocystis sp.
A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C; Accession: 874785
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N. O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud BNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti A;Residues: 1-136 <KAN>
A;Cross-references: EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAA16936.1; PID:g16520
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein slr0489 hypothetical protein slr1082 - Synechocystis sp. (strain PCC 6803) A; Reference number: S74322; MUID:97061201; PMID:8905231 A,Accession: S74785 A,Status: preliminary A,Molecule type: DNA

Gaps ; 0 h Score 35; DB 2; Length 136; Similarity 100.0%; Pred. No. 17; 6; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches 6; Conserv

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|||||| LDWSFL 47 1 LDWSFL 6 42 ઠ В

RESULT 2

hypothetical protein F16B4.2 - Caenorhabditis elegans

A;Cross-references: EMBL:AF039048; PIDN:AAB94233.1; GSPDB:GN00023; CESP:F16B4.2 A;Experimental source: strain Bristol N2; clone F16B4

C;Genetics: A;Gene: CESP:F16B4.2

A;Map position: 5 A;Introns: 48/2; 112/2; 160/3; 255/3; 291/2; 333/3

100.0%; Score 35; DB 2; Length 362; Query Match

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hypothetical protein F17L22.160 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 24-Nov-1999
C;Accession: T05845
R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Basumitted to the Protein Sequence Database, February 1999
A;Reference number: 215454
A;Accession: T05845
A;Molecule type: DNA
A;Residues: 1-962 cBEV>
A;Cross-references: EMBL:AL035527
A;Experimental source: cultivar Columbia; BAC clone F17L22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conserved hypothetical protein Atu1999 [imported] - Agrobacterium tumefaciens (strain Cf C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Spacession: AB2822 R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, T; Kwood, D.W.; Setubal, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell'; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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A;Experimental source: strain Bristol N2; clone F42A6
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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C;Superfamily: Arabidopsis thaliana hypothetical protein F17L22.160
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Pred. No. 2.9e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T32618
R;Du, Z.; Scheet, P.; Andrews, S.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid F42A6.
A;Reference number: Z21201
A;Accession: T32618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 2;
Pred. No. 77;
1; Mismatches (
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A;Molecule type: DNA
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83.3%;
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83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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A;Introns: 51/3; 109/3
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                                                                                                                                                                                                                                                                         sulfate permease family protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Accession: AE1969
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUD:21595285; PMID:11759840
A;Scatus: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
C.A.; Althors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., I.J. J.H.; Li, Y.; Lin, X.; Liu, Z.K.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C.C., J.J. J.H.; R.S.; Romley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.Authors: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.Reference number: A86141; MUD:21016719; PMID:11130712
A.Authors: preliminary
A.Molecule type: DNA
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C;Genetics:
A;Gene: T22G18.2
A;Map position: 1
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A86216
                                 Gaps
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                              Indels
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   Pred. No. 46;
0; Mismatches
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100.08;
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Best Local Similarity 100.0
Matches 6; Conservative
   Similarity 100.
6; Conservative
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                                                                                                                                             26 LDWSFL 31
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   Best Local
Matches
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probable glycolate oxidase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C;Accession T36246
R;Saunder, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M..
submitted to the EMBL Data Library, March 1999
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N;Alternate names: low affinity sulfate transporter; protein slr0096
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S76624
R;Kancko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypotherical protein H10396 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C;Accession: A64151
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, ...
Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kirkness, T.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
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A;Molecule type: DNA
A;Residues: 1-404 <TIGR>
A;Coss-references: GB:U32723; GB:L42023; NID:g1573363; PIDN:AAC22055.1; PID:g1573367;
A;Note: best homolog was a hypothetical protein from Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                      A.Scatus: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Rosidues: 1-377 - 65NJ>
A.Scross-references: EMBL.AL035640; PIDN:CAB38520.1; GSPDB:GN00070; SCOEDB:SCE63.05
A.Experimental source: strain A3(2)
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C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: C86874
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A66625; MUID:21235186; PMID:11337471
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A;Molecule type: DNA
A;Residues: 1-319 <2770>
A;Cross-references: GB:AE005176; PID:912725040; PIDN:AAK06093.1; GSPDB:GN00146
A;Experimental source: strain IL1403
                                                                           A;Cross-references: GB:AE008688; PIDN:AAL42992.1; PID:g17740453; GSPDB:GN00186 A;Experimental source: strain C58 (Dupont) C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE007869; PIDN:AAK87755.1; PID:g15157123; GSPDB:GN00169
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83.3%; Pred. No. 1.5e+02;
ive 1; Mismatches 0; Indels
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Pred. No. 89;
1; Mismatches
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                                                                                                                                                                                                      A,Gene: Atu1999
A,Map position: circular chromosome
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Matches 5; Conservative
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140 LDWTFL 145
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140 LDWTFL 145
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A; Residues: 1-203 <KUR>
                                                                    A; Residues: 1-203 < KUR>
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A;Status: preliminary A;Molecule type: DNA
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Search completed: February 18, 2004, 14:38:50 Job time: 7.5921 secs
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                                             A;Accession: S76624
A;Status: nucleic acid sequence not shown; translation not shown
A;Status: nucleic acid sequence not shown; translation not shown
A;Noleucleitype: DNA
A;Residues: 1-556 <KAN>
A;Cross-references: EMBL:D64004; GB:AB001339; NID:g1001701; PIDN:BAA10568.1; PID:g100173
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: integral membrane protein HP0228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: AG1739
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Doninguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A;Authors: Kreft, J.; Kuhn, M.; Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1739
A;Accession: AG1739
A;Residues: 1-927 AG1A>
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R.Glaser, P.; Frangeul, L.; Buchtieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
Science 294, 849-852, 2001
A,Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Simose, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A,Reference number: AB1077; MUID:21537279; PMID:11679669
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A;Molecule type: DNA
A;Residues: 1-27 <GLA
A;Cross-references: GB:NC 003210; PIDN:CAD00438.1; PID:g16411848; GSPDB:GN00177
A;Experimental source: strain EGD-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AL592022; PIDN:CAC97687.1; PID:g16414982; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
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Pred. No. 4.2e+02;
1; Mismatches 0; Indels
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A;Reference number: S74322; MUID:97061201; PMID:8905231
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83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch: Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, E. Nakazaki, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, E. A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; WUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                   hypothetical protein alr3756 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AE2275
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-339 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB75455.1; PID:g17132890; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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Score 32; DB 2; Length 927;
Pred. No. 4.2e+02;
1; Mismatches 0; Indels
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83.3%;
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Similarity 83.3%;
5; Conservative
     Query Match
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; Search time 22.7763 Seconds (without alignments) 41.814 Million cell updates/sec
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| SIDSI / gggdata / geneseq_geneseq_embl / Ah1993 DAT: *
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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Maximum DB e
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result		Query				
No.	Score	Match	Match Length DB	DB	ΩI	Description
-	35	000			ABB08736	Mitatod TKKhota NR
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7	35	100.0	φ	23	AAM48519	NBD mutant peptide
n	. 35	100.0		24	ABU08429	Human NEMO binding
4	35	100.0	•	23	ABB77300	Human IKKbeta muta
ß	33	94.3		22	AAU58740	Propionibacterium
Q	33	94.3		23	ABP30274	Streptococcus poly
7	33	94.3	216	23	ABP25952	Streptococcus poly
80	33	94.3		22	ABB64315	Drosophila melanod
6	32	91.4	9	23	ABB08737	Mutated IKKbeta NE

WO200183547-A2

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AAM48520 ABU08430 AAG59894 AAG60632 ABB03835	4027	AAGOULO / AAUS5876 AABS8122 AAG67051 AAG23584	AAG91029 AAG49093 AAG49116 ABB91342 AAB26244	AAB16701 AAG11935 AAR48747 AAW02719 AAG11934 AAG1934	AAG49115 AAB69701 AAG69607 AAAG49114 AAW013968 AAW00496 AAW00496
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ALIGNMENTS

ABB08736 standard; peptide; 6 AA.

ABB0873

ABB08736;

IKKDeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
autoimmune disease; transplant rejection; osteoporosis; cancer;
Alzheimmer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;
antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
dermatological; antibacterial; antipsoriatic; antiheumatic;
antiarthritic; osteopathic; antiulcer; mutant; mutein. Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 14. /note= "Wildtype Trp substituted by Phe" Location/Qualifiers (first entry) Key Misc-difference Homo sapiens. Synthetic. 14-JUN-2002 antiasthmatic; cytostatic; antipsoriatic; nootropic;

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The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB087721-ABB08725-ABB08742) comprising at least one NEWO binding domain (ABB77313). The compound has acts through selective inhibition of (ABB0877313). The compound has acts through selective inhibition of vytokine-mediated NF-kB activation by blocking the interaction of NEWO with INKObeta at the NEWO binding domain. Blockage of IKKbeta-NEWO interaction results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IKKbeta kinase activation and subsequent decreased phosphorylation of IKKbeta kinase activation and cat (directly or indirectly) by blocking the recruitment of leukocytes cat differentiation. The compound is useful in treating NF-kB mediated cat cate sites of acute and chronic inflammation, by down-regulating the expression of E-selection on leukocytes or by blocking osteoclast differentiation. Where the compound is useful in treating NF-kB mediated conditions, where the compound is useful in treating of isoase, atherosclerosis, a viral infection or ataxia autoimmune disease, ratherosclerosis, a viral infection or ataxia categoricaria, anaphylaxis, cutaneous inflammatory disease, vasculitie and cuticaria, anaphylaxis, cutaneous inflammatory disease, vasculities and cuticaria, anaphylaxis, cutaneous inflammatory disease, vasculities and colling booriatis are architis, psoriatis, psoriatis, psoriatis, psoriatis, psoriatis, creaming or multiple sclerosis. For chronic obstructive or herpes simplex. Other viral cypolymyalgia, scleroderma Wegner's granulomatosis, temporal arteritis, cryomegalovirus or herpes simpled HIV and influenza. The compound may also be useful for treating anaphylaxis, drug and food sensitivity, contact dermatitis, cumburn or aging. The compound may be useful for the propound may be deministered alone or in combination with other known catiinflammatory agents. The present sequence is that of a mutated NEW Paterior. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                              Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting a cell with an anti-inflammatory compound comprising at least one NEMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                          Claim 23; Page 45; 82pp; English.
02-MAY-2001; 2001WO-US40654
                            02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                  WPI; 2002-179350/23
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Best Local Similarity
Matches 6; Conserv
                                                                      (UYYA ) UNIV YALE.
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                                                                                                       Ghosh S;
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                                                                                                                                                                                                            binding domain
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(AAM48525-AAM48619). The antiinflammatory compounds have antiaethmatic, cytostatic, antiperentic, antirheumatory compounds have antiaethmatic, antibacterial, immunosupressive, dermatological, neuroprotective, antibacterial, immunosupressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of KappaB kinase beta (IKKDeta) at the NEWO binding domain that results in inhibition of IKKDeta kinase activation and subsequent decreased phosphorylation of IKKDeta kinase compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, costeoporesis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, grannlomatosis, multiple sclerosis; transplant rejection; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermacological; neuroprotective; antiatherososlerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alzheimer's disease, atherosclerosis, viral infections, and ataxia
telangiectasia. The compounds are also useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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100.0%; Pred. No. 9.3e+05;
ive 0; Mismatches 0;
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ID ABU08429 standard; peptide; 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAY-2001; 2001WO-US14346.
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22-AUG-2000; 2000US-0643260.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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AAM48519 standard; Peptide; 6 AA

RESULT 2

NBD mutant peptide SEQ ID NO 14.

20-MAR-2002 (first entry)

AAM48519;

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ABB77300;

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The present invention relates to antiinflammatory compounds comprising NEMO binding domain (NBD) peptides. The NEWO binding domains are found on IkappaB kinase-beta (IKMCALs) and IkappaB kinase-beta (IKMCALs) and IkappaB kinase-alpha cound on IkappaB kinase-beta (IKMCALs) and IkappaB kinase-alpha are useful for modulating nuclear factor kappaB (NF-kappaB) induction in a cell, where the compounds are capable of blocking the interaction in a cell, where the compounds are useful for modulating and IKMCALs, and NEMO. The antiinflammatory compound further comprises at least one membrane translocation domain. The compounds are useful for treating in a finiammatory disease, atherosclerosis, viral infections, Ataxia telangiecterasis, and for transplantation detection. The compounds of the invention block NF-kappaB induction by IKK but do not inhibit the basal activity of NF-kappaB. ABU08412 represent human
                                                                                                                                            IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB; nuclear factor-kappaB induction; inflammatory disorder; autoimmune disease; osteoporosis; cancer; Alzheimer's disease; atherososis; viral infection; Ataxis telangiectasia; transplantation detection; immunosuppressive; osteopathic; cytostatic; nootropic; neuroprotective; antiatherosolerotic; virucide; vasotropic; antirheumatic; antiathatic; mutant; mutein.
                                                                                                                            Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel antiinflammatory peptide compounds comprising NEMO binding domain, useful for modulating NF-kappaB induction in a cell and for treating NF-kappaB-mediated inflammation disorders e.g., asthma,
                                                                                         Human NEMO binding site (NBD) mutant peptide #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 22; Page 17; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-2001; 2001US-0847940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
                                                     12-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 psoriasis, vasculitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ghosh S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MAYM/) MAY M J. (GHOS/) GHOSH S.
                                                                                                                                                                                                                                                                                                                                                             JS2002156000-A1.
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               ABU08429;
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100.0%; Score 35; DB 24; Length 6; 100.0%; Pred. No. 9.3e+05; ive 0; Mismatches 0; Indels Query Match

6; Conservative Best Local Similarity Matches 6; Conserv

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Gaps

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ABB77300 standard; protein; 756 AA. ABB77300 ID ABB7 XX RESULT 4

LDWSFL

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1 LDWSFL

IXXDeat; IXXalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB; kinase activation; leukocyte; inflammation; B-selectin; osteoclast; autoimmune disease; transplant rejection; osteoporosis; cancer; Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis; rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; antiinflammatory; immunosuppressive; osteopathic; cytostatic; nootropic, neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antiashmatic; antiallergic; dermacological; antibacterial; antipsoriatic; antiallergic; antiallergic; antiarthritic; osteopathic; antiulcer; mutant; mutein. Human IKKbeta mutant W741F. (first entry) 14-JUN-2002

Homo sapiens Synthetic Location/Qualifiers Misc-difference

/note= "Wildtype Trp substituted by Phe"

WO200183547-A2

08-NOV-2001.

02-MAY-2001; 2001WO-US40654.

02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.

(UYYA) UNIV YALE.

May MJ,

WPI; 2002-179350/23.

Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting a cell with an anti-inflammatory compound comprising at least one NEMO binding domain

Example 11; Page -; 82pp; English.

The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB077313). The comprision at least one NEMO binding domain (ABB077313). The compound has acts through selective inhibition of cytokine-mediated NF-kB activation by blocking the interaction of NEMO cytokine-mediated NF-kB activation by blocking the interaction of NEMO conflains domain. Blockage of IKKDeta-NEMO interaction results in inhibition of IKKDeta kinase activation and subsequent decreased phosphorylation of IKKDeta kinase activation and interaction results in inhibition of IKKDeta kinase activation and subsequent decreased phosphorylation of IKKDeta kinase activation and cat (directly or indirectly) by blocking the recruitment of leukocytes into sites of acute and chronic inflammation, by down-regulating the expression of B-selectin on leukocytes or by blocking osteoclast conflictions, where the compound is useful in treating osteoclast conflictions, where the complition is an inflammatory disorder, an autoimmune disease, transplant rejection, osteoporosis, cancer, autoimmune disease, transplant rejection, osteoporosis, cancer, contingual anaphylaxis, cutaneous inflammatory disorder and allergies, urticaria, anaphylaxis, cutaneous inflammation, sepsis psoriasis, crematicis, osteoarthritis, psoriatic arthritis, lupus and the susting soriatic arthritis, lupus and susting sporiations of spondylarthritis. Also for Crohn's disease, ulcerative colitis, spondylarthritis. Also for Crohn's disease, ulcerative colitis, spondylarthritis, shortederma, wegner sprandown and anaphylaxis, drug and food sensitivity, contact dermatitis, creating anaphylaxis, drug and food sensitivity, contact dermatitis,

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sunburn or aging. The compound may be used to replace corticosteroids in any application in which corticosteroids are used, including immunosuppression in transplants and cancer therapy. Also for identifying antiinflammatory compounds and for diagnosis of an inflammatory disorder. The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of an IKKbeta mutant, useful in examples of the invention.

Note: The present sequence is not given in the specification but is derived from GenBank Accession No. 014920 (ABB77294).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory presence or absence of P. acnes in a patient comparises contacting the sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                      100.0%; Score 35; DB 23; Length 756; 100.0%; Pred. No. 3.9e+02;
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                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skeiky YAW, Persing DH, Mitcham JL, Wang SS,
L'maisonneuve J, Zhang Y, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID No 19935; 1069pp; English.
                                                                                                                                                                                                                                                                             0; Mismatches
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                                                                                                                                           Best Local Similarity
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polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downrequlate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus, GAS, GBS, group B streptococcus, Streptococcus agalactiae, group A streptococcus, Streptococcus pyogenes; antibacterial, antiinflammatory; infection; vaccine; meningitis; gene therapy.
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                                                                                                                                                                                                                                  Score 33; DB 22; Length 59;
Pred. No. 61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP30274 standard; Protein; 208 AA.
                                                                                                                                                                                                                                94.3%;
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24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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N-PSDB; ABN70905.
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Tettelin H;
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ID ABP
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used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying Streptococcus proteins.
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                                                                                    94.3%;
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11-JUL-2000; 2000US-0614150.
                                                                   Query Match
Query Match
Best Local Similarity 83.30,
Best Local Similarity 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
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                                                          216 AA;
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                                                                                                                                                                                                                                                                                                                                                              pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (31, given in the specification. The proteins have antibacterial and antinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to biological sample. (I) is used to anucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be
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                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus, GAS, GBS, group B streptococcus, Streptococcus agalactiae, group A streptococcus, Streptococcus pyogenes; antibacterial, antilnflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
used as a vaccine or diagnostic composition. The disease caused by Strepprococcus that is prevented or treated may be meningitis. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity chromatography, immunoassays, and distinguishing/identifying
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                                                                                                                         Score 33; DB 23; Length 208;
Pred. No. 2.3e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                             Streptococcus polypeptide SEQ ID NO 1080.
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                                                                                                                                                                                                                                                                           ABP25952 standard; Protein; 216 AA.
                                                                                                                         94.3%;
83.3%;
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24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
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                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus agalactiae.
                                                                      Streptococcus proteins.
                                                                                                           Query Match
Best Local Similarity
5, Conserve
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198 MDWSFL 203
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                                                                                                           Gaps
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Score 33; DB 23; Length 21:
Pred. No. 2.4e+02;
Ored. No. D. 1 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 19737.
                                                                                                   1; Mismatches
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The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB008725-ABB08742) comprising at least one NBMO binding domain (ABB77313). The compound has acts through selective inhibition of cytokine-mediated NF-kB activation by blocking the interaction of NEMO interaction results in inhibition of IKKDeta kinase activation and subsequent decreased phosphorylation of IKKDeta kinase activation and subsequent decreased phosphorylation of IKMDeta kinase activation the compound subsection by down-regulating the expression of E-selectin on leukocytes or by blocking osteoclast conditions, where the condition is an inflammatory disorder, an autoimmune disease, transplant rejection, osteoporosis, cancer, alteriance, alternation, selection or ataxia telangiectasia. The inflammatory disorder is asthma, allergies, cheumatory disease, chronic obstructive pulmonary disease, vasculitis and bursitis. The inflammatory disorder may also be dermatitis, eccema, psoriasis, osteoarthritis, psoriatic arthritis, lupus and psoriasis, osteoarthritis, lupus and
                                                                                                                                                                                              kinase activation; leukocyte; inflammation; E-selectin; Osteoclast; autoimmune disease; transplant rejection; osteoporosis; cancer; Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis; rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; antiinflammatory; immunosuppressive; osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antiashmatic; antiallergic; dermatological; antibacterial; antipsoriatic; antiallergic; antialretic; osteopathic; antiulcer; mutant; mutein.
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                                                                                                                                                                           IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
                                                                                                                                Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 15.
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ABB08737 standard; peptide; 6 AA
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                                                                                    (first entry)
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Synthetic.
                                                                                       14-JUN-2002
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                                           ABB08737;
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spondylarthritis. Also for Crohn's disease, ulcerative colitis, polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis, cryoglobulinaemia or multiple sclerosis. For chronic viral infections caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral diseases include HIV and influenza. The compound may also be useful for treating anaphylaxis, drug and food sensitivity, contact dermatitis, subburn or aging. The compound may be used to replace corticosteroids in any application in which corticosteroids are used, including immunosuppression in transplants and cancer therapy. Also for identifying antiinflammatory compounds and for diagnosis of an inflammatory disorder. The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of a mutated NEMO binding domain of IKKbeta. Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis. Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation, Gaps The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 ö 91.4%; Score 32; DB 23; Length 6; 83.3%; Pred. No. 9.3e+05; ive 1; Mismatches 0; Indels Phillips K; Example 6; Page 48; 88pp; English. AAM48520 standard; Peptide; 6 AA. NBD mutant peptide SEQ ID NO 15. Findeis MA, 02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260. 02-MAY-2001; 2001WO-US14346. (first entry) (PRAE-) PRAECIS PHARM INC. (UYYA) UNIV YALE. 5; Conservative WPI; 2002-121889/16. Local Similarity Ghosh S, 1 LDWSFL 6 6 AA; WO200183554-A2 20-MAR-2002 08-NOV-2001. Synthetic. psoriasis AAM48520; Sequence Query Match May MJ, Best Loc Matches RESULT 10 AAM48520 8888888888888888888888888 à 셤 æ

psoriasis, vasculitis -

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(AAM48625-AAM88619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antintheumatic, antiarrhitic, osteopathic, antibactatic, antipsoriatic, antintheumatic, antiarrhitic, osteopathic, notropic, antiatherosclerotic, vincide and antiallargic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB cativation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEWO binding domain that results in inhibition of IKKbeta antians and subsequent decreased phosphorylation of IKAppaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telanglectasis. The compounds are also useful for treating pro-inflammatory responses such as allergies, unticaria, anaphylaxis, arthritis or food sensitivity, eczema, dermatitis, sunburn, aging and
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    fused, to a NEMO binding sequence
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22-AUG-2000; 2000US-0643260.
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N-PSDB; ABX94271, ABX94272.
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acid residues,
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                                                                                                                                                                                                                                                                                                                                                                                           6 AA;
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Synthetic.
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                                                 The present invention relates to antinflammatory compounds comprising NEMO binding domain (NBD) peptides. The NEMO binding domains are found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha (IKKalpha) proteins. The antinflammatory compounds of the invention are useful for modulating nuclear factor-kappaB (NF-kappaB) induction in a cell, where the compounds are capable of blocking the interaction between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The antinflammatory compound further comprises at least one membrane translocation domain. The compounds are useful for treating
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                         inflammatory disorders, autoimmune diseases, osteoporosis, cancer, Alzheimer's disease, atherosclerosis, viral infections, Ataxia telangiectasis, and for transplantation detection. The compounds of the invention block NP-kappas Induction by IKK but do not inhibit the basal activity of NP-kappas. ABU08418-ABU08432 represent human NBD mutant peptides.
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                          Claim 22; Page 17; 47pp; English.
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2000US-0179065. 2000US-0180628.

17-JAN-2001; 2001WO-US01338

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Pred. No. 57;
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83.3%;
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08-NOV-2000;
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Rosen CA, Barash SC, Ruben SM;
      17.NOV-2000; 2000US-0249208.
17.NOV-2000; 2000US-0249208.
17.NOV-2000; 2000US-0249211.
17.NOV-2000; 2000US-0249211.
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17.NOV-2000; 2000US-0249211.
17.NOV-2000; 2000US-0249211.
17.NOV-2000; 2000US-0249211.
17.NOV-2000; 2000US-0249218.
17.NOV-2000; 2000US-0249218.
17.NOV-2000; 2000US-0249245.
17.NOV-2000; 2000US-0249265.
17.NOV-2000; 2000US-0249265.
17.NOV-2000; 2000US-024929.
17.NOV-2000; 2000US-024929.
17.NOV-2000; 2000US-024929.
17.NOV-2000; 2000US-024929.
17.NOV-2000; 2000US-024929.
17.NOV-2000; 2000US-0251988.
05.DEC-2000; 2000US-0251988.
06.DEC-2000; 2000US-0251868.
08.DEC-2000; 2000US-0251868.
08.DEC-2000; 2000US-0251868.
08.DEC-2000; 2000US-0251868.
                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
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2000US-0254097
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N-PSDB; AAL35417.
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Isolated polypeptide for treating, preventing and or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis

Claim 11; SEQ ID NO 1782; 781pp + Sequence Listing; English.

The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB01087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the disgnossis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colifis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

56 AA Sequence

Gape ö 91.4%; Score 32; DB 22; Length 56; 83.3%; Pred. No. 87; 1.1 Mismatches 0; Indels Query Match 91.4 Best Local Similarity 83.3 Matches 5; Conservative

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2000US-237038P 2000US-237039P 2000US-237040P 2000US-240960P 2000US-241785P

2000US-239935P

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08-DEC-2000; 2000US-251869P
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02-OCT-2000; 2
13-OCT-2000; 2
20-OCT-2000; 2
20-OCT-2000; 2
                                  02-OCT-2000;
                                                                                                       01-NOV-2000;
Musculoskeletal system antigen; cancer; metastasis;
re-vascularisation; thrombosis; arteriosclerosis; mineral content;
re-vascularisation; thrombosis; arteriosclerosis; mineral
re-vascular condition; wound; injury; burn; angiogenesis; ulcer;
post-operative tissue repair; limb regeneration; neuronal growth;
meurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
MAIDS-related complex; chondrocyte growth; bone regeneration;
periodontal regeneration; tissue transport; bone graft; skin aging;
periodontal regeneration; tissue transport; bone growth; cell prouth; organ transplant; cell differentiation; body height;
weight; hair colour; eken; percentage of adipose tissue;
pigmentation; cosmetic surgery; metabolism; biorhythm; caricadic rhythm;
depression; tendency for violence; pain; reproductive capability;
normelevel; endocrine level; appetite; libido; memory; stress;
storage capability; fat content; libid content; protein content;
warbohydrate content; vitamin content; cofactor content;
                                                                                                               Novel human musculoskeletal system antigen #749.
                                                            ABU13129 standard; Protein; 56 AA
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2000US-225758P.
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Barash SC;

(ROSE/) ROSEN C A. (RUBE/) RUBEN S M. (BARA/) BARASH S C.

2000US-251856P

2000US-244617P 2000US-249299P

17-NOV-2000;

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The invention describes an isolated mucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful confluence or cancer metastases, in animals or the nucleic acid: stimulates re-vascularisation of isohaemic tissues associated with conditions; treats wounds due to injulies, and other cardiovascular conditions; treats wounds due to injulies, and other cardiovascular conditions; treats wounds due to injulies, and limb regenerative tissue repair, and ulcers; stimulates angiogenesis and limb regeneration; stimulates neuronal growth; can treat and prevent contitions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-related complex; stimulates chondrocyte growth, thus they can be conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-related complex; stimulates chondrocyte growth, thus they can be cused to enhance bone and periodontal regeneration and aid in tissue transports or bone grafts; prevents skin aging due to sunburn by stimulating keratinocyte growth; prevents hair loss, since FGF family estimulates growth and differentiation of hematopoietic cells and bone marrow cells when used in combination with other cytokines; maintains cignas before transplantation or for supporting cell culture of primary tissues; induces tissue of mesodermal origin to differentiate in early embryonic stem cells, besides, hematopoietic lineage; modulates mammalian characteristics such as, body height, weight, hair colour, eye colour, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery); modulates mammalian metabolism; changes mammal's metal state or physical state by influencing biorhythms, caricadic rhythms, depression, tendency for violence, tolerance for pain, reproductive capabilities, hormonal or endocrine levels, appetite, contour, everyment, lipid, protein, caricades the menry, or stress; increases the productive violence of a contour contour contour chem untitional components. This is the amino acid sequence of a coro
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Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer
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                                                                                                                                                                               Claim 11; SEQ ID NO 1782; 321pp; English
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ö Score 32; DB 24; Length 56; Pred. No. 87; 0; Indels 1, Mismatches 91.4%; Query Match Best Local Similarity 83.5.

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Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                    "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                             Pfam; PF01381, HTH 3; 1.
SWART; SM00530; HTH XRE; 1.
PROSITE; PS00687; ALDEHYDB DEHYDR GLU; 1.
HYPOCHACICAL protein; Complete proteome.
SEQUENCE 295 AA; 32188 MW; 91AF744D77736075 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 33; DB 16; 100.0%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                     EMBL, AL939105; CAB55664.1; -.
InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR001387; HTH_3.
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01-OCT-2000 (TrEMBLrel. 15, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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MEDLINE=20365717; PubMed=10910347;
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EMBL; AE003996; AAF84542.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                 coelicolor A3(2).";
Nature 417:141-147(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 LDWSAL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               xylella fastidiosa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LDWSAL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2371;
                                                                                                                                          Hopwood D.A.;
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Dan H., Prescott J.F.;
ENDA sequence and comparison of virulence plasmids from Rhodococcus equi ATCC 33701 and 103.";
Infect Immun. 68:6840-6847(2000).
EMBL; ARD01204; BAB16664.1;
EMBL; AR116907; AAG21758.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE FROM N.A.
STRAIN=ATCC33701, and 103; PLASMID=pREAT701 (p33701), and virulence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC33701; PLASMID=PREAT701 (p33701);
Takai S., Sekizaki T., Kakuda T., Nakamura M., Suzuki K., Ogino N.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium equii (Rhodococcus equi).
Plasmid pREAT701 (p33701), and Plasmid virulence.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Nocardiaceae; Rhodococcus.
                                                                                                                                              Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 266;
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Pred. No. 4.5e+02;
                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Plasmid.
SEQUENCE 266 AA; 29450 MW; 26B9B0B9717FF8B6 CRC64;
                                                                                               20309 MW; 38474F2CAC40A7D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Hypothetical 29.4 kDa protein.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CG8191 protein (RE17665p).
                                                                                                                                         Score 31; DB 16; I
Pred. No. 3.2e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                266 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
InterPro; IPR001226; Flavodoxin.
Pfam; PF00258; flavodoxin; 1.
PROSITE; PS00201; FLAVODOXIN; 1.
Complete proteome.
SEQUENCE 192 AA; 20309 MW; 38
                                                                                                                                            93.9%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.9%;
                                                                                                                Query Match
Best Local Similarity 83.3%,
Pera 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                        43 MDWSAL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                           1 LDWSAL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=11083803;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STATAS=306 / ATCC 13902 / XV 101;

STRATAS=306 / ATCC 13902 / XV 101;

A SILVA A.C.R.; Ferro J.A.; Reinach F.C.; Farah C.S.; Furlan L.R.;

A SILVA A.C.R.; Monteiro-Vitorello C.B.; Van Sluye M.A.; Almeida N.F.;

Alves L.M.C.; do Amaral A.M.; Bertolini M.C.; Camarogo L.E.A.;

A Alves L.M.C.; do Amaral A.M.; Bertolini M.C.; Camarogo L.E.A.;

Camarotte G.; Cannavan F.; Cardozo J.; Chambergo F.; Ciaplina L.P.;

Cararolli R.M.B.; Coutinho L.L.; Cursino-Santos J.R.; El-Dorry H.;

Faria J.B.; Ferreira A.J.S.; Ferreira R.C.C.; Gruber A.;

Katsuyama A.M.; Kishi L.T., Leite R.P.; Lemos E.G.M.; Lemos M.V.F.;

Locall E.C.; Machado M.A.; Madeira A.M.B.M.; Mayaki C.Y.; Moon D.H.;

Moreira L.M.; Novo M.T.M.; Okura V.K.; Oliveira M.C.; Oliveira V.R.;

Pereira H.A.; Rossi A.; Sena J.A.D.; Silva C.; de Souza R.F.;

A Trindade dos Santos M.; Truffi D.; Tsai S.M.; White F.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.";
                                     Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xanthomonas axonopodis (pv. citri).Bacteria; Yanthomonadales;Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                         STRAIN=Friedlin;
MEDLINE=98146435; PubMed=9477341;
IVONS A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                         "A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
Bents, ALIG1416; CAB77684.1; -.
Hypothetical protein.
SEQUENCE 399 AA; 43458 MW; BB86021C2BBB3E18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.9%; Score 31; DB 5; Length 399
83.3%; Pred. No. 6.78+02;
Migmatches 0; Indels
                                                                                                                                                                        Maeny D., Purnelle B., Goffeau A., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monooxygenase; Complete proteome.
SEQUENCE 455 AA; 50857 MW; D4D9F44E9761A618 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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InterPro; IPR000733; Plav monooxygnae.
InterPro; IPR013042; Rng mnoxygenaee.
Pfan; Pf01360; Monooxygenaes; I.
PRINTS; PR00420; RNGMNOXGNASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kynurenine 3-monooxygenase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                           SEQUENCE FROM N.A. STRAIN=Friedlin;
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                             Leishmania major.
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Q8PM34
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          RC STRAIN-BERKELEY,
RA Manatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans G.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Asburners M., Henderson S.N.,
R. George R.A., Lewis S.E., Richards S., Asburners M., Henderson S.N.,
R. George R.A., Lewis S.E., Richards S., Asburners M., Henderson S.N.,
R. Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Félifer B.D.,
R. Man K.H., Doyle C., Baxendal B.R., Chalson C.R., Miklos G.L.G.,
R. Ballew R.M., Basu A., Baxendal J., Bayaktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendal J., Bayaktaroglu L., Beasley E.M.,
Ballew R.M., Basu D.A., Baxendal J., Bayaktaroglu L., Beasley E.M.,
Ballew R.M., Cawley S., Dahlke C., Daverdort P., Brother P.,
R. Burtis K.C., Bueam D.A., Buller H., Cadieu E., Center A., Londra I.,
R. Burtis K.C., Bueam D.A., Buller H., Cadieu E., Center A., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dagan-Rocha S., Dunkov B.C.,
Dodson K., Doup L.E., Downes M., Dagan-Rocha S., Dunkov B.C.,
R.D. Dougeliste C.C., Ferraz C., Ferraz C., Ferraz C.,
R. Gong F., Gorrell J.H., Gu Z., Kennison J.A., Reckhum N.,
R.D. Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Alalli M., Kalush F., Karpen G.H., Re. Z., Kennison J.A., Ketchum K.A.,
R.M. Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
Alalli M., Matuphy B., Murphy L., Marzhy D.M., Nachoon D.L.,
Roch P., Led Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,
Reiner S., Mattei B., McIntoeh T.C., Morris J., Wohrefi A.,
Reiner K., Remingron K.A., Nixon K., Unixon K., Wanger D., Puri V., Welson D.R.,
Roller E., Spadding A.C., Stamber S., Poller S., Wang X.,
Nang Z.-Y., Wassarman D.A., Weinstcock M., Weissenbach J.,
Nang Z.-Y., Wassarman D.A., Weinstcock J.C.,
R. Walles R., Tector C., Turner R., Venter E., Wang X., Zhu X., Smith H.O.,
R. Walles R., Arodage T., Worley G., Wu D., Yen S., Zhu X., Smith H.O.,
R. Walles R., Rocher E., Rocher E., Wang G., Zhon S., Ra,
R. Hose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   345 AA; 39831 MW; 0613409F8F007B9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE003500; AAF48496.1; -. EMBL; AY071134; AAL48756.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0030675; CG8191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 93.9
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 LDWSAI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LDWSAL 6
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01-OCT-2000 (
01-MAR-2001 (
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Q9NE98 Q9NE98;

RESULT 5 Q9NE98

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Gaps

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Length 399;

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                                                                                                         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
Score 31; DB 16; Length 455;
Pred. No. 7.7e+02;
          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 75752 MW; 2728764810039458 CRC64;
                                                                                    Last annotation update)
                                                                              Last sequence update)
                                                              652 AA
           1; Mismatches
                                                                         Created)
                                                                                                     Drosophila melanogaster (Fruit fly)
                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE003834; AAF58967.1; -
FlyBase; FBgn0033392; CG8027.
InterPro; IPR000800; Notch.
93.9%;
83.3%;
                                                                   Q9V553;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2003 (TrEMBLrel. 23,
     Local Similarity 83.3
les 5; Conservative
                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00066; notch;
SEQUENCE 652 AA; 75
                                 435 IDWSAL 440
                                                                                                                                      SEQUENCE FROM N.A.
                      1 LDWSAL 6
                                                                                                                                           STRAIN-BERKELEY
                                                                                         CG8027 protein.
Query Match
                                                             09V553
                                                                                                CG8027
          Matches
                                                  RESULT Q
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93.9%; Score 31; DB 5; Length 652;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                    "Sequence and Characterization of the Cytochrome bo Operon of Vitreoscilla.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
EMBL; AF439739; AAM20915.1; -..
INTERPRO; IRROO0893; COXI.
PROSITE; PRO1165; CYCOXIDASEI.
PROSITE; PRO0077; COXI; 1.
COPPET; Electron transport; Heme; Oxidoreductase; Respiratory chain;
                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzallez M., Guaralin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.d., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                              Webster D.A., Hwang K.-W., Kim S.-K., Kim K.-J., Chung Y.-T.,
                                                                                                                                                                                                                                          Vitreoscilla sp. (strain C1).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Vitreoscilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 666;
              Indels
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY089618; AAL90356.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74470 MW; B5F3EAEB67282E7C CRC64;
                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Cytochrome bo subunit B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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Pred. No. 1.1e+03;
1; Mismatches 0;
  1.1e+03;
                                                                                                                                             666 AA
              Mismatches
                                                                                                                                                                        Created)
                                                                                                                                            PRT;
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83.3%;
                                                                                                                                                                        22,
                5; Conservative
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                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transport
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                                                                                                                                                                        01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; Trans
                                                                   447 LDWSAM 452
 Best Local Similarity
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LDWSAI 10
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                                          1 LDWSAL
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01-JUN-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                         Stark B.C.;
                                                                                                                                                                                                                                                                                                                                STRAIN=C1;
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                                                                                                                                                          081311;
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              Matches
                                                                                                              RESULT 8
Q8L311
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Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Pettersson B., Sterky F., Uhlen.M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 355-1394 FROM N.A.
De haan M., Grivell L.A., Maarse A.C.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIPS; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequenc
01-MAR-2003 (TrEMBLrel. 23, Last annotat
Chromosome XV reading frame ORF YOROIIW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR00359; AAA ATPase.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR001202; WW Rsp5_WWP.
Pfam; PF00005; ABC_tran; 2.
ProDom; PD000006; ABC transporter; 2.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.9%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 83.3.
For S; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                01-MAR-2003 (TrEMBLrel
ORF YOR011W (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON TER
SEQUENCE
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Dumont M_E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy G.,
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
Iwolecular cloning of a gene, DHS1, which complements a drughypersensitive mutation of the yeast Saccharomyces cerevisiae.";
Biosci. Biocechnol. Blocchem. 58:391-395(1994).
InterPro. IPR003593; AAA ATPase.
InterPro; IPR003439; ABC transporter.
InterPro; IPR001202; WW Rsp5_WWP.
Probom; PD000006, ABC transporter;
Probom; PD000006, ABC transporter;
Probom; PD000006, ABC transporter;
Probom; PAAS, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TEMBLE). 01, Last sequence update)
01-MAR-2003 (TEMBLE). 01, Last sequence update)
ATP dependent permease (Yeast homolog).
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotales; Saccharomycetales; Saccharomyceta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "CYC2 encodes a factor involved in mitochondrial import of yeast cytochrome c.";
Mol. Cell. Biol. 13:6442-6451(1993).
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                                                                                                                                         Length 666;
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Pred. No. 1.7e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1006 AA; 113961 MW; 0EA9408A1AD1CA7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       De haan M.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                  77745 MW; F6FDB6D1C1C39248 CRC64;
                                                                                                                                   Query Match 93.9%; Score 31; DB 5; I Best Local Similarity 83.3%; Pred. No. 1.1e+03; Matches 5; Conservative 1; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1006 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               007324;
01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10, Created)
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FlyBase; FBgn0033392; CG8027.
InterPro; IRR00880; Notch.
FBan; PF00066; notch; 1.
SEQUENCE 666 Ab; 77745 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.9%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                   461 LDWSAM 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       629 IDWSAL 634
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Best Local Similarity
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                                                                                                                                                                                                                                                   1 LDWSAL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=FY1679;
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Gaps
                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; S
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1040 AA; 117840 MW; B32B0F1D33906B5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-488 FROM N.A.
Pettersson B., Sterky F., Uhlen M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               De haan M., Grivell L.A., Maarse A.C.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 3; I
Pred. No. 1.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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InterPro; IPR001599; AAA ATPBSS.
InterPro; IPR001309; ABC_transporter.
InterPro; IPR001202; WW Rsp5_WWP.
ProDom; PD000006; ABC_transporter; 1.
SWART; SW00382; AAA; 1.
PROSITE; PS01159; WW_DOMAIN_1; 1.
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SEQUENCE FROM N.A.
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01-DEC-2001 (
01-OCT-2002 (
                                                                                                                            Query Match
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                                                                                                                                                   Matches
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"A set of cordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Harper D., Bateman A., Brown S., Chandra G. T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitesh E., Rajandream M.A., Rutherford K., Rutter S.,
Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Complete genome sequence of the model actinomycete Streptomyces
                                                                                 ö
                                                                                                                                                                                                                                                                   Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                     Score 31; DB 3; Length 1394;
Pred. No. 2.4e+03;
1; Mismatches 0; Indels
                                1394 AA; 157749 MW; 357A35A0FCF0C93B CRC64;
                                                                                                                                                                                                                                                                                                                                                   Oliver K., Harris D.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=A3(2);
Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                          Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                     PRT; 2297 AA
                                                                              1; Mismatches
PROSITE; PS01211; ABC_TRANSPORTER; 1.
PROSITE; PS01159; WW_DOMAIN_1; 1.
                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001227; Ac transferase.
InterPro; IPR003408; Ala synthase.
InterPro; IPR004839; Aminotransf1/2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000873; AMP-bind.
InterPro; IPR000794; Ketoacyl synt.
InterPro; IPR001917; NHtransf 2.
InterPro; IPR006163; Pp_bind.
Pfam; PF00699; Acyl_transf; 1.
Pfam; PF02490; ALA_synthase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
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Nature 417:141-147(2002).
EMBL; AL939125; CAA16183.1; -.
                                                       h
Similarity 83.3%;
5; Conservative 1
                                                                                                                                                                                                          01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MR-2003 (TrEMBLrel. 23, Polyketide synthase. SCOS892 OR SC3F7.12.
                                                                                                                                                                                     PRELIMINARY;
                                                                                                                     1017 IDWSAL 1022
                                                       Query Match
Best Local Similarity
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                                                                                                       1 LDWSAL 6
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                       ATP-binding
                                   SEQUENCE
                                                                                                                                                                                     054155
                                                                                                                                                             RESULT 13
054155
                                                                              Matches
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PAMILY.

RASSTOL; AAK73514.1; -.

RICEPPCO; IPRO01227; Ac transferase.

RICEPPCO; IPRO01228; AbH zinc.

RICEPPCO; IPRO0410; FabD.

RICEPPCO; IPRO0410; FabD.

RICEPPCO; IPRO06163; Pp bind.

RICEPPCO; IPRO06163; Pp bind.

RICEPPCO; IPRO06163; Pp bind.

REATH, PPO0107; adh zinc; 1.

REATH, PPO0109; ketcacyl-synt; 6.

REATH, PPO0500; pp-binding; 6.

RICEPPCO; RECACOLISE; Labb; 6.

REATH, PPO0500; ADH ZINC; 1.

REATH, PPO0500; ADH ZINC; 1.

ROSITE; PS00005; ADH ZINC; 1.

ROSITE; PS00005; ADH ZINC; 1.

ROSITE; PS00005; ADH ZINC; 1.

ROSITE; PS000012; PHOSPHOPANTETHEINE; 5.

WHEAL-binding; Oxidoreductase; Phosphopantetheine; Transferase; Zinc.

SEQUENCE 10917 AA; 1132905 MW; 15AC5956BBS810A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- COFACTOR: ZINC (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
FAMILY.
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                                                                                                                                                                                                                                                                                                                   93.9%; Score 31; DB 16; Length 2297;
83.3%; Pred. No. 4e+03;
ative 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces nodosus.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Pred. No. 1.9e+04;
1; Mismatches 0; Indels
Pfam; PF00155; aminotran_1_2; 1.
Pfam; PF00101; AMP-binding; 1.
Pfam; PF00109; ketoacyl-synt, 1.
Pfam; PF00109; ketoacyl-synt_C; 1.
Pfam; PF00550; pp-binding; 1.
PROSTE: P500059; AT TRANSFER CLASS_2; 1.
PROSITE; P500066; B KETOACYL SYNTHASE; 1.
PROSITE; P500606; B KETOACYL SYNTHASE; 1.
PROSIDED AT TRANSFER CLASS 2: 1.
PROSPROPARTE STANDE CLASS 3: 1.
PROSPROPARTE STANDE CLASS 3: 1.
PROSPROPARTE STANDE CLASS 3: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nodosus.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
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nes 5; Conservative
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8165 IDWSAL 8170
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AC GSO164 PRELIMINARY; PRT; 90 AA.
C GSO164, PRELIMINARY; PRT; 90 AA.
C 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
C Corymbacterium leprae.
C Corymbacterium leprae.
C Corymbacterium leprae.
NCBI TaxID=1769;
RN SEQUENCE FROM N.A.
RA Smith D.R.;
RA Smith D.R.;
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	34	53	87.9	9	-	GLMS HALN1	
GenCore version 5.1.6	35	53	87.9	630	-4	GLMS_SYNY3	
t (c) 1993 - 2004 Compugen Ltd.	36	53	87.9	644	-	VP4 BTV11	
	37	59	87.9	644	-	VP4_BTV13	
	38	59	87.9	644	-	VP4_BTV2A	
h, using sw model	39	29	87.9	654	-	VP4 BTV10	
	40	53	87.9	754	-	RIRI BPT4	
8, 2004, 13:39:39 ; Search time 3.55263 Seconds	41	53	87.9	842	-	PKL2 RAT	
(without alignments)	42	29	87.9	926	-	MAY3 SCHCO	
79.423 Million cell updates/sec	43	29	87.9	941	-	GCSP_MYCTU	
	44	29	87.9	946	-	PKL1 RAT	
260-13	45	29	87.9	928	п	YA7B_SCHPO	

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Q9ht00 P72720 P3428 P33429 P33427 P07132 P32282 C08874 P37934 Q56433

ALIGNMENTS

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ovis aries
synechocyst
bradyrhizob
homo sapien
deinococcus
bacillus su

YZ37_SYNY3 CO14_BRAJA PKL2_HUMAN TRPF_DEIRA YFJR_BACSU Y4WD_RHISN PROD_HUMAN SAMP_PIG

O28938 archaeoglob

Description

Length DB

Query Match

Score

Result

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:*

Database :

127863 segs, 47026705 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

US-09-643-260-13 33 1 LDWSAL 6

Title: Perfect score: Seguence:

OM protein - protein search

February 18

Run on:

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chlamydia p chlamydia m chlamydia t spirochaeta

GUDH PSEPU UHPT CHLPN UHPT CHLMU UHPT CHLTR TRPE SPIAU

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Query Match 100.0%; Score 33; DB 1; Length 330; Best Local Similarity 100.0%; Pred. No. 38; Matches 6; Conservative 0; Mismatches 0; Indels

treponema p xenopus lae brachydanio gallus gall

P46691 P980480

homo sapien mus musculu rattus norv bos taurus

BRARE CHICK HUMAN MOUSE RAT BOVIN

sus scrofa mesocricetu rattus norv

PIG

RAT ECOLI RHOSH TREPA XENLA

escherichia rhodobacter

homo sapien homo sapien

mus musculu bradyrhizob

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Gene 143:73-77(1994).
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Best Local Similarity
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NCBI_TaxID=1148;
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P98057;
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                                                                                                                                                  Gaps
                                                                                             Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Caprinae; Ovis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
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                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation update)
dep junction beta-2 protein (Connexin 26) (Cx26)
GJB2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7237_SYNY3 STANDARD; PRT; 333 AA. Q55480. [Abc. 1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical sugar kinase 81r0537.
          226 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 61;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB
Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
          PRT;
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                                                                                                                                                                                                                                                                                                                         EMBL, U17592; AAA67446.1; -.
InterPro; IPR000500; Connexin.
Pfam; PF000029; connexin; 1.
PRINTS; PR00206; CONNEXIN.
SMART; SM00037; CNX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26215 MW;
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                                                                                                                                                                                                                                                                                                                                                                                             Gap junction; Transmembrane. DOMAIN 1 20
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         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216
226 AA;
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Best Local Similarity
                                                                          Ovis aries (Sheep)
                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                               NCBI_TaxID=9940;
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         SHEEP
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                   P46691;
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CXB2 SHEEP
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SEQUENCE FROM N.A.
MEDLINE=96127529; PubMed=8590279;
MEDLINE=96127529; PubMed=8590279;
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium
Sequence analysis of the genome of the unicellular region Erom positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

BEDILINE-24559305, PubMed-8200541;
Surpin M.A., Moshiri F., Murphy A.M., Maier R.J.;
"Genetic evidence for a fourth terminal oxidase in Bradyrhizobium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Probable cytochrome c oxidase polypeptide I (EC 1.9.3.1) (Fourth
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PRINYS; PR00990; RIBOKINASE.
PROSITE; PS00584; PFKB KINASES 1; FALSE NEG.
PROSITE; PS00584; PFKB KINASES 2; 1.
Hypothetical protein; Transferase; Kinase; Complete proteome. SEQUENCE 333 AA; 35184 MW; CBCE13D0F7EEF90D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.9%; Score 31; DB 1; Length 333; 83.3%; Pred. No. 89; 0; Indels ative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, Q9TVW2; 1DGY.
InterPro; IPR002173; PfkB.
InterPro; IPR002139; Ribokinase.
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(Rel. 41, Last seq
(Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D64006; BAA10827.1; -. PIR; S75980; S75980.
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Eur. J. Biochem. 227:344-351(1995)
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CONFLICT
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                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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    c + 2 H(2)O.
    -!- PATHWAY: Respiratory chain; terminal step.
    -!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.

CATALYTIC ACTIVITY: 4 ferrocytochrome c + 0(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKL2 HUMAN STANDARD; PRT; 984 AA.
016513; Q9HHW4;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protein kinase C-like 2 (EC 2.7.1.-) (Protein-kinase C-related kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
1'-histidyl-3'-tyrosine (By similarity).
G -> D (IN REF. 1).
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MEDLINE=95154310; PubMed=7851406;
Palmer R.H., Ridden J., Parker P.J.;
"Cloning and expression patterns of two members of a novel protein-kinase-C-related kinase family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95080426; Pubmed=7988719;
Palmer R.H., Ridden J., Parker P.J.;
"Identification of multiple, novel, protein kinase C-related gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY).

COPPER B (BY SIMILARITY).

COPPER B (BY SIMILARITY).

COPPER B (BY SIMILARITY).

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COPPER B (BY SIMILARITY).

IRON (HIGH-SPIN HEME AXIAL LIGAND)

IRON (LOW-SPIN HEME AXIAL LIGAND)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                           EMBL; AP005944; BAC47980.1; -.
HSSP; P18401; 1FFT.
InterPro; IPR000883; COX1.
PFfam; PF00115; COX1; COX1.
PRINTS; PR01165; COX1; 1.
PROSITE; PS00077; COX1; 1.
Oxidoreductase; Heme; Copper; Transmembrane; Respiratory chain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (LOW-SPIN HEME AXIAL LIGAND)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F04F4870CD039861 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          IRON
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                                                                                                                                                                                                                                                          EMBL; L25841; AAA26210.1;
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FEBS Lett. 356:5-8(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 83.3 ies 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          105
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204 2
666 AA;
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METAL 105
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287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CROSSLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
METAL
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METAL
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δ
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                                                                                                              SUBSTRATES (BY SIMILARITY).

BUXYME REGULATION: ACTIVATED BY LIPIDS, PARTICULARLY CARDIOLIPIN
AND TO A LESSER EXTENT BY OTHER ACIDIC PHOSPHOLIPIDS AND
UNSATURATED PATTY ACIDS (BY SIMILARITY).

PUBCELLULAR LOCATION: Cycoplasmic (By similarity).

PTM: AUTOPHOSPHORYLATED
PTM: ACTIVATED BY LIMITED PROTEOLYSIS WITH TRYPSIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapa
                                                                                                                                                                                                                                                                                                                        SIMILARITY).
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
PKC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R GORGAGE HONG: 940b; PKKCL2.

R MMY, 602549; --

R GO; GO:0006468; P:protein amino acid phosphorylation; TAS.

GO; GO:0000468; P:signal transduction; TAS.

GO; GO:0000168; P:signal transduction; TAS.

GO; GO:0000169; Pkinase.C.

InterPro; IPR000861; Pkinase.C.

InterPro; IPR000861; REM_repeat.

R InterPro; IPR000861; REM_repeat.

R InterPro; IPR000801; Prot kinase.

R Ffam; PF00185; HRI; 3.

R Ffam; PF000433; pkinase; 1.

R SMART; SM00139; CZ; 1.

R SMART; SM00139; CZ; 1.

R SMART; SM00133; STK X; 1.

R RROSITE; PS001003; PROTEIN KINASE ST; 1.

R PROSITE; PS001007; PROTEIN KINASE DOM; 1.

R PROSITE; PS00110; PROTEIN KINASE DOM; 1.

R TRANSFEASE, ATP-binding; Serine/threonine-protein kinase; 2.

R TRANSFEASE.
                                                    Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      663 671 ATP (BY SIMILARITY).

686 686 ATP (BY SIMILARITY).

782 PR SIMILARITY.

207 N -> NGDGINCPEYEHN (IN REF. 3)

984 AA; 112034 MW; 687EC417A0F51C1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.9%; Score 31; DB 1; Length 984
83.3%; Pred. No. 2.6e+02;
iive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, U33052, AAC50208.1, -..
EMBL, S7548; AAB33346.1, -..
EMBL, AL1363B1, CAC17575.1; -..
PIR, S67527, S67527
HSSP, Q63450; LA06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6

TRPF DEIRA STANDARD;

1D TRPF DEIRA STANDARD;

1AC Q9RYZ8;

DT 15-SEP-2003 (Rel. 42, Created)
SEQUENCE OF 17-984 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGNC: 9406; PRKCL2.
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les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          919 IDWSAL 924
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RA Runate Paragravaus) Furneracasasas, 1, 1, Albertini A.M., Alloni G., Runate R.A. Gogaswara N., Moszer I., Albertini A.M., Borchert S., Ravedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., R. Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Entiator F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., R.A. Eritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Anisan S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guiseppi G., Guy B.J., Hagage K., Haiech J., Harwood C.R., Henaut A., R.A. Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., R.A. Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., K. Mellado R.P., Mallado R.P., Mauler G., Moestl D., Nazarevic V., R.A. Medlado R.P., Mallado R.P., Muzuno M., Moestl D., Nakai S., Noback M., Reynon D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Persecan B., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Schleich S., Schroeter R., Scoffone F., Takengain H., Tamakoshi A., Tanaka T., Takengain H., Takemaru A., Tanakoshi A., Tanaka T., Takengain H., Takemaru M., Tanakoshi A., Tanakoni R., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto R., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A., Huller R., Wiblet Gram-positive bacterium Bacillus R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., Rubhils R., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Bropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:249-256(1997).
-!- SIMILARITY: BELONGS TO THE 3-HYDROXYISOBUTYRATE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D83967; BAA23388.1; -.
EMBL; D78509; BAA24303.1; -.
EMBL; Z99108; CAB12628.1; -.
PIR; A69807; A69807; AFIR.
Interpro; IPR002204; 3hydroxisobut_dh.
PROSITE; P800895; 3 HYDROXISOBUT_DH; FALSE NEG.
Hypothetical protein; Oxidoreductase; NAD; Complete proteome. ACT SITE 146 BY SIMILARITY.
SEQÜENCE 261 AA; 27866 MW; 6C9ABCACBC71CA66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.9%; Score 30; DB 1; Length 261
83.3%; Pred. No. 1.18+02;
ive 1; Mismatches 0; Indels
for trehalose metabolism and acetoin utilization."; Microbiology 142:3057-3065(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                             [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LDWSAL 6
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P55682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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        HAU
HAU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the SWIS outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@iabb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 286.1571.1577(1999).
-!- CATALYTIC ACTIVITY: N-(5-phospho-beta-D-ribosyl)-anthranilate = 1-
(2-carboxyphenylamino)-1-deoxy-D-ribulose 5-phosphate.
-!- PATHWAY: Tryptophan biosynthesis; third step.
-!- SIMILARITY: BELONGS TO THE TRPF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=AC327;
MEDLINE=97124190; PubMed=8969503;
Yamamoto H., Uchiyama S., Sekiguchi J.;
"Cloning and sequencing of a 40.6 kb segment in the 73 degrees-76 degrees region of the Bacillus subtilis chromosome containing genes
                                                                                                                                                                                                                                                                            STRAINER / ATCC 13939 / DSM 20539 / NCIB 9279;
MEDLINE-20036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Wonfet K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
  15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
N-(5'-phosphoribosyl)anthranilate isomerase (EC 5.3.1.24) (PRAI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.9%; Score 30; DB 1; Length 208; 83.3%; Pred. No. 85;
                                                                                                                                             Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isomerase, Tryptophan biosynthesis, Complete proteome.
SEQUENCE 208 AA, 21156 WW, CF98D22E23AC2833 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Hypothetical oxidoreductase yfjR (EC 1.1.-.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE001875; AAF09715.1; -. PIR; D75556; D75556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequ
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                             Deinococcaceae; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, Q56320; IDL3.
TIGR; DR0123; --
HAMAP, WF 20135; -; 1.
INTECFPC; IPR001240; PRAI.
PÉRM; PF00697; PRAI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.3%,
Best Local Similarity 83.3%,
                                                                                                                  Deinococcus radiodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 LDWAAL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus subtilis.
                                                                                                                                                                                                        NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LDWSAL
                                                                                     TRPF OR DR0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               radiodurans R1
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034969;
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Gaps

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377 AA

PRT;

Length 261;

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hyperprolinaemia.";
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                                                                                          in mice.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUB=Brain;
MEDLINE=980464348; PubMed=9385373;
Campbell H.D., Webb G.C., Young I.G.;
"A human homologue of the Drosophila melanogaster sluggish-A (proline oxidase) gene maps to 22q11.2, and is a candidate gene for type-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                           MEDLINE-97305956; PubMed-9163424;
Fraiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
Perret X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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30-MAY-2000 (Rel. 39, Last sequence update)
18-SEP-2003 (Rel. 42, Last annotation update)
Proline oxidase, mitochondrial precursor (EC 1.5.3.-) (Proline
                                                            Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30; DB 1; Length 377; Pred. No. 1.5e+02; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                           Hypothetical protein; Transmembrane; Transport; Plasmid TRANSMEM 4 24
                                               Plasmid sym pNGR234a.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobia
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                49CF6E44AA0D74BD CRC64;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical transport protein Y4WD.
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InterPro; IPR007114; MFS.
                                         (strain NGR234).
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221 LDWSAV 226
                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dehydrogenase).
                                                                              NCBI_TaxID=394;
                                         Rhizobium sp.
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DISEASE: Defects in PRODH are the cause of type I hyperprolinaemia [MIM:239500]; a disorder characterized by elevated serum proline levels. May be involved in the psychiatric and behavioral phenotypes associated in the 22q11 velocardiofacial syndrome. SIMILARITY: BELONGS TO THE PROLINE OXIDASE FAMILY.
                                                                                                                                                                                                                   Nadler J.V., Karayiorgou M.;
"The gene encoding proline dehydrogenase modulates sensorimotor gating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Serum amyloid P-component precursor (SAP) (9.5S alpha-1-glycoprotein).
                                                                                                                                                                                                                                                                                                           Nat. Genet. 21:434-439 (1999).
-!- FUNCTION: CONVERTS PROLINE TO DELTA-1-PYRROLINE-5-CARBOXYLATE.
-!- PATHWAY. CONVERTS EACH From proline to glutamate; first step.
-!- SUBCELLULAR LOCATION: Mitochondrial matrix.
-!- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SKELETAL MUSCLE AND BRAIN,
TO A LESSER EXTENT IN HEART AND KIDNEY, AND WEAKLY IN LIVER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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TRANSIT 1 7 MITOCHONDRION (POTENTIAL).
CHAIN 7 516 PROLINE OXIDASE.
CONFLICT 80 80 S -> T (IN REF. 2).
SEQUENCE 516 AA; 59216 MW; 2PASBIE4481C450A CRC64;
                                                                                                                                   MEDLINE-99206616; PubMed-10192198;
Gogos J.A., Santha M., Takacs Z., Beck K.D., Luine V., Lucas L.R.,
Nadler J.V., Karayiorgou M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=85207828; PubMed=2987268;
Mantzouranis E.C., Dowton S.B., Whitehead A.S., Edge M.D.,
Bruns G.A.P., Colten H.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 516;
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83.3%; Pred. No. 2.1e+02;
iive 1; Mismatches 0;
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                                                                 SEQUENCE FROM N.A.
TISSUE=Cerebellum, and Kidney;
Hum. Genet. 101:69-74(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:9453; PRODH. GK; 043272; -.
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Homo sapiens (Human)
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231 LDWSSL 236
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X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).

X MEDLINE=97360233; PubMed=9217261;
A Hohenseter E., Hutchinson W.L., Pepys M.B., Wood S.P.;
Hohenseter E., Hutchinson W.L., Pepys M.B., Wood S.P.;
Component with bound dAMP.";
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                                                                                                                                                                                                                                                                   TISSUE=Skeletal muscle;

MEDLINE=2288257; PubMed=12477932;

MEDLINE=2288257; PubMed=12477932;

MEDLINE=2288257; PubMed=12477932;

MALAUSER R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hookins R.F., Jordan H., Moore T., Max S.I., Wang J., Hasheh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshlywis S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W., Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Ablakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Ghneration and initial analysis of more than 15,000 full-length human and mouse CDNA sequences."
uman serum amyloid P component. cDNA isolation, complete sequence pre-serum amyloid P component, and localization of the gene to
                                                                                                    SEQUENCE FROM N.A.
MEDLINE=87137351; PubMed=3029048;
Ohnishi S., Maeda S., Shimada K., Arao T.;
Isolation and characterization of the complete complementary and genomic DNA sequences of human serum amyloid P component.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=86033713; PubMed=4055725;
Prelli F., Pras M., Frangione B.;
The primary structure of human tissue amyloid P component from a patient with primary diopathic amyloidosis.";
J. Biol. Chem. 260:12895-12898 (1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=79042150; PubMed=81686;
Thompson A.R., Enfield D.L.;
"Human plasma P component: isolation and characterization.";
Biochemistry 17:4304-4311(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=94159098; PubMed=8114934;
Emsley J., White H.E., O'Hara B., Oliva G., Srinivasan N.,
Tickle I.J., Blundell T.L., Pepys M.B., Wood S.P.;
"Structure of pentameric human serum amyloid P component.";
Nature 367:338-345(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                               Biol. Chem. 260:7752-7756(1985)
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                                                                                                                                                                                                                MIM; 104770; -
60; GO:0005615; C:extracellular space; TAS.
GO; GO:0003794; F:acute-phase response protein activity; TAS.
GO; GO:0003764; F:chaperone activity; TAS.
GO; GO:0005201; F:chaperone activity; TAS.
GO; GO:000521; F:plasma glycoprotein; TAS.
GO; GO:0006462; P:prasma glycoprotein; TAS.
GO; GO:0006462; P:protein complex assembly, multichaperone pa. . .; TAS.
InterPro; IPR001759; Pentaxin.
between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00159; PTX; 1.
PROSITE; PS00289; PENTAXIN; 1.
Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin; Signal; Polymorphism;
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/FTIG=VAR 006055.
S -> P (IN REF. 1).
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/FTId=VAR_006054.
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                                                                                                                                                  EMBL; BC007039; AAH07039.1; -. EMBL; BC007058; AAH07058.1; -.
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                                                                               EMBL; D00097; BAA00060.1; -. EMBL; M10944; AAA60302.1; -.
                                                                                                         CAA28275.1; -.
                                                                                                                                                                                                                                                                                                                                  Pfam; PF00354; pentaxin; 1.
PRINTS; PR00895; PENTAXIN.
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PTX2 OR SAP.
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              RESULT 12
SAMP_MESAU
ID SAMP_MESAU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Landrace; TISSUE-Liver;
Olawa A., Mateumoto M., Kajikawa M., Hanazono M., Yasue H.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBUNIT: HOMOPENTAMER: PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
-!- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
-!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SERUM AMYLOID P-COMPONENT.
PENTAXIN.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
9D1867691EBBEDC66 CRC64;
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                                                                                                        Length 223;
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                                                                                                                                       1; Indels
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Pfam; PR00154; pentaxin. 1.
PRINTS; PR00895; PENTAXIN.
Prodom, PD002153; Pentaxin; 1.
SMART; SM00159; PTX; 1.
PROSITE; PS00289; PENTAXIN; 1.
Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin; Signal.
                                                                          223 AA; 25387 MW; 6C88A515FE88B393 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.9%; Score 29; DB 1; I
83.3%; Pred. No. 1.4e+02;
ive 0; Mismatches 1;
                                                                                                       87.9%; Score 29; DB 1; 1
83.3%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                      16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serum amyloid P-component precursor (SAP).
                                                                                                                                                                                                                                                                              224 AA
                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB005546; BAA21474.1; -.
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                                                                                                                                                                                                 202 LDWQAL 207
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                                                                                                                       Local Similarity
les 5; Conserv
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les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P02743; 1SAC
                                                                                                                                                                  1 LDWSAL 6
                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                           SAMP_PIG
019063;
                                                           STRAND
SEQUENCE
                                                                                                       Query Match
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TURN
STRAND
                                           STRAND
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Matches
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203 LDWQAL 208

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=81241327; PubMed=6166709; Coe J.E., Margossian S.S., Slayter H.S., Sogn J.A.; Margossian S.S., Slayter H.S., Sogn J.A.; Hamster female protein. A new Pentraxin structurally and functionally similar to C-reactive protein and amyloid P component."; J. Exp. Med. 153:977-991(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Comparative analyses of pentraxins: implications for protomer assembly and ligand binding.";

Structure 2:1017-1027(11994).

-!- SUBUNIT: HOWOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.

-!- SUBCELIGUAR LOCATION: Secreted.

-!- SIBCELIGUAR LOCATION: Secreted.

-!- SIBCELIGUAR DESTINON: THAT ELICIT AN ACUTE PHASE RESPONSE.

-!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY. ORTHOLOG OF HUMAN SAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0895; PENTAXIN.
PRODOM: PROD0153; Pentaxin; 1.
PROSITE; PRO0159; PTX; 1.
PROSITE; PRO0289; PENTAXIN; 1.
Lectin; Pentaxin; Plasma; Acute phase; Signal; Amyloid; Glycoprotein; SIGNAL.
                                                    01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Serum amyloid P-component precursor (Female protein) (FP) (SAP(FP)).
                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE=85218787; PubMeda2408337; Dowton S.B., Woods D.E., Mantzouranis E.C., Colten H.R.; Dowton S.B., amaner female protein: analysis of female protein primary structure and gene expression."; Science 228:1206-1208(1985).
                                                                                                                               Mesocricetus auratus (Golden hamster).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                        Rudnick C.M., Dowton S.B.; "Serum amyloid P (female protein) of the Syrian hamster. Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95187705; PubMed=7881902; Srintvasan N., White H.E., Emsley J., Wood S.P., Pepys M.B., Blundell T.L.;
234 AA.
                                                                                                                                                                                                                                                                                                                              structure and expression.";
J. Biol. Chem. 268:21760-21769(1993)
                                                                                                                                                                                                                                                                    MEDLINE=94012761; PubMed=7691816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L22024; AAA03577.1; -.
EMBL; M1342; AAA36980.1; -.
PIR; A4417; A44177.
PIR; A4859; A46593.
PDB; 1HAS; 15-OCT-95.
InterPro; IPR001759; Pentaxin.
                                01-APR-1988 (Rel. 07, Created)
01-FBB-1995 (Rel. 31, Last seq
28-FBB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 24-234 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00354; pentaxin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 25-48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1] --
SEQUENCE FROM N.A.
SERQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=94316500; PubMed=8041620;
Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
"Analysis of the Escherichia coli genome. V. DNA sequence of the region from 76.0 to 81.5 minutes.";
Nucleic Acids Res. 22:2576-2586(1994).
materials of low mw diffuse from one cell to a neighboring cell.
-!- SUBRINIT: A connexon is composed of a hexamer of connexins.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUB SPECIFICITY: Expressed in testis.
-!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reizer J., Charbit A., Reizer A., Saier M.H. Jr.;
"Novel phosphotransferases system genes revealed by bacterial genome
analysis: operons encoding homologues of sugar-specific permease
domains of the phosphotransferase system and pentose catabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-UUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative hexulose-6-phosphate isomerase (EC 5.-.-) (HUMPI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.9%; Score 29; DB 1; Length 286; 100.0%; Pred. No. 1.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                             A585266ACA2ACCF2 CRC64;
                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enzymes.";
Genome Sci. Technol. 1:53-75(1996).
                                                                                                                                                                                                                                                                      SMART; SM00037; CNX; 1.
PROSITE; PSO0407; CONNEXINS_1; 1.
Gap junction; Transmedrane.
DOMAIN CYTO
                                                                                                                                                                                                  EMBL; M76534; AAA40998.1; -.
PIR; C42053; C42053.
InterPro; IPRO00500; Connexin.
Pfam; PF00029; connexin; 1.
PRINTS; PR00206; CONNEXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1994 (Rel. 30, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                             32860 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
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99
151
174
209
232
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                                                                     SUBFAMILY.
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TRANSMEM
DOMAIN
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SGBU_ECOLI
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MEDLINE=92112940; PubMed=1370487;
Medling=1.3.4., Bruzzone R., Jenkins N.A., Gilbert D.J.,
Copeland N.G., Paul D.L.;
"Four novel members of the connexin family of gap junction proteins.
Molecular cloning, expression, and chromosome mapping.";
Molecular cloning, expression, and chromosome mapping.";
J. Biol. Chem. 267:2057-2064(1992).
J. Biol. Chem. 267:2057-2064(1992).
PUNCTION: One gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.9%; Score 29; DB 1; Length 234
83.3%; Pred. No. 1.5e+02;
.ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234
26463 MW; 6161F0383062D2DB CRC64;
    SERUM AMYLOID P-COMPONENT
                                          01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1993 (Rel. 41, Last annotation update)
Gap junction alpha-6 protein (Connexin 33) (Cx33).
GJA6 OR CXN-33.
               PENTAXIN.
BY SIMILARITY.
N-LINKED (GLCNAC. .
T -> S (IN REF. 3).
K -> N (IN REF. 3).
A -> T (IN REF. 2).
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234 AA;
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Best Local Similarity
Matches 5; Conserv
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                            DISULFID
CARBOHYD
CONFLICT
CONFLICT
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                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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J. Bacteriol. 177:4311-4320(1995).

-! FUNCTION: DIHEME C-TYPE CYTOCHROME, THAT IS PARTICULARLY EXPRESSED WHEN CELLS GENERATE ENERGY VIA AEROBIC RESPIRATION.

-! SUBCELLULAR LOCATION: Membrane-bound.

-! PTM: BINDS TWO HEME GROUPS PER MOLECULE (POTENTIAL).

-! SIMILARITY: TO ACETOBACTER ALCOHOL DEHYDROGENASE CYTOCHROME C
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
-!- FUNCTION: ISOMERIZATION OF D-ARABINO-6-HEXULOSE 3-PHOSPHATE TO
                                -!- PATHWAY: PROBABLY PART OF A SUGAR METABOLIC PATHWAY ALONG WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Flory J.E., Donohue T.J.; "Organization and expression of the Rhodobacter sphaeroides cycFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
NCBI_TaxID=1063;
                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                              Length 286;
                                                                                                                                                                                                                                                                                                                                                                                           87.9%; Score 29; DB 1; Length 286
100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                           Isomerase, Complete proteome. SEQUENCE 286 AA; 32455 MW; 4C849F575E937BF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
MEDLINE-95362655; Pubmed-7543472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 31, Last annotation update)
Diheme cytochrome C-type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 AA.
                                                                 - !- SIMILARITY: BELONGS TO THE HUMPI FAMILY
                                                                                                                                                                                                                                                                  Ecodone, EG12286; sgbU.
InterPro, IPR004560; Hxl6Piso_put.
Pfam, PF03809; Hxl6Piso_put, 1.
TIGRFAMS; TIGR00542; hxl6Piso_put; 1.
                                                                                                                                                                                                                                       EMBL; U00039; AAB18559.1; ALT INIT.
EMBL; AE000435; AAC76606.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro, IPR003088; Cyt_CI.
InterPro, IPR003219; CytC_adh.
InterPro, IPR000345; CytC_heme_bind.
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DR ProDom; PD011584; CytC_adh; 1.

DR PROSITE; PS00190; CYTOCHROME C; 2.

KW Electron transport; Heme; Membrane.
FT BINDING 52 55 HEME 1 (COVALENT) (BY SIMILARITY).
FT BINDING 55 55 HEME 1 (COVALENT) (BY SIMILARITY).
FT BINDING 202 202 HEME 2 (COVALENT) (BY SIMILARITY).
FT BINDING 205 205 HEME 2 (COVALENT) (BY SIMILARITY).
FT BINDING 205 205 HEME 2 (COVALENT) (BY SIMILARITY).
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FT BINDING 205 206 HEME 2 (COVALENT) (BY SIMILARITY).
FT BINDING 205 206 HEME 2 AIAL LIGAND)
FT METAL 206 206 (BY SIMILARITY).

SQ SEQUENCE 296 AA; 31727 MW; 4C4A9DBF695BSBFD CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.86+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 1 LDWSA 5

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Db 241 LDWSA 245

Search completed: February 18, 2004, 14:28:11
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

February 18, 2004, 14:12:09; Search time 6.5921 Seconds Run on:

(without alignments) 87.531 Million cell updates/sec

US-09-643-260-13 Perfect score:

1 LDWSAL 6 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 segs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	o	hypothetical prote	protein kinase (EC	ATP-dependent tran	polyketide synthas	hypothetical prote	phosphoribosylanth	3-hydroxyisobutyra	probable xylanase/	transcription regu	chromate resistanc	probable membrane	beta-ketoadipyl Co	hypothetical prote		hypothetical prote		hypothetical prote	orsellinic acid sy	protein F22013.8 [helicase homolog F	gap junction prote	вроваве в		transposase slr211	transposase slr085	transposase sll125	_
SUMMARIES	ID	B69416	F82645	S75980	S67527	866876	T34918	D84320	D75556	A69807	D97195	F82398	D82088	AG0149	D83618	T20638	E82758	T37128	F75547	T39612	T30871	F86218	T00713	A24047	7704	S74925	S75488	7.4	875590	A83754
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transposase slr152	hypothetical prote	female protein - g	probable permease	conserved hypothet	serum amyloid P-co	conserved hypothet	Berum amyloid P-co	hypothetical prote	hypothetical prote	transposase s11043	transposase slr023	transposase slr035	transposase slr135	transposase s11199	gap junction prote
S75475	AG2498	A44177	G83488	H82830	YLHUP	F82729	A48593	G87696	F70612	876906	S76382	876312	S77237	875484	C42053
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171	177	211	214	215	223	232	234	242	279	282	282	282	282	282	286
87.9	87.9	87.9	87.9	87.9	87.9	87.9	87.9	87.9	87.9	87.9	87.9	87.9	87.9	87.9	87.9
29	5	29	53	53	29	29	59	53	53	53	59	53	53	29	29
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

hypothetical protein AF1331 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: O5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: B69416
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodso.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S A;Atthors: Utcerback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S A;Accession: B69416
A;Accession: B69416
A;Accession: B69416
A;Accession: B69416
A;Residues preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-30 oKLEA
A;Residues: 1-30 oKLEA
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A; Cross-references: GB: AE001012; GB: AE000782; NID: 92689335; PIDN: AAB89926.1; PID: 926492

100.0%; Score 33; DB 2; Length 330; 100.0%; Pred. No. 69; Cive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 6; Conservative

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Gapa

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177 LDWSAL 182 1 LDWSAL 6 ò 유

RESULT 2 F82645

F82645
C.Species: Xylella fastidiosa
C.Species: Xylella fastidiosa
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C.Species: Xylella fastidiosa
C.Species: The Xylella fastidiosa
Nature 406, 151-157, 2000
Nature 406, 151-157, 2000
Nature 406, 151-157, 2000
NATILE: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Notes: for a complete list of authors see reference number A59128 below
A;Status: preliminary
A;Residues: preliminary
A;Residues: preliminary
A;Residues: 1-192 cSINA
A;Residues: 1-192 cSINA
A;Residues: 1-192 cSINA
A;Residues: Brain a55C
A;Experimental source: strain a55C
A;Experimental s

Gaps

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1; Mismatches

Length 984; Indels

DB 2; 5e+02;

Score 31; Pred. No.

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F;663-671/Region: protein kinase ATP-binding motif F;686/Active site: Lys #status predicted
                                                                                                                              Similarity 83.3%; 5; Conservative
                                                                                                                                                                                                                                                                                                            919 IDWSAL 924
                                                                                                                              Query Match
Best Local Similarity
Matches 5; Conserv
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chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, B.C.; Miyaki, C.Y.; Y. G.; Nunes, L.R.; Oliveira, M.A.; de Goliveira, M.C.; de Oliveira, R.C.; Palmieri, D.M. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.; Genetics: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: S75980
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:D64006; GB:AB001339; NID:g1001291; PIDN:BAA10827.1; PID:g100134
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: probable ribokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RiPalmer, R.H.; Ridden, J.; Parker, P.J.
Blochem. 227, 344-351, 1995
A;Title: Cloning and expression patterns of two members of a novel protein-kinase-C-rela A;Reference number: 153327; MUID:95154310; PMID:7851406
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein kinase (EC 2.7.1.-) PRK2 - human
C;Species: Homo sapiens (man)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 21-Jul-2000
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A; Molecule type: mRNA
A; Residues: 1-984 < PAL>
A; Esperimental source: fetal brain
A; Experimental source: fetal brain
A; Accession: 167464
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-984 < RES>
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A;Accession: S75980
A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-333 <KAN>
                                                                                                                                                                                                                                                                                                                                                                     Length 192;
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83.3%;
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Best Local Similarity
Matches 5; Conserv
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Yeast 12, 1091-1095, 1996
A/Title: The sequence of a 30 kb fragment on the left arm of chromosome XV from Sacchard
A/Reference number: S72130, MUID:97051599, PMID:8896276
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A;Cross-references: EMBL:U43491; NID:g1150992; PIDN:AAC49491.1; PID:g1151007
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
ATP-dependent transport protein homolog YOR011w - yeast (Saccharomyces cerevisiae NATP-dependent transport protein homolog; protein 02601; protein UNA841 C;Species: Saccharomyces cerevisiae homolog; protein 02601; protein UNA841 C;Species: Saccharomyces revisian 12-Jul-1996 #text_change 19-Apr-2002 C;Accession: $66876; $66877; $534617; $61995; $72144 B. Protein Si, Sterky, F.; Uhlen, M. Submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 389-841 <STE>
A;Cross-references: EMBL:U43491; NID:g1150992; PIDN:AAC49491.1; PID:g1151007
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F;421-437/Domain: transmembrane #status predicted <TM2>
F;476-492/Domain: transmembrane #status predicted <TM3>
F;501-517/Domain: transmembrane #status predicted <TM4>
F;527-543/Domain: transmembrane #status predicted <TM4>
F;640-656/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the Protein Sequence Database, July 1996 A;Reference number: 866877 A;Accession: 866877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Risterky, F.; Uhlen, M. submitted to the EMBL Data Library, December 1995 A;Reference number: S61981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:Z74919; MIPS:YOR011w
A;Experimental source: strain S288C
R;de Haan, M.; Grivell, L.A.; Maarse, A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 355-1394 <DEH>
A;Cross-references: EMBL:Z74919; MIPS:YOR011w
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R;de Haan, M.; Maarse, A.C.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A;Reference number: $54617
A;Accession: $54617
A;Molecule type: DNA
A;Residues: 355-1394 <DEM>
A;Cross-references: EMBL;X87331
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A,Cross-references: SGD:S0005537
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A;Cross-references: GB:S75548; NID:g914099; PIDN:AAB33346.1; PID:g914100 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein Kinases; protein kinase homold C;Keywords: ATP; phosphotransferase F;655-916/Domain: protein Kinase homology <KIN>

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C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: D75556
C;Accession: D75556
R;White, O; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
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F;2-240/Domain: 3-hydroxyisobutyrate dehydrogenase homology #status atypical <HIB>
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A;Experimental source: strain 168
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Pred. No. 2e+02;
1; Mismatches 0; Indels
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Pred. No. 1.5e+02;
1; Mismatches 0; Indels
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Best Local Similarity 83.3%;
Matches 5; Conservative 1
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Best Local Similarity 83.3%;
Matches 5; Conservative
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144 LDWAAL 149
                                                                                          142 LDWAAL 147
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A; Status: preliminary
            1 LDWSAL
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R;Ag, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Frattas, T.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Frattas, T., 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
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C;Genetics:
A;Gene: SCOEDB:SC3PF.12
C;Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I homology; acetate-CoA ligase
C;Keywords: carrier protein
C;Keywords: carrier protein
F;R0-583/Domain: acetate-CoA ligase homology <ACL>
F;R0-583/Domain: acetate-CoA ligase homology <ACCP>
F;R0-583/Domain: acyl-carrier-protein homology <ACCP>
F;R0-583/Domain: acyl-carrier-protein] S-malonyltransferase homology <AMT>
F;1115-1600/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
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A;Experimental source: strain A3(2)
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A;Cross-references: GB:AE004437; NID:g10581148; PIDN:AAG19928.1; GSPDB:GN00138
C;Genetics:
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb_2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 17-Nov-2000
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R,Ollver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. Submitted to the EMBL Data Library, January 1998
A;Reference number: 221558
A;Accession: T34918
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                                                                                                                                                                                                                                                Score 31; DB 2; Length 139
Pred. No. 7.2e+02;
1; Mismatches 0; Indels
                                      F;782-789/Region: nucleotide-binding motif A (P-loop)
F;1107-1123/Domain: transmembrane #status predicted <TM7>
F;1166-1183/Domain: transmembrane #status predicted <TM9>
F;1226-1242/Domain: transmembrane #status predicted <TM9>
F;766-954/Domain: ATP-binding cassette homology <ABC2>
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A;Molecule type: DNA
A;Residues: 1-2297 <OLI>
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83.3%;
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Best Local Similarity 83.33
Matches 5; Conservative
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1017 IDWSAL 1022
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1641 IDWSAL 1646
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Best Local Similarity
Matches 5; Conserva
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Best Local Similarity
Matches 5; Conserv
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A,Molecule type: DNA,
*Residues: 1-380 <HEL-
A;Cross-references: GB:AE004304; GB:AE003852; NID:99656905; PIDN:AAF95482.1; GSFDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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A;Molecule type: DNA
A;Residues: 1-401 <STO>
A;Cross-treferences: GB:AE004460; GB:AE004091; NID:g9946055; PIDN:AAG03617.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
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A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Reference number: AB0001; MUID:21470413; PMID:11586360
       H.; Dragoi, I.; Sellers,
                                                           A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Reference number: A82035; MUID:20406833; PMID:10952301
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A; Cross-references: GB:AL590842; PIDN:CAC90058.1; PID:g15979278; GSPDB:GN00175
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AG0149
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Pred. No. 2.9e+02;
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chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera patho
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Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                             A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 1
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                                                                                                                                                                                                                                                                 probable xylanase/chitin deacetylase [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: D97195 #Schooling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001 #S.V.; Smith, D.R. A;File: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Status: preliminary A;Residuest type: DNA A;Residuest Lype: D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: F8238
R;Heidelbery, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: F8238
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-365 <HEID
A;Cross-references: GB:AE004420; GB:AE003853; NID:g9658361; PIDN:AAF96823.1; GSPDB:GN001
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcription regulator AraC/XylS family VCA0926 [imported] - Vibrio cholerae (strain N1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: D82088
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
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A,Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics: CAC2396
A,Gene: CAC2396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Vibrio cholerae
Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
Accession: F82398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 30; DB 2; Length 280 Pred. No. 2.1e+02; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30; DB 2; Length 365
Pred. No. 2.8e+02;
1; Mismatches 0; Indels
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83.3%;
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Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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70 VDWSAL 75
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submitted to the EMBL Data Library, June 1995
Alkeference number: 219914
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Alkeference number: 219914
Alkeference number: 219914
Alkeference in 2002
Alkeference: DNA
Alkeferences: EMBL: 249889; PIDN: CAA90069.1; GSPDB: GN00028; CESP: F06H11.4
Alkeferences: EMBL: 249889; PIDN: CAA90069.1; GSPDB: GN00028; CESP: F06H11.4
Alkeferences: EMBL: 2408411
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Alkeferences: CSP: F06H1.4
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T20618; T24630
R;Kercenson: T20638; T24630
R;Kershaw, J.
submitted to the EMBL Data Library, June 1995
A;Reference number: Z19303
A;Accession: T20638
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-442 <WIL.>
A;Coss-references: EMBL:Z49887; PIDN:CAA90060.1; GSPDB:GN00028; CESP:T06H11.4
A;Experimental source: clone F09B9
                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                      Query Match 90.9%; Score 30; DB 2; Length 401; Best Local Similarity 83.3%; Pred. No. 3e+02; Matches 5; Conservative 1; Mismatches 0; Indels
A,Gene: pcaF; PA0228
C,Superfamily: acetyl-CoA acetyltransferase
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Query Match 90.9%; Score 30; DB 2; Length 442; Best Local Similarity 83.3%; Pred. No. 3.4e+02; Matches 5; Conservative 1; Mismatches 0; Indels

Search completed: February 18, 2004, 14:38:49 Job time : 7.5921 secs

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Database

Sequence 106, App Sequence 10, Appl Sequence 23433, A Sequence 24401, A Sequence 14428, A Sequence 397, Appl Sequence 2, Appl Sequence 2, Appl Sequence 4, Appl Sequence 4, Appl Sequence 2, Appl Sequence 1, Appl Sequence 2, Appl Sequence 14, Appl Sequence 2, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 14290, A

Sequence 11, Appl Sequence 7691, Ap Sequence 34, Appl Sequence 702, Appl

Sequence 113, Sequence 115, Sequence 113, Sequence 115, Sequence 28, Appl Sequence 3236, Ap

Sequence Sequence 2

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; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants US-09-847-940B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: May, Michael J.
APPLICANT: Ghosh, Sankar
TILLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-117CP
CURRENT APPLICATION UNDER: US/09/847,940B
CURRENT FILING DATE: (2001_05-02)
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
                     100.0%; Score 33; DB 10; Similarity 100.0%; Pred. No. 7e+05; 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-289-762-702
US-10-024-298A-113
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US-09-847-946A-13
Sequence 13, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 13, Application US/09847940B; Patent No. US20020156000A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
  Best_Local Similarity
Matches 6; Conserv
\begin{array}{c} \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \\ \mathbf{
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     Query Match
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                                                                                                                                                                        February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds (without alignments) 75.239 Million cell updates/sec
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'(gnz_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
'(gnz_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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'(gnz_6/ptodata/1/pubpaa/NEW_PUB.pep:*
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2 US-10-148-786A-8
2 US-10-148-786A-8
2 US-10-369-493-2852
2 US-10-217-554-18
2 US-10-217-555-18
0 US-09-895-072-13
0 US-10-023-894-16
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2 US-10-023-898-16
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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APPLICANT: Ghosh, Sankar

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: 08/09/847,946A

CURRENT APPLICATION NUMBER: 09/641,261
PRIOR PPLICATION NUMBER: 09/643,260
PRIOR PLING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160

SEQ ID NO 13

LENGTH: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide US-09-847-946A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 33; DB 11; Length 6; 100.0%; Pred. No. 7e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25, Application US/10148786A
PUDLICATION NO. US20030143656A1
GENERAL INFORMATION:
APPLICANT: Alessi, Dario
APPLICANT: Blondi, Richardo
TITLE OF INVENTION: Protein Kinase Regulation
FILE REFERENCE: 002.00210
CURRENT APPLICATION NUMBER: US/10/148,786A
CURRENT FILING DATE: 2003-01-08
NUMBER: OF SEQ ID NOS: 68
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Biondi, Richardo
APPLICANT: Biondi, Richardo
FILE REFERENCE: 002.00210
CURRENT APPLICATION NUMBER: US/10/148,786A
NUMBER OF SEQ ID NOS: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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Best Local Similarity 100.(
Matches 6; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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1 LDWSAL 6
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US-10-148-786A-25
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Sequence 2852, Application US/10369493
; Bedication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Blater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE OF STORMER: US/10/369,493
; CURRENT APPLICANTION NUMBER: US/10/369,493
; CURRENT PILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2852
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; OTHER INFORMATION: Description of Artificial Sequence: Polypeptide
US-10-148-786A-8
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Pred. No. 8.9e+02;
1; Mismatches 0; Indels
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APPLICANT: Yang, Jing
APPLICANT: Hemmings, Brian A
APPLICANT: Cron, Peter D
TITLE OF INVENTION: Kinase Crystal Structures
FILE REFERENCE: 4423
CURRENT APPLICATION NUMBER: US/10/217,574
CURRENT APPLICATION NUMBER: GB 0119860.5
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2002-05-01
PRIOR APPLICATION NUMBER: GB 0216215.4
PRIOR FILING DATE: 2002-05-01
PRIOR FILING DATE: 2002-07-12
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/10217574
Publication No. US20040005687A1
GENERAL INFORMATION:
APPLICANT: Barford, David
APPLICANT: Yang, Jing
                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 83.3%;
Matches 5; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 77
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Best Local Similarity 83...
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12 IDWSAL 17
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Sequence 13, Application US/09986552

Fatent No. USGO020150981A1

GENERAL INFORMATION.

APPLICANT: CANFIELD, William

TITLE OF INVENTION: WETHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES

TITLE OF INVENTION UNMBER: US/09/986,552

CURRENT APPLICATION NUMBER: US/09/986,552

CURRENT APPLICATION NUMBER: US/05/35,872

PRIOR APPLICATION NUMBER: 60/153,831

PRIOR APPLICATION NUMBER: 60/153,831

PRIOR APPLICATION NUMBER: 60/153,831

PRIOR APPLICATION NUMBER: 60/153,831

PRIOR APPLICATION NUMBER: 50/153,831

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PRIOR APPLICATION NUMBER: 60/153,831

PRIOR APPLICATION NUMBER: 00/153,831
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Sequence 16, Application US/10023894

Sequence 16, Application US/10023894

Sequence 16, Application US/10023894

Sequence 16, Application US/10023894

Sequence 16, Application US/10023891

GENERAL INFORMATION:

APPLICANT: CANFIELD, William

APPLICANT: CANFIELD, William

APPLICANT: CANFIELD, WILLIam

APPLICANT: CANFIELD, WILLIAM

TITLE OF INVENTION: ACETYLGLUCOSAMINE-1-PHOSPHODIESTER ALPHA-N-ACETYL GLUCOSIMANIDA

FILE REFERENCE: 217139US77

CURRENT APPLICATION NUMBER: US/10/023,894

CURRENT PILLING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin version 3.1
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83.3%; Pred. No. 1.38+03;
cive 1; Mismatches 0; Indels
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                                                                     Score 31; DB 9; Length 502;
Pred. No. 1.3e+03;
1; Mismatches 0; Indels
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, ORGANISM: Drosophila melanogaster
US-09-986-552-13
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: LENGTH: 502

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-10-023-894-16
  , ORGANISM: Drosophila melanogaster US-09-895-072-13
                                                                          93.9%;
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Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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372 LDWSAM 377
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LENGTH: 502
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Badent No. US2002025550A1

GREERAL INFORMATION:
GREERAL INFORMATION:
GREERAL INFORMATION:
HILLIAM M
TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOWAL HYDROLASES
FILE REFERENCE: 210119USOCONT
CURRENT PAPLICATION NUMBER: US/09/895,072
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: 60/153,831
PRIOR APPLICATION NUMBER: US 09/635,872
PRIOR APPLICATION NUMBER: US 09/635,872
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 502
                                                                                                                                                                                                                                                                                                                                                                    US-10-217-555-18

US-10-217-555-18

Sequence 18, Application US/10217555

Publication No. US20040009569A1

GENERAL INFORMATION:
APPLICANT: Yang, Jing
APPLICANT: Yang, Jing
APPLICANT: True OF INVENTION: Kinase Crystal Structures and Materials and Methods for TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for TITLE OF INVENTION: Kinase Activation
FILE REFERENCE: 44236
CURRENT FILING DATE: 2002-12-05
PRIOR FILING DATE: 2001-08-14
PRIOR PLICATION NUMBER: GB 0119860.5
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-08-14

PRIOR FILING DATE: 2002-05-01

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 18

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                                         FEATURE:
COTHER INFORMATION: Description of Unknown Organism: Sequence source;
COTHER INFORMATION: uncertain
US-10-217-574-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Description of Unknown Organism: Sequence source; OTHER INFORMATION: uncertain US-10-217-555-18
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TYPE: PRT
ORGANISM: Unknown Organism
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269 IDWSAL 274
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269 IDWSAL 274
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Length 502;

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US-10-023-889-16

Sequence 16, Application US/10023889

Sequence 16, Application WS/10023889

Sequence 16, Naplication WS/10023889

Publication No. US20030124652A1

GENERAL INFORMATION:

APPLICANT: CANFIELD, William

TITLE OF INVENTION: DEFICIENT CELLS

FILE REFERENCE: 203512US77

CURRENT APPLICATION UNDER: US/10/023,889

CURRENT FILING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 21

SEQ ID NOS: 21

SEQ ID NO 16

LENGTH: 502
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Sequence 16, Application US/10023890

Publication No. US20030124653A1

GENERAL INFORMATION:

APPLICANT: CANFIELD, William

TITLE OF INVENTION: MARMALIAN CELLS

FILE REFERENCE: 203510US77

CURRENT APPLICATION NUMBER: US/10/023,890

CURRENT FILING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 21
                                                            Score 31; DB 15; Length 50 Pred. No. 1.3e+03; 1; Mismatches 0; Indels
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Pred. No. 1.3e+03;
1; Mismatches 0;
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Pred. No. 1.3e+03;
1; Mismatches 0;
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) ORGANISM: Drosophila melanogaster US-10-023-888-16
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ORGANISM: Drosophila melanogaster
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SEQ ID NO 16
LENGTH: 502
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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Publication No. US20030148460A1
GENERAL PURCAWATION
TITLE OF INVERMENTON: PHOSHODIESTER ALPHA-GLCNAcase OF THE LYSOSOWAL TARGETING PATHWAY
FULLE APPLICATION NUMBER: US/10/306,686
CURRENT APPLICATION NUMBER: US/10/306,686
CURRENT FILING DATE: 2002-11-29
PRIOR FILING DATE: 2000-08-10
PRIOR FILING DATE: 1999-08-14
NUMBER OF SEQ ID NOS: 52
SOSTWARE: Patentin version 3.1
            Sequence 16, Application US/10024197
Publication No. US20030133924A1
GENERAL INFORMATION:
TITLE OF INVENTION: HIGHLY PHOSPHORYLATED ACID BETA-GLUCOCEREBROSIDASE AND METHODS (TITLE OF INVENTION: TREATING GAUCHER'S DISEASE
TITLE OF INVENTION: TREATING GAUCHER'S DISEASE
TITLE OF INVENTION: TREATING GAUCHER'S DISEASE
CURRENT APPLICATION NUMBER: US/10/024,197
CURRENT PILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.1
SEQ ID NO 16.
LENGTH: 502
TYPE: PRT
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Pred. No. 1.3e+03;
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93.9%; Score 31; DB 12; Length 50
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels
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GENERAL INFORMATION

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GENERAL OF INVENTION:
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GURRENT APPLICATION NUMBER:
GURRENT FILING DATE:
NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patentin version 3.1

SEQ ID NO 16

LENGTH: 502
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US-10-023-888-16
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US-10-306-686-13
    US-10-024-197-16
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February 18, 2004, 13:37:19; Search time 22.7763 Seconds (without alignments) 41.814 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Description	Mutated IKKbeta NE	NBD mutant peptide	Human NEMO binding	Human IKKbeta muta	Region A of protei	Protein kinase der	3-phosphoinositide	AGC protein kinase	Drosophila melanog
SUMMARIES	. 4	AAM48518	ABU08428	ABB77299	AAY94732	AAB99802	AAB99793	AAB99835	ABB63738
DB	33	23	24	23	21	22	22	22	22
% Query e Match Length DB I	9	9	9	756	53	53	77	315	345
& Query Match	100.0	100.0	100.0	100.0	93.9	93.9	93.9	93.9	93.9
Score	33	33	33	33	31	31	31	31	31
Result No.	п	7	£,	4	S	9	7	80	6

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	212			1891	18	AAW23720	Platenolide syntha
	22			1891	18	AAW22610	Platenolide syntha
	23		0	19938	24	ABP76678	Streptomyces virid
	24	6	7.	35	22	AA008947	Human polypeptide
	25	6	7.	98	21	AAG00108	Human secreted pro
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	27	σ	7	134	22	AAU48444	֚֚֚֓֡֝֝֞֜֞֜֝֡֞֝֞֜֡֞֜֜֡֡֡֡֡֡֡֝֡֡֡֡֡֡
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	53	σ,	٠.	210	16	AAR74769	Female hamster pro
	30	σ.		223	13	AAR29923	SAP. Homo sapiens
	31	σ.	٠.	228	7.	ABP76686	8 V171
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	,	n 0	٠,	175	9 6	77170027	Dropi on bacterium
	4.7	n or	: -	382	9 (72019727 7201972	Conexin protein C
	43	. 01		385	23	ABP61480	activ
	44	σ.	7	382	23	48	Human NF-kB activa
	45	0	7	394	22	6238	Drosophila melanog
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AC	ABB0873	35;					
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. P.	14-JUN-2002	-2002	(Ilret	set entry)	2		
1 E	Marten		4	TKKheta NEMO binding	קישי	domain nentide SEO	TD NO 13
ž	200		3		5	ממווי של מליכו המווים	2
KW	IKKbeat; IKKalpha;	; IKK	alphe	1; NEMO; NEMO	NEW	binding	
K	kinase	activ	ation	1; leuko	cyte	; inflammation; E-selectin;	ectin; osteoclast;
<u>X</u>	autoim	nune d	iseae	se; tran	ıspla	autoimmune disease; transplant rejection; osteoporosis; cancer;	rosis; cancer;
X.	Alzheir	ner's	disea	18e; Vir	a.	infection; asthma; an	aphylaxis; psoriasis;
X.	rneumat	told a	renri	TIB; CE	uuo.	s disease; multiple s	•
¥ 24	COLLIC	Thirt	, ,	ootato.	יין קיין מיין קיין	ssion; ancimitammaco	ve. anti-HIV. human.
¥ ¥	antiart	erios.	֓֞֝֝֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓	ידוטייי,	3 5	osteopathic; cytostatic; modificatic; metropictective; amti-miv; antiarteriosclerotic: virucide: antiasthmatic: antialleraic:	
		111111	;		,		() I I I I I I I I I I I I I I I I I I

antiarteriosclerotic; virucide; antiasthmatic; antiallergic; dermatological; antibacterial; antipsoriatic; antirheumatic; antiarthritic; osteopathic; antiulcer; mutant; mutein. Homo sapiens Synthetic.

Location/Qualifiers Key Misc-difference

/note= "Wildtype Trp substituted by Ala"

WO200183547-A2

08-NOV-2001

antiasthmatic; cytostatic; antipsoriatic; nootropic;

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antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosolerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NRkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an antiinflammatory compound (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Page 48; 88pp; English.
                                                                                                                                                                                                                                                                                                                                   02-MAY-2001; 2001WO-US14346.
                                                                                                                                                                                                                                                                                                                                                                       02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
                                                                                                                                                                                                                                                                                                                                                                                                                                (PRAE-) PRAECIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-121889/16.
                  Antiinflammatory;
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                                                                                                                                                                                                                                                        WO200183554-A2.
                                                                                                                                                                                                                                                                                             38-NOV-2001.
                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         May MJ,
  The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting act least one NEWO binding domain (ABB08773-ABB08742) comprising at least one NEWO binding domain (ABB77313). The compound has acts through selective inhibition of (ABB0877313). The compound has acts through selective inhibition of NEWO binding domain. Blockage of IXKbeta-NEWO with IXKbeta at the NEWO binding domain. Blockage of IXKbeta-NEWO interaction results in inhibition of IXKbeta kinase activation and subsequent decreased phosphorylation of IXKbeta kinase activation and subsequent decreased phosphorylation of IXKbeta kinase activation and cat (directly or indirectly) by blocking the recruitment of leukocytes at the orapound is useful in treating NP-KB mediated atfrementation. The compound is useful in treating NP-KB mediated conditions, where the condition is an inflammatory disorder, an autoimmume disease, transplant rejection, osteoporosis, cancer, Alzheimer's disease, transplant rejection, osteoporosis, cancer, and anaphylaxis, cutaneosclerosis, a viral infection or ataxia catomicaria, anaphylaxis, cutaneosclerosis, a viral infection or ataxia utcidaria, anaphylaxis, cutaneosclerosis, a viral infection or ataxia catomicaria, anaphylaxis, uttaineous inflammatory disease, vasculitis and bursitis. The inflammatory disease, vasculitis and cutoidaria, school obstructive pulmonary disease, vasculitis and colymyalgia, scleroderma Wegner's granulomatosis, temporal arteritis, corpusing sponiatis. The inflammatory disease, ulcerative colitis, popolymyalgia, scleroderma Wegner's granulomatosis, temporal arteritis, colons caused by Epstein-barr, cytomegalovirus or herpes simpled. Corpusione and food sensitivity, contact dermatitis, curbating anaphylaxis, drug and food sensitivity, contact dermatitis, cumburn or aging. The compound may be useful for treating anaphylaxis, drug and food sensitivity, contact dermatitis, mumunosuppression in transplants and compound may be useful for the compound may be definitedered alone or
                                                                                                                                                                                                              Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting a cell with an anti-inflammatory compound comprising at least one NEMO
                                                                                                                                                                                                                                                                                                                 Claim 23; Page 45; 82pp; English.
02-MAY-2001; 2001WO-US40654.
                                    02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
                                                                                                                                                                           WPI; 2002-179350/23
                                                                                            (UYYA ) UNIV YALE.
                                                                                                                                     Ghosh S;
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                                                                                                                                                                                                                                                                        binding domain
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Phillips K;

Findeis MA,

Ghosh S,

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(AAM48620-AAM48619). The antinflammatory compounds have antiasthmatic, cytostatic, antipeoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, antibacterial, immunosuppressive, dermatological, neuroprotective, notropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB crivation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEWO binding domain that results in inhibition of IKAbpaB. The activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, burstitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, carantlematosis, multiple sclerosis, transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis, transplant rejection; and ataxia telangiectasia. The compounds are also useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 33; DB 23; Length 6 100.0%; Pred. No. 9.3e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU08428 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LDWSAL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 AA;
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ABU08428
ID ABU0
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Gaps ö

100.0%; Score 33; DB 23; Length 6; 100.0%; Pred. No. 9.3e+05; Live 0; Mismatches 0; Indels

6; Conservative

1 LDWSAL 6

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Query Match Best Local Similarity Matches 6; Conserv

AAM48518 standard; Peptide; 6 AA.

RESULT 2 AAM48518 NBD mutant peptide SEQ ID NO 13

20-MAR-2002 (first entry)

AAM48518;

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Human; antinflammatory compound; NEMO binding domain; NBD; IXXDeta; IkappaB kinase-beta; IkappaB kinase-alpha; IKXalpha; NF-kappaB; nuclear factor-kappaB induction; inflammatory disorder; autoimmune disease; osecoporosis; cancer; Alzheimer's disease; atherosclerosis; viral infection; Ataxia telangiectasia; transplantation detection; immunosuppressive, osteopathic; cytostatic; nociropic; neuroprotective; antiatherosclerotic; virucide; vasotropic; antirheumatic; antiatheritic; muteni.
                                                                                                                                                                                                                                                                                                                                                                                                             Novel antiinflammatory peptide compounds comprising NEMO binding domain, useful for modulating NF-kappaB induction in a cell and for treating NF-kappaB-mediated inflammation disorders e.g., asthma,
                                                      Human NEMO binding site (NBD) mutant peptide #11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 22; Page 17; 47pp; English.
                                                                                                                                                                                                                                                                      02-MAY-2001; 2001US-0847940.
                                                                                                                                                                                                                                                                                            02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
                                12-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-209142/20.
                                                                                                                                                                                                                                                                                                                                                                Ghosh S;
                                                                                                                                                                                                                                                                                                                              (MAYM/) MAY M J. (GHOS/) GHOSH S.
                                                                                                                                                                                                                       US2002156000-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 AB;
                                                                                                                                                                                                                                               24-OCT-2002.
                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
          ABU08428;
                                                                                                                                                                                                                                                                                                                                                                 May MJ,
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The present invention relates to antiinflammatory compounds comprising NEMO binding domain (NBD) peptides. The NEMO binding domains are found on INABDAB kinase-beta (IXKOAETA) and IXABDAB kinase-balpha kinase-beta (IXKOAETA) and IXABDAB kinase-balpha antiinflammatory compounds of the invention are useful for modulating nuclear factor-kappaB (NF-kappaB) induction in a cell, where the compounds are capable of blocking the interaction between one or more IKKS such as IKKABIPHA or IKKDeta, and NEMO. The antiinflammatory compound further comprises at least one membrane translocation domain. The compounds are useful for treating inflammatory disorders, autoimmune diseases, osteoporosis, cancer, alzheimer's disease, atherosclerosis, viral infections, Ataxia telangiectesia, and for transplantation detection. The compounds of the invention block NF-kappaB induction by IKK but do not inhibit the basal activity of NF-kappaB. ABU08418-ABU08432 represent human Length 6; 100.0%; Score 33; DB 24; 100.0%; Pred. No. 9.3e+05; ive 0; Mismatches 0;

6; Conservative Query Match Best Local Similarity Matches

1 LDWSAL 6

LDWSAL

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Indels

ABB77299 RESULT

ABB77299 standard; protein; 756 AA.

ABB77299;

(first entry) 14-JUN-2002 Human IKKbeta mutant W741A.

IXXXbeat, IXXXalpha, NEMO, NEMO binding domain, NBD, NF-kappaB; NF-kB; kinase activation; leukocyte, inflammation; E-selectin; osteoclast; autoimmune disease; transplant rejection; osteoporosis; cancer; Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis; rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; antinflammatory; immunosuppressive; osteopathic; cytostatic; nootropic; neuroprotective; antiatientialianiateriosclerotic; virucide; antiasthmatic; antialergic; dermatological; antibacterial; antipsoriatic; antirheumatic; antiarthritic; osteopathic; antiulcer; mutant; mutein.

Homo sapiens. Synthetic. Location/Qualifiers 741 Misc-difference

/note= "Wildtype Trp substituted by Ala"

WO200183547-A2

08-NOV-2001

02-MAY-2001; 2001WO-US40654.

02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.

(UYYA) UNIV YALE.

۸ay MJ,

WPI; 2002-179350/23.

Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting a cell with an anti-inflammatory compound comprising at least one NEMO

Example 11; Page -; 82pp; English.

The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB077313). The comprising at least one NEMO binding domain (ABB077313). The compound has acts through selective inhibition of cytokine-mediated NF-kB activation by blocking the interaction of NEMO cytokine-mediated NF-kB activation by blocking the interaction of NEMO compound in inhibition of IKKDeta kinase activation and subsequent decreased phosphorylation of IKKDeta kinase activation and interaction results in inhibition of IKKDeta kinase activation and cat (directly or indirectly) by blocking the recruitement of leukocytes into sites of acute and chronic inflammation, by down-regulating the expression of E-selectin on leukocytes or by blocking osteoclast confiferentiation. The compound is useful in treating NF-kB mediated confitients, where the compound is useful in treating osteoclast confitients, where the compound is useful in fraction or ataxia autoimmune disease, transplant rejection, osteoporosis, cancer, conditions, where the condition is an inflammatory disorder an autoimmune disease, transplant rejection, osteoporosis, cancer, contication, anaphylaxis, cutaneous inflammation, sepsis, psoriasis, crementation or ataxia crementation or ataxia crementation or ataxia crementation of arthritis, osteoarthritis, psoriatic arthritis, lupus and computed the sporiatic arthritis, lupus and substains, osteoarthritis, psoriatic arthritis, lupus and spondylarthritis. Also for Crohn's granulomatosis, temporal arteritis, cryoglobulinaemia or multiple sclerosis. For chronic viral infections caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral diseases include HIV and influenza. The compound may also be useful for treating anaphylaxis, drug and food sensitivity, contact dermatitis,

us-09-643-260-13.rag

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sunburn or aging. The compound may be used to replace corticosteroids in any application in which corticosteroids are used, including immunosuppression in transplants and cancer therapp. Also for identifying antiinflammatory compounds and for diagnosis of an inflammatory disorder. The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of an IKKbeta mutant, useful in examples of the invention.

Note: The present sequence is not given in the specification but is derived from GenBank Accession No. 014920 (ABB77294).
                                                                                                                                                                                                                                                                                                                                                                                      Substrate specificity; phosphoinositide-dependent protein kinase 1; PRK1; protein kinase Crelated protein kinase 2; PRK2; cancer; apoptosis; mechanical tissue damage; ischaemic disease; stroke; myocardial infarction, antigenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Altering substrate specificity of phosphoinositide-dependent protein kinase 1, to phosphorylate Ser473 in addition to Thr308 by exposing to
                                                                                                                                                                            Gaps
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                                                                                                                                                  100.0%; Score 33; DB 23; Length 756; 100.0%; Pred. No. 7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Downes P,
                                                                                                                                                                                                                                                                                                                                                              Region A of protein kinase C related protein kinase 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Currie R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 12; 103pp; English.
                                                                                                                                                                                                                                                                                       AAY94732 standard; peptide; 53 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deak M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAR-2000; 2000WO-GB01004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99GB-0006245
                                                                                                                                                                                                                                                                                                                                        29-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interacting polypeptide -
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                                                                                                                                                                Local Similarity
                                                                                                                           756 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
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survival signal that protects cells from apoptosis induced in a variety of ways. Reduction of the activity of PDK1 may promote apoptosis and may be useful in treating cancer. Conditions in which aiding apoptosis may be of benefit may also include resolution of inflammation. A compound capable of increasing the activity of PDK1 may be useful in treating diabetes or obesity, or may be useful in inhibiting apoptosis. Increased activity of PDK1 may lead to increased levels of leptin, which may lead to weight loss. The compounds may suppress apoptosis, which may aid cell survival during or following cell damaging processes and in treating disease in which apoptosis is involved. Examples of the diseases include, mechanical (including heat) tissue injury or ischaemic disease, for example stroke and myocardial infarction, or neural injury. The present sequence represents a region of protein kinase C related protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a method for identifying a compound that modulates protein kinase activity. The method comprises measuring the ability of the compound to inhibit, promote or mimic the interaction of a hydrophobic pocket-containing protein kinase with an interacting polypeptide. The interacting polypeptide interacts with the hydrophobic pocket of the protein kinase and/or comprises the amino acid sequence Phe/Tyr.Xaa.Xaa.Aaa.Phe/Tyr (I). The method is useful in screening assays for developing pharmaceutical compounds or drugs. Compounds, polypeptides or polynucleotides from the present invention are useful in medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying modulators of protein kinase (PK) activity, useful in developing drugs for treating cancer or diabetes, by measuring the ability of the compound to modulate or mimic the interaction of PK with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein kinase; identification; hydrophobic pocket; interacting; cancer; diabetes; inhibition; apoptosis; tissue injury; stroke.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 21; Length 53;
Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.9%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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in need of modulation of signalling by a hydrophobic pocket-containing protein kinase. Specifically, the patient has cancer or diabetes or is in need of inhibition of apoptosis, e.g. a patient suffering from tissue injury or ischaemic injury, including stroke. The compound or composition is also useful for inhibiting the degree or rate of phosphorylation by the protein kinase. The interacting polypeptide or compound is useful in methods of stabilising a hydrophobic pocket. Containing protein kinase, where the protein kinase is exposed to the compound or polypeptide or the protein kinase is exposed to the sequences, and AAH44210 and AAH44211 represent oligonucleotide sequences, used in the exemplification of the present invention.
   particularly in the manufacture of a medicament for treating a patient
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53 AA; Sequence

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                               Gaps
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93.9%; Score 31; DB 22; Length 53; 83.3%; Pred. No. 91; ive 1; Mismatches 0; Indels
            Local Similarity 83.3
 Query Match
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12 IDWSAL 17 1 LDWSAL 6 ઠ 유

RESULT 7 AAB99793

AAB99793 standard; Peptide; 77 AA. AAB99793;

3-phosphoinositide-dependent protein kinase 1 binding peptide PIF. (first entry) 20-SEP-2001

Protein kinase; identification; hydrophobic pocket; interacting; cancer; diabetes; inhibition; apoptosis; tissue injury; stroke.

sapiens Ношо

Synthetic.

WO200144497-A2.

21-JUN-2001

04-DEC-2000; 2000WO-GB04598

99US-0168559. 02-DEC-1999;

(UYDU-) UNIV DUNDEE.

Alessi D, Biondi R;

WPI; 2001-390252/41.

Identifying modulators of protein kinase (PK) activity, useful in developing drugs for treating cancer or diabetes, by measuring the ability of the compound to modulate or mimic the interaction of PK with interacting polypeptides

Disclosure, Page 22; 180pp; English.

modulates protein kinese activity. The method comprises measuring the ability of the compound to inhibit, promote or mimic the interaction of a hydrophobic pocket-containing protein kinase with an interacting polypeptide interacts with the hydrophobic pocket of the protein kinase and/or comprises the amino acid sequence phe/Tyr-Xaa-Xaa-Phe/Tyr (1). The method is useful in screening assays for developing pharmaceutical compounds or drugs. Compounds, polypeptides or polynucleotides from the present invention are useful in medicine, particularly in the manufacture of a medicament for treating a patient in need of modulation of signalling by a hydrophobic pocket-containing The present invention describes a method for identifying a compound that

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protein kinase. Specifically, the patient has cancer or diabetes or is in need of inhibition of apoptosis, e.g. a patient suffering from tissue injury or ischaemic injury, including stroke. The compound or composition is also useful for inhibiting the degree or rate of phosphorylation by the protein kinase. The interacting polypeptide or compound is useful in methods of stabilising a hydrophobic pocketcontaining protein kinase, where the protein kinase is exposed to the compound or polypeptide. AAB99786 to AAB9947 reppresent amino acid sequences, and AAH44210 and AAH44211 represent oligonucleotide sequences, used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying modulators of protein kinase (PK) activity, useful in developing drugs for treating cancer or diabetes, by measuring the ability of the compound to modulate or mimic the interaction of PK with
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                                                                                                                                                                                                                                                        Score 31; DB 22; Length 77; Pred. No. 1.4e+02; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGC protein kinase family member PRK2 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB99835 standard; Protein; 315 AA.
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                                                                                                                                                                                                                                                            93.9%;
83.3%;
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Query Match
Best Local Similarity 83.35,
Berhan 5; Conservative
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injury or ischaemic injury, including stroke. The compound or composition is also useful for inhibiting the degree or rate of phosphorylation by the protein kinase. The interacting polypeptide or compound is useful in methods of stabilising a hydrophobic pocketcontaining protein kinase, where the protein kinase is exposed to the compound or polypeptide. AAB19718 for AAB198147 represent amino acid sequences, and AAH44210 and AAH44211 represent oligonucleotide sequences, used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 une sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                            Length 315;
                                                                                                                           Score 31; DB 22; Length 31
Pred. No. 6.3e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 18006.
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                                                                                                                                                                                                                                                       ABB63738 standard; Protein; 345 AA.
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                                                                                                                             93.9%;
83.3%;
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11-JUL-2000; 2000US-0614150.
                                                                                                                                                    Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                              pharmaceutical
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Length 345;

Score 31; DB 22; Pred. No. 6.9e+02;

93.9%; 83.3%;

Query Match Best Local Similarity

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The present invention describes a method for identifying a compound that modulates protein kinase activity. The method comprises measuring the ability of the compound to inhibit, promote or mimic the interaction of a pultophobic pocket-containing protein kinase with an interacting polypeptide interacts with the hydrophobic pocket-containing polypeptide interacts with the hydrophobic pocket of the protein kinase and/or comprises the amino acid sequence. The protein kinase and/or comprises the amino acid sequence. The protein kinase and/or compounds or drugs. Compounds, polypeptides or polyputoleotides from the present invention are useful in medicine, or polyputoleotides from the present invention are useful in medicine, or particularly in the manufacture of a medicament for treating a patient or in need of modulation of signalling by a hydrophobic pocket-containing containing in hinses. Specifically, the patient has cancer or diabetes or is in need of inhibition of apoptosis, e.g. a patient suffering from tissue injury or ischaemic injury, including stroke. The compound or compound is useful for inhibiting the degree or rate of phosphorylation by the protein kinase. The interacting polypeptide or compound is useful for kinase. The interacting polypeptide or compound is useful in methods of stabilising a hydrophobic pocket-compound or polypeptide. AAB99786 to AAB9947 represent amino acid sequences, and AAH4410 and AAH4411 represent invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein kinase; identification; hydrophobic pocket; interacting; cancer; diabetes; inhibition; apoptosis; tissue injury; stroke.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGC protein kinase family member PRK2 protein sequence.
                                                                                                                                                                                                                                                                                              AAB99822 standard; Protein; 385 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                               136 LDWSAI 141
1 LDWSAL 6
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The interaction relates to a mechanist the substrate of a preparation relates to a mechanist de-dependent protein kinase 1 (PDKI), by exposing it to an interacting polypeptide. Included in the invention are a preparation comprising PDKI and an interacting polypeptide. PDKI with altered specificity is useful for phosphorylating polypeptide. PDKI with altered specificity is useful for phosphorylating residue of a substrate with the following peptide contemponding to the Ser/Thr residue of a substrate with the following peptide compound identified by methods of the invention that are capable of altering the substrate specificity of PDKI. PLOSE OF PRK2 or altering the substrate specificity of PDKI, PDK2 or PRK2 signalling a compound identified by methods of the invention that are capable of the insulin signalling pathway and/or PDKI, PDK2 or PRK2 signalling a compound that is capable of reducing the activity of PDKI may be useful in treating cancer. PDKI, e.g. compound that is capable of reducing the activity of PDKI may be useful in treating cancer. Conditions in which aiding apoptosis may be useful in treating cancer. Conditions in which aiding apoptosis may be benefit in treating cancer. Conditions in which aiding apoptosis may be benefit concreased levels of inflammation. A compound capable of cobesity, or may be useful in inhibiting apoptosis. Increased activity of PDKI may successes and in treating disease in cobesity, or may be useful in inhibiting apoptosis. Increased activity of PDKI may lead to increased levels of leptin, which may lead to weight cobesity, or may be useful in inhibiting apoptosis. Increased activity of PDKI may successes and in treating disease in which apoptosis is involved. Examples of the diseases include, mechanical confirms or following cell damaging processes and in treating disease in the course of the invention.

C represents a protein kinase C related protein kinase 2 amino acid certices requence, used in the course of the invention.
                                   Substrate specificity; phosphoinositide-dependent protein kinase 1; PDK1; protein kinase C related protein kinase 2; PRK2; cancer; apoptosis; mechanical tissue damage; ischaemic disasse; stroke; myocardial infarction; antigent peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Altering substrate specificity of phosphoinositide-dependent protein kinase 1, to phosphorylate Ser473 in addition to Thr308 by exposing to interacting polypeptide -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a method for altering the substrate
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                                                                                                                                                                                                                                                                                                                                                            Downes P,
                                                                                                                                                                                                                                                                                                                                                            Currie R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
Protein kinase C related protein kinase 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 11; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA015489 standard; Protein; 984 AA.
                                                                                                                                                                                                                                                                                                                                                              Deak M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.9%;
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                                                                                                                                                                                                                                                                                                                                                            Balendran A,
                                                                                                                                                                                                                                                                                                                      (UYDU-) UNIV DUNDEE
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-647155/62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               984 AA;
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                                                                                                                                                                     WO200056864-A2
                                                                                                                                                                                                                                                                                 19-MAR-1999;
                                                                                                                               Inidentified
                                                                                                                                                                                                          28-SEP-2000.
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ID AAO1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                 developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 4074.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY94736 standard; Protein; 984 AA.
                                                                                                                             ABB59094 standard; Protein; 652 AA
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83.3%;
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
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320 IDWSAL 325
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447 LDWSAM 452
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Best Local Similarity
Matches 5; Conserv
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1 LDWSAL 6
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                                                                                                                                                                                                                                                                                                                                                                 The invention comprises a method for determining whether a substance is an activator or an inhibitor of a DHAM-kinase (deregulated in hyperactive macrophage kinase). DHAM-kinases used in the invention include guarylate kinase 1 (GUK1), serin-threonin-kinase PRK2 and serin-threonin-kinase PRK2. The method of the invention is useful for identifying substances that influence inflammatory conditions of chronic inflammatory airway diseases (e.g. chronic bronchitis or chronic obstructive pulmonary serin-threonin-kinase PRK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                             Determining activators or inhibitors of 'deregulated in hyperactive macrophage' (DHAM)-kinase for treating chronic inflammatory airway diseases, by measuring DHAM-kinase function after it is contacted with a test substance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                 Human, DHAM-kinase inhibitor; guanylate kinase 1; PRK2; deregulated in hyperactive macrophage kinase inhibitor; GUK1; serin-threonin-kinase; PAK2; inflammatory condition; chronic inflammatory airway disease; chronic bronchitis; chronic obstructive pulmonary disease; COPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31; DB 23; Length 984;
Pred. No. 2.1e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 72196.
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                                                                                                                                                                                                                             (BOEH ) BOEHRINGER INGELHEIM PHARMA KG.
                                                                                                                                                                                                                                                                                                                                                  Claim 8; Page 41-47; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG56197 standard; Protein; 53 AA.
                                               Human serin-threonin-kinase PRK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.9%;
83.3%;
                                                                                                                                                                                        15-DEC-2001; 2001WO-EP14844
                                                                                                                                                                                                         22-DEC-2000; 2000US-257854P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.3%;
                            (first entry)
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                                                                                                                                                                                                                                                 Mueller S,
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919 IDWSAL 924
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                                                                                                                                                WO200252036-A2
                                                                                                                              Homo sapiens.
                            03-OCT-2002
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         AA015489;
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990S-0141842.
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01-JUL-1999;
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02-JUL-1999;
06-JUL-1999;
09-JUL-1999;
12-JUL-1999;
13-JUL-1999;
14-JUL-1999;
15-JUL-1999;
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Protein identification; aignal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGS6196 standard; Protein; 57 AA.
      990S-0154779
990S-0155139
990S-0155686
990S-0156458
990S-0156758
990S-0157117
990S-0157753
990S-0157753
990S-0158029
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990S-0160741.
990S-0160767.
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990S-0160815.
990S-0160815.
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Similarity 83.3%;
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99US-0160989
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99US-0161406
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Best Local Similarity
Matches 5; Conserv
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VDWSAL 35
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28-0CT-1999;
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5. FEB-1999 5. MAR. 1999 9. MAR. 1999 9. MAR. 1999 9. MAR. 1999 6. APR. 1999 6. APR. 1999 9. APR. 1999 9. APR. 1999 9. ARR. 1999	0. APR-1999 4. MAX-1999 6. MAX-1999 6. MAX-1999 11. MAX-1999 4. MAX-1999 4. MAX-1999 9. MAX-1999 9. MAX-1999 9. MAX-1999 10. MAX-1999 10. MAX-1999 10. MAX-1999 10. MAX-1999 10. MAX-1999 10. MAX-1999 10. MAX-1999 10. MAX-1999 10. MAX-1999 10. MAX-1999 10. MAX-1999 10. MAX-1999 10. MAX-1999 10. MAX-1999 10. MAX-1999 10. MAX-1999 10. MAX-1999 10. MAX-1999	11-UIN-1999 3-UIN-1999 4-UIN-1999 8-UIN-1999 8-UIN-1999 0-UIN-1999 6-UIN-1999 6-UIN-1999 6-UIN-1999 8-UIN-1999	8-UN-1999 1-UN-1999 1-UN-1999 3-UN-1999 3-UN-1999 6-UN-1999 1-UL-1999 1-UL-1999 6-UL-1999 6-UL-1999 8-UL-1999 8-UL-1999 8-UL-1999
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PR 13-JUL-1999; 99US-0143542.

PR 14-JUL-1999; 99US-0144005.

PR 15-JUL-1999; 99US-0144005.

PR 16-JUL-1999; 99US-0144006.

PR 19-JUL-1999; 99US-0144006.

PR 19-JUL-1999; 99US-0144006.

PR 19-JUL-1999; 99US-0144322.

PR 20-JUL-1999; 99US-0144331.

PR 20-JUL-1999; 99US-0144332.

PR 20-JUL-1999; 99US-0144332.

PR 20-JUL-1999; 99US-0144332.

PR 22-JUL-1999; 99US-014508.

PR 22-JUL-1999; 99US-014508.

PR 23-JUL-1999; 99US-014508.

PR 23-JUL-1999; 99US-014508.

PR 23-JUL-1999; 99US-014508.

PR 23-JUL-1999; 99US-0145119.

PR 13-JUL-1999; 99US-0145119.

PR 11-AUG-1999; 99US-0145119.

PR 11-AUG-1999; 99US-0145119.

PR 12-AUG-1999; 99US-0145119.

PR 23-AUG-1999; 99US-015106.

PR 24-AUG-1999; 99US-015106.

PR 24-AUG-1999; 99US-015106.

PR 24-AUG-1999;

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PR 04-OCT-1999; 99US-0157117.
PR 06-OCT-1999; 99US-015753.
PR 06-OCT-1999; 99US-015753.
PR 06-OCT-1999; 99US-0158029.
PR 07-OCT-1999; 99US-0158029.
PR 12-OCT-1999; 99US-0158232.
PR 13-OCT-1999; 99US-0158233.
PR 13-OCT-1999; 99US-0158235.
PR 14-OCT-1999; 99US-0158236.
PR 14-OCT-1999; 99US-0158231.
PR 14-OCT-1999; 99US-0158231.
PR 14-OCT-1999; 99US-015831.
PR 14-OCT-1999; 99US-015818.
PR 14-OCT-1999; 99US-015818.
PR 14-OCT-1999; 99US-015818.
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PR 14-OCT-1999; 99US-015818.
PR 21-OCT-1999; 99US-016818.
PR 21-OCT-1999; 99US-016818.
PR 22-OCT-1999; 99US-016818.
PR 22-OCT-1999; 99US-016818.
PR 22-OCT-1999; 99US-016818.
PR 22-OCT-1999; 99US-016198.
PR 22-OCT-1999; 99US-016198.
PR 22-OCT-1999; 99US-016199.
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PR 23-OCT-1999; 99US-016199.
PR 23-OCT-1999; 99US-016199.
PR 24-OCT-1999; 99US-016199.
PR 24-OCT-1999; 99US-016199.
PR 25-OCT-1999; 99US-016199.
PR 28-OCT-1999; 99US-016199.
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Search completed: February 18, 2004, 14:26:24 Job time: 23.7763 secs

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Sequence 12, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; TTPLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF;
; TTLE REPERENCE: PPI-117CP
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US/09/847,940B
; PRIOR PRILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
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US-09-864-761-36612

US-09-969-730-172

US-10-220-511-11

US-10-369-493-11197

US-11-10-4047-2545

US-11-10-4047-2545

US-10-264-237-1879

US-10-264-237-1879

US-08-847-9468-2

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US-08-847-9468-2

US-09-847-9468-3
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US-09-847-946A-12
Sequence 12, Application US/09847946A
Publication No. US20030054999A1
GENERAL INPORMATION:
APPLICANT: May, Michael J
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ORGANISM: Artificial Sequence
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum DB seq length: 200000000
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Result

Sequence 8, Appli Sequence 11197, A Sequence 1879, Ap Sequence 1879, Ap Sequence 2, Appli Sequence 2, Appli

Sequence

Sequence 88, App Sequence 81, App Sequence 80, App Sequence 83, App Sequence 86, App Sequence 87, App Sequence 82, App Sequence 82, App Sequence 171, App Sequence 171, App Sequence 171, App

Scoring table:

Searched:

Database

Perfect score:

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Sequence:

Sequence 1 Sequence 4 Sequence 8

Sequence Sequence Sequence

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APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
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APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findlips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Gerhard
TILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT APPLICATION NUMBER: 60/201,261
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-00-847-946A-95

Sequence 95, Application US/09847946A

Publication No. US20030054999A1

SEQUENCE 95, Application US/09847946A

PUBLICANT: May, Michael J

APPLICANT: Ghosh, Sankar

APPLICANT: Findeis, Mark A

APPLICANT: Phillips, Kathryn

APPLICANT: Phillips, Kathryn

APPLICANT: Phillips, Gerhard

TILLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REFERENCE: PPI-119

CURRENT PRILICATION NUMBER: 05/09/847,946A

CURRENT PLICATION NUMBER: 00/201.05-02

PRIOR PLILOR DATE: 2000-05-02

PRIOR PLILOR DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide US-09-847-946A-12
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Best Local Similarity 100.0%; Pred. No. 7e+05;

Matches 6; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100
Best Local Similarity 100
Matches 6; Conservative
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LENGTH: 6
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APPLICANT: Glosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Rathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPL-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 160
SEQ ID NOS: 160
SEQ ID NO 92
LINNGTH: 8
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFFWARE: PALENTIN VET: 2.0
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OTHER INFORMATION: Description of Artificial Sequence: NEWO binding
OTHER INFORMATION: sequence
US-09-847-946A-99
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US-09-847-946A-92
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; Sequence 92, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100..
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Best Local Similarity 100.
Matches 6; Conservative
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RESULT 6

; Sequence 99, Application US/09847946A; Publication No. US20030054999A1

US-09-847-946A-100

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TYPE: PRT
ORGANISM: Artificial Sequence
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Sequence 91, Application US/09847946A

Publication No. US2003005499A1

GENERAL INFORMATION:

APPLICANT: Way, Michael J

APPLICANT: Ghosh, Sankar

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Hannig, Gerhard

TITLE OF INVENTION: ANTI-IN9

FILE REFERENCE: PPI-119

FILE REFERENCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT APPLICATION NUMBER: 00/201,261

PRIOR APPLICATION NUMBER: 60/201,261

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR PILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 91

LENGTH: 9
Sequence 100, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
    APPLICANT: May, Michael J
; APPLICANT: Phideis, Mark A
APPLICANT: Phideis, Mark A
APPLICANT: Phideis, Mark A
APPLICANT: Phideis, Mark A
APPLICANT: Phideis, Mark A
APPLICANT: Phideis, Mark A
APPLICANT: Phideis, Mark A
APPLICANT: Phideis, Mark A
APPLICANT: Phideis, Mark A
APPLICANT: Phideis, Mark A
APPLICANT: Phideis, Mark A
APPLICANT: Phideis, Mark A
CURRENT FILING GATI: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR PLICATION NUMBER: 09/643,260
; PRIOR PLICATION NUMBER: 09/643,260
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR PLING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SEQ ID NO 100
; SEQ ID NO 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence:NEMO binding OTHER INFORMATION: sequence US-09-847-946A-100
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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US-09-847-946A-91
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Sequence 97, Application US/09847946A

Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Phillips, Kathryn

APPLICANT: Phillips, Kathryn

APPLICANT: Hannig, Gerhard

ITIER BEFERRNCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2000-05-02

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR PILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: Patentin Ver. 2.0

LENGTH- 9
Sequence 94, Application US/09847946A

Sequence 94, Application US/09847946A

Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

SELICANT: Hannig, Gerhard

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REPRENCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT PILING DATE: 2001-05-02

PRIOR FILING DATE: 2000-06-02

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 94
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US-09-847-946A-97
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Best Local Similarity 100.
Matches 6; Conservative
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US-09-847-946A-90
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LENGTH: 10
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; Publication No. US20030054999A1
; GENERAL INFORMATION:
    APPLICANT: May, Michael J
; APPLICANT: Pindeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: ANION: ANI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT FILING DATE: 2000-05-02
PRIOR PLING DATE: 2000-05-02
PRIOR PLING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 93
LENGTH: 10
                                                                                                                                                                                                                    US-09-847-946A-98

| Sequence 98, Application US/09847946A |
| Publication No. US2003005499A1 |
| Publication No. US2003005499A1 |
| Publication No. US2003005499A1 |
| APPLICANT: Ghosh, Sankar |
| APPLICANT: Findeis, Mark A |
| APPLICANT: Findeis, Mark A |
| APPLICANT: Findeis, Mark A |
| APPLICANT: Findeis, Mark A |
| APPLICANT: Findeis, Mark A |
| TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF |
| FILE REFERENCE: PPI-119 |
| CURRENT APPLICATION NUMBER: US/09/847,946A |
| CURRENT FILING DATE: 2000-05-02 |
| PRIOR APPLICATION NUMBER: 60/201,261 |
| PRIOR PILING DATE: 2000-05-02 |
| PRIOR PILING DATE: 2000-05-02 |
| PRIOR PILING DATE: 2000-05-02 |
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| PRIOR PILING DATE: 2000-05-03 |
| PRIOR PILING DATE: 2000-05-02 |
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US-09-847-946A-98
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 6; Conservative
                                                                      3 LDYSWL 8
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100.0%; Score 36; DB 11; Length 10;

Query Match

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; Sequence 90, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Glosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Findeis, Mark A
; APPLICANT: Findeis, Mark A
; APPLICANT: Findeis, Mark A
; PERENENCH Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT FILING NATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                            APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Ghosh, Sankar
APPLICANT: Phillishs, Kathryn
APPLICANT: Phillishs, Kathryn
APPLICANT: Hannig, Gerhard
ITILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US/09/847,946A
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR PILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
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                                            Indels
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100.08;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 6; Conserv
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ITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
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                                                                                                                                                                                                                                   91.7%; Score 33; DB 12; Length 73; 83.3%; Pred. No. 1.4e+02; ive 1; Mismatches 0; Indels
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Taupler Jr, Raymond J
Moore, No. US20040010119Allle
Shenoy, Suresh
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PRIOR FILING DATE: 2001-02-12
PRIOR PELING DATE: 2001-02-12
PRIOR PELING DATE: 2001-02-12
PRIOR PELING DATE: 2001-031
PRIOR PELING DATE: 2001-031
PRIOR APPLICATION NUMBER: 60/268,496
PRIOR PELING DATE: 2001-02-13
PRIOR PELING DATE: 2001-03-16
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PRIOR PELING DATE: 2001-10-18
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. Spytek, Kimberly A
. Guo, Xiaojia (Sasha)
. Fernandes, Elma
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Blalock, Angela
Ballinger, Robert
Vernet, Corine
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Malyankar, Uriel M
Gusev, Vladimir
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Millet, Isabelle
Peyman, John
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Mezes, Peter S
Ellerman, Karen
Heyes, Melvin P
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Gunther, Erik
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Liu, Xiahong
Casman, Stacie
Boldog, Ferenc
                              SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 310
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Matches 5; Conservative
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Pena, Carol E
   NUMBER OF SEQ ID NOS: 547
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                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-074-978A-310
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46 LDYTWL 51
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                                                          100.0%; Score 36; DB 11; Length 11; 100.0%; Pred. No. 8.9;
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Pena, Carol E A
Shimkets, Richard A
Taupier Jr, Raymond J
Moore, No. US20040010119A11le
Shenoy, Suresh
Edinger, Shlomit
Gunther, Erik
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APPLICANT: SPYCEK, Kimberly A
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Fernandes, Elma
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Malyankar, Uriel M
Guev, Vladimir
Rastelli, Luca
Mezes, Peter S
Ellerman, Karen
Heyes, Melvin P
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Casman, Stacie
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Ballinger, Robert
Vernet, Corine
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Millet, Isabelle
Peyman, John
                                                       Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
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Kekuda, Ramesh
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US-10-074-978A-310
US-09-847-946A-90
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Search completed: February 18, 2004, 15:41:59 Job time : 17.7529 secs

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36 100.0 9 23 AAM48851 36 100.0 9 23 AAM488595 36 100.0 10 23 AAM488590 36 100.0 10 23 AAM488590 36 100.0 11 23 AAM488593 36 100.0 11 23 AAM48887 36 100.0 11 23 AAM48887 36 100.0 12 23 ABB77297 37 91.7 390 22 ABB77297 39 91.7 404 19 AAW59035 31 91.7 404 19 AAW31344		32 88.9 9 23 32 88.9 9 82 33 32 88.9 9 82 33 32 88.9 9 9 23 32 88.9 9 9 23 32 88.9 9 9 23 32 88.9 9 9 23 32 88.9 9 10 23 32 88.9 9 11 23 32 88.9 9 69 22 88.9 9 9 69 22 88.9 9 9 69 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9 9 22 88.9 9	SUL	KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis; rhumandendarond arthritis; Crohn's disease; multiple solerosis; HIV; rhumancotorotectorid; immunosuppression; antiinflammatory; immunosuppressive; corticosterorid; immunosuppression; antiantatory; anti-HIV; human; watiarteriosclerotic; virucide; antiasthmatic; antiallergic; dermatological; antibacterial; antipsoriatic; antirheumatic; KW antiarthritic; osteopathic; antiulcer; mutein. XX Anno sapiens. Synthetic. Location/Qualifiers FT Key Misc-difference 3 Motoe 13 Motoe 147 Misc-difference 3 Motoe 15847-A2. XX XX XX XX XX XX XX XX XX
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. protein - protein search, using sw model on: February 18, 2004, 13:37:19; Search time 22.7763 Seconds (without alignments) 41.814 Million cell updates/sec	Title: DS-09-643-260-12 Perfect score: 36 Sequence: 1 LDYSWL 6 Scoring table: BLOSUM62 Searched: 1107863 seqs, 158726573 residues Total number of hits satisfying chosen parameters: 1107863 Manimum DB seq length: 0 Manimum DB seq length: 0 Manimum DB seq length: 0 Manimum DB seq length: 0 Manimum DB seq length: 0 Manimum DB seq length: 0 Manimum DB seq length: 0	Docessing: Minimum Match Of Maximum Match 10 Listing first 10 Listing first 10 Listing first 11: /SIDSI/gcgdat 2: /SIDSI/gcgdat 3: /SIDSI/gcgdat 4: /SIDSI/gcgdat 5: /SIDSI/gcgdat 6: /SIDSI/gcgd	8: /SIDS1/gcgdata/geneseq/geneseqp-emb]/AA1987.DAT:* 9: /SIDS1/gcgdata/geneseq/geneseqp-emb]/AA1980.DAT:* 10: /SIDS1/gcgdata/geneseqg/geneseqp-emb]/AA1980.DAT:* 11: /SIDS1/gcgdata/geneseqg/geneseqp-emb]/AA1990.DAT:* 12: /SIDS1/gcgdata/geneseqg/geneseqp-emb]/AA1991.DAT:* 13: /SIDS1/gcgdata/geneseqg/geneseqp-emb]/AA1992.DAT:* 14: /SIDS1/gcgdata/geneseqg/geneseqp-emb]/AA1992.DAT:* 15: /SIDS1/gcgdata/geneseqg/geneseqp-emb]/AA1993.DAT:* 16: /SIDS1/gcgdata/geneseqg-emb]/AA1994.DAT:* 17: /SIDS1/gcgdata/geneseqg-emb]/AA1995.DAT:* 18: /SIDS1/gcgdata/geneseqg-emb]/AA1997.DAT:* 19: /SIDS1/gcgdata/geneseqg-emb]/AA1997.DAT:* 20: /SIDS1/gcgdata/geneseqg-emb]/AA1999.DAT:* 21: /SIDS1/gcgdata/geneseqg-emb]/AA1999.DAT:* 22: /SIDS1/gcgdata/geneseqg/geneseqg-emb]/AA2001.DAT:* 23: /SIDS1/gcgdata/geneseqg/geneseqg-emb]/AA2001.DAT:* 24: /SIDS1/gcgdata/geneseqg/geneseqg-emb]/AA2001.DAT:* 24: /SIDS1/gcgdata/geneseqg/geneseqg-emb]/AA2001.DAT:* 24: /SIDS1/gcgdata/geneseqg-emb]/AA2001.DAT:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Summaries Result Ouery No. Score Match Length DB ID 1 36 100.0 6 23 AAB808734 Mutated IKKbeta NE AAA48517 AAA4852 AAA48592 AAA48592 AAA48592 AAA48596 AAA48596 AAA48596 AAA48596 AAA48596 AAA48596 AAA48596 AAA48596 AAA48596 AAA48596 AAA48596 AAA48596 AAA48596 AAA48596 AAA48596 AAA48596 AAA48597 AAA48597 AAA48597 AAA48597 AAA48597 AAA48597 AAA48597 AAA48597 AAA48597 AAA48597 AAA48597 AAA48597 AAA48597 AAA48597 AAA48597 AAA48597 AAA48597 AAA445888

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antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive, dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NRkappaB; IkappaB kinase beta; IKKOeta, cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antiabacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatheroscletoric, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkAppaB. The compounds are useful for treating inflammatory disorders, e.g. asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lung inflammation or cancer, psoriagis, rheumatoid arthritis, osteoarthritis, inflammatcory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia relangiactesia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
                                         Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM48620-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an antiinflammatory compound (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 6; Page 48; 88pp; English.
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22-AUG-2000; 2000US-0643260.
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    The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB00725-ABB00725-ABB00725-ABB00725-ABB00725-ABB00725-ABB00725-ABB00725-ABB00725-ABB00725-ABB00725-ABB00725-ABB00725-ABB00725-ABB00725-ABB00725-ABB00725-ABB00725-ABB00725-ABB00725-ABB00725-ABB00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-ABF00725-
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting a cell with an anti-inflammatory compound comprising at least one NEMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               urticāria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis, rheumatorid arthritis, ostecarthritis, psoriatic arthritis, inflammatory bowel disease, chronic obstructive pulmonary disease, vasculitis and bursitis. The inflammatory disorder may also be dermatitis, eczema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        psoriasis, osteoarthritis, psoriatic arthritis, lupus and spondylathritis. Also for Crohn's disease, ulcerative colitis, bolymyalqia, scleroderma, Wegner's granulomatosis, temporal arteritis, cryoglobulinaemia or multiple sclerosis. For chronic viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 23; Page 45; 82pp; English.
                                                                          02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
02-MAY-2001; 2001WO-US40654
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                                                                                                                                                                                              (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                Ghosh S;
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Phillips K;

Findeis MA,

Ghosh S,

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Gaps
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                                             Length 6;
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                                            100.0%; Score 36; DB 23;
100.0%; Pred. No. 9.3e+05;
ive 0; Mismatches 0;
                                                                                                                                                                             AAM48540 standard; Peptide; 6 AA.
                                                                     6; Conservative
                                                         Local Similarity
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ID AAM4
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arthritis

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Indels

100.0%; Score 36; DB 23; Length 6; 100.0%; Pred. No. 9.3e+05;

0; Mismatches

6; Conservative

1 LDYSWL 6

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Query Match Best Local Similarity Matches 6; Conserv

AAM48517 standard; Peptide; 6 AA

RESULT 2 AAM48517 NBD mutant peptide SEQ ID NO 12.

20-MAR-2002 (first entry)

AAM48517;

EXEXEX B

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WPI; 2002-121889/16.
                                                  (UYYA ) UNIV YALE.
                                                                                                                 Sequence 6 AA;
                                 WO200183554-A2.
                                    38-NOV-2001
                             Synthetic.
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                                                                  psoriasis
 AAM48540;
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Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirhoumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NBMO binding domain; ezcema; cytokine; NPkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel antinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                        Anti-inflammatory peptide SEQ ID NO 95.
                                                     AAM48592 standard; Peptide; 6 AA.
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                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     psoriasis
                     AAM48592
                                                                             The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48629-AAM48645), comprising a membrane translocation domain (AAM48629-AAM48620). The AAM486651 which compounds from 6-15 anino acid residues, fused to a NEWO binding sequence (AAM48619). The antiinflammatory compounds have antiasthmatic, antibacterial, antipacriatic, antirheumatic, antiarthitic, osteopathic, corpounds act as selective inhibitors of cytokine-mediated NFkappaB compounds act as selective inhibitors of cytokine-mediated NFkappaB compounds act as selective inhibitors of cytokine-mediated NFkappaB compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, pooriasis, rheumatoid arthritis, actiommune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis, transplant rejection; osteoporosis, catheimer's disease; atherosclerosis; viral infections; and ataxia telangiectusia. The compounds are also useful for treating to treating to treating the corpounds of scenesh, anaphylaxis, and disease atherosclerosis; viral infections; and ataxia telangiectusia. The compounds are also useful for treating and ataxia arthritis, arthritis, anticommune diseases, and setul for treating corfored or food sensitivity, eczema, dermatitis, sunburn, aging and
                                                                                          Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; noctropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; defendation of the manatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEWO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteopoxosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phillips K;
                                                Anti-inflammatory peptide SEQ ID NO 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 61; 88pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAY-2001; 2001WO-US14346.
20-MAR-2002 (first entry)
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Findeis MA, Phillips K;

The invention relates to an antiinflammatory compound (especially AMM48628-AMM48645), comprising a membrane translocation domain (AMM48628-AMM48646), comprising a membrane translocation domain cand residues, fused to a NEWO binding sequence (AAM48619). The antiinflammatory compounds have antisthmatic, ortostatic, antipocriatic, antiheumatic, antiathritic, osteopathic, corpounds act as selective inhibitors of cytokine-mediated NRRappaB activation and subsequent decreased phosphorylation of IKKbeta kinase activation by blocking interaction of IkappaB kinase beta (IKKbeta kinase activation and subsequent decreased phosphorylation of IKKppaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, orticalmantory bowel disease, sepsie, vasculitis, bursitis, untiple sclerosis; viral infections; and etaxia telemer's diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's diseases, and seases the compounds are also useful for treating profilemer, and seases conditions; and ataxia telangiectasia. The compounds are also useful for treating and crais arthritis; arthritis, and prompanes such as allergies, urticaria, anaphylaxis, arthritis arthritis; arthritis, and ataxia telangiectasia. The compounds are also useful for treating and ataxia arthritis; arthritis; arthritis; anaphylaxis, arthritis; arthritis; arthritis; anaphylaxis, arthritis; arthritis; anaphylaxis, arthritis; arthritis; anaphylaxis, arthritis; arth Claim 6; Page 62; 88pp; English.

Sequence

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Gaps ; 0

100.0%; Score 36; DB 23; Length 6; 100.0%; Pred. No. 9.3e+05; Artive 0; Mismatches 0; Indels

6; Conservative

Query Match Best Local Similarity Matches 6; Conserv

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Similarity
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Matches
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                                                                                                                                                                                                                                                      RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; antiinflammatory compound; NEMO binding domain; NBD; IKKDeta; IkappaB kinase-alpha; IKKAlpha; NF-kappaB; nuclear factor-kappaB induction; inflammatory disorder; autoimmune disease; osteoporosis; cancer; Alzheimer's disease; atherosclerosis; viral infection; Ataxia telangiectasia; transplantation detection; immunosuppressive, osteopathic; cytostatic; nootropic; neuroprotective; antiatherosclerotic; virucide; vasotropic; antirheumatic; antiatherosclerotic; virucide; vasotropic; antirheumatic; antiatheritic; mutant; mutein.
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   Score 36; DB 23; Length 6; Pred. No. 9.3e+05;
                                                                Indels
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                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                 ABU08427 standard; peptide; 6 AA.
   100.0%;
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22-AUG-2000; 2000US-0643260.
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                                                                    Conservative
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Query Match
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Matches 6; Conserv
                                                                                                                              1 LDYSWL 6
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100.0%; Score 36; DB 24; Length 6;

Query Match

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AMM48620-AMM48645), comprising a membrane translocation domain (APM48620-AMM48645), comprising a membrane translocation domain (AAM48620-AMM48645), comprising a membrane translocation domain amino acid residues, fused to a NEMO binding sequence (AAM48620-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antitheumatic, antiarthritic, osteopathic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKkbeta kinase activation and subsequent decreaced phosphorylation of IKkpeta kinase activation and subsequent decreaced phosphorylation of IKkpeta kinase activation and subsequent decreaced phosphorylation of IKkpeta kinase compounds are useful for treating inflammatory disorders, e.g. asthma, ungitial antimities, osteoparthritis, inflammatory bowel disease, seepsis, vasculitis, osteoparthritis, inflammatory bowel disease, sepsis, vasculitis, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiactasia. The compounds are also useful for treating anaphylaxis, pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
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                        Gaps
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100.0%; Pred. No. 9.3e+05; ive 0; Mismatches 0;
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22-AUG-2000; 2000US-0643260.
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(UYYA ) UNIV YALE.
                          6; Conservative
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                                                                   1 LDYSWL 6
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                                                                                                              LDYSWL
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sepsis, vasculitis,

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WO200183554-A2
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                                                                                                                                                                                                                                                                                                  Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEWO binding domain; ezzema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatold arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporogis; Alzheimer's disease; atherosclerosis; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AM48621) comprising a membrane translocation domain acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antisperiatic, antimhematic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, antibacterial, immunosuppressive, dermatological, neuroprotective, oncorpola ac as selective inhibitors of cytokine-mediated NEMAppaB activation by blocking interaction of IkappaB kinase beta (IKKbeta kinase the NEWO binding domain that results in inhibition of IKKbeta kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis,
                                                                                        Gaps
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drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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                                                              100.0%; Score 36; DB 23; 100.0%; Pred. No. 9.3e+05;
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                                                                                                                                                                                                  AAM48589 standard; Peptide; 8 AA.
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Best Local Similarity
Matches 6; Conserv
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               arthritis.
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bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 36; DB 23; 100.0%; Pred. No. 9.3e+05;
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(AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15

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compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEWO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatory disorders, e.g. asthma, osteoarthritis, inflammatory bowel disease, sepsis, vascultis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis, Alzheiner's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, utiliamia, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain

Claim 6; Page 62; 88pp; English.

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(AAM48525-AAM48619). The antinflammatory compounds have antiasthmatic, cytostatic, antipostriatic, antinflammatory compounds have antiasthmatic, cytostatic, antipostriatic, antimostriatic, antimostriatic, antimostriatic, antimostriatic, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB compounds act as selective inhibitors of cytokine-mediated NFkappaB compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psociasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, dranning diseases such as lupus, polymyladia, scleroderma, granulomatosis, multiple sclerosis, transplant rejection; osteoprosis; dranning compounds are also useful for treating inflammatoris, and ataxia the compounds are also useful for treating centering inflammatoris, and ataxia the compounds are also useful for treating centering cente
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Live 0; Mismatches 0;
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(AAM48620-AAM48645). Comprising a membrane translocation domain.

(AAM48620-AAM48645). The antiniflammatory compounds have antiasthmatic, amino acid residues, fused to a NEWO binding sequence of cytostatic, antipactatic, antiarbardatic, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-inflammatory peptide SEQ ID NO 97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM48594 standard; Peptide; 9 AA.
                                    Claim 6; Page 62; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.
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psoriasis
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The invention relates to an antiinflammatory compound (especially AAM48629, comprising a membrane translocation domain (AAM48620-AAM48619), comprising a membrane translocation domain (AAM48620-AAM48619). The antiinflammatory compounds have antiathmatic, amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiathmatic, antipacterial, immunosuppressive, dermatological, neuroprotective, ortipacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerocic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB cativation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKkpeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, inflammatory no cancer, psoriasis, rheumatory disorders, e.g. asthma, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, undiminantory bowel disease, sepsis, vasculitis, and ataxia telangiectasia. The compounds are also useful for treating inflammatory responses such as allergies, unicaria, and ataxia telangiectasia. The compounds are also useful for treating provinced and allergies, unicaria, and ataxia decreases.
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                                                                             Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
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WPI; 2002-121889/16.
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Best Local Similarity
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Phillips K;

Findeis MA,

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The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48628-AAM48629), comprising a membrane translocation domain (AAM48629-AAM48629). The AAM486519 which comproises from 6-15 amino acid residues, fused to a NERWO binding sequence (AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, antibacterial, immunosuppressive, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NERapaB activation by blocking interaction of IxapaB kinase beta (IKKbeta) at the NEWO binding domain that results in inhibition of IxapaBs. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, bowel disease, sepsis, vasculitis, bursitlammatory bowel disease, sepsis, vasculitis, bursitial autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating conflammatory responses such as allergies, urticaria, anaphylaxis, arthritis, anticonflammatory responses such as allergies, urticaria, anaphylaxis, arthritis, anticonflammatory responses such as allergies, urticaria, anaphylaxis, arthritis, anticonflammatory responses such as allergies, urticaria, anaphylaxis, anticonflammatory descena, dermatitis, sunburn, aging and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 62; 88pp; English.
                                                                                                                                                  02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.
                                                                                          02-MAY-2001; 2001WO-US14346.
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Best Local Similarity
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                                                                                                                                                                                                                                                                           (UYYA ) UNIV YALE.
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                                  08-NOV-2001.
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AMM48620-AMM48645), comprising a membrane translocation domain

(AAM48620-AMM48645), comprising a membrane translocation domain

(AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15

amino acid residues, fused to a NEWO binding sequence

(AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,

crostatic, antistoriatic, antiinflammatory compounds have antiasthmatic,

antibacterial; immunosuppressive, dermatological, neuroprotective,

compounds act as selective inhibitors of cytokine-mediated NEKAppaB

activation by blocking interaction of IkappaB kinase beta (IKKbeta) at

the NEMO binding domain that results in inhibition of IKKbeta kinase

activation and subsequent decreased phosphorylation of IKAppaB. The

compounds are useful for treating inflammatory disorders, e.g. asthma,

compounds are useful for treating inflammatory disorders, e.g. asthma,

compounds are useful for treating inflammatory disorders, e.g. asthma,

compounds are useful for treating inflammatory disorders, e.g. asthma,

compounds are useful for treating inflammatory disorders, e.g. asthma,

compounds are useful for treating inflammatory disorders, e.g. asthma,

compounds are diseases such as lupus, polymyalgia, scleroderma,

granulomatosia, multiple sclerosis, transplant rejection; osteoporosis,

clangiectasia. The compounds are also useful for treating

pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

chang or food sensitivity, eczema, dermatitis, sunburn, aging and
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                                                                                                                                                                                                                                                                                                 domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to an antiinflammatory compound (especially
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                                                                                                                                                  Ghosh S, Findeis MA, Phillips K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-inflammatory peptide SEQ ID NO 93.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 62; 88pp; English.
22-AUG-2000; 2000US-0643260.
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                                                        (PRAE-) PRAECIS PHARM INC (UYYA ) UNIV YALE.
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                              Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
                                          Gaps
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100.0%; Score 36; DB 23; Length 10; 100.0%; Pred. No. 3.9;
                                          0; Indels
                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                               Anti-inflammatory peptide SEQ ÍD NO 96.
                                                                                                                                                                                                                            AAM48593 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                                           20-MAR-2002 (first entry)
                                          6; Conservative
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LDYSWL 7
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Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic, antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEWO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.

RESULT 13 AAM48590

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WO200183554-A2

Synthetic.

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AMM48620-AMM48645), comprising a membrane translocation domain.

(AAM48620-AMM48645), comprising a membrane translocation domain and residues, fused to a NEMO binding sequence.

(AAM48520-AMM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antiinflammatory compounds have antiasthmatic, antibacterial, immunosuppressive, dermatological, neuroprotective, ontorpic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKkbeta kinase activation and subsequent decreased phosphorylation of IKAppaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoparessis, costeoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis, transplant rejection, osteoporosis, continents and seases atherocalenosis; viral infections; and ataxia
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                                                                                                                                                                                                                                                                                                                                                                                                   Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an antiinflammatory compound (especially
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                 staxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                             Phillips K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 62; 88pp; English.
                                                                                                                                                                                                                                                                                                                             May MJ, Ghosh S, Findeis MA,
                                                                                                                                                                                                         02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
                                                                                                                                                                   02-MAY-2001; 2001WO-US14346.
                                                                                                                                                                                                                                                                 (PRAE-) PRAECIS PHARM INC. (UYYA ) UNIV YALE.
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                                                                                                                               08-NOV-2001
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arthritis.
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compounds are useful for treating inflammatory derivation of IKKbeta kinase compounds are useful for treating inflammatory compounds have antiasthmatic, cytostatic, antiporiatic, antiheumatic, antiarthriar, osteopathic, antiboriatic, antiheumatic, antiarthriar, osteopathic, compounds are as selective, inhibitors of cytokine mediated NR appas activation by blocking interaction of Ikappas kinase beta (IKKbeta kinase the NBMO binding domain that results in inhibition of IKKbeta kinase compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases such as lungs, polymyalgia, scleroderma, cytomulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
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                 immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NENO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKDeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alzheimer's disease, atherosclerosis, viral infections, and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
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antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
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Similarity 100.0%; Pred. No. 4.3;
6; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Findeis MA,
                                                                                                                                                                                                                                                                                                                                                         02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.
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Similarity 100.0%; Score 35; DB 11; Length 179; Similarity 100.0%; Pred. No. 37; 6; Conservative 0; Mismatches 0; Indels (Nature 420:563-573(2002).
EMBL, AK033531; BAC28343.1; -.
Hypothetical protein.
SEQUENCE 179 AA; 21321 MW; CBF710227B0CDB18 CRC64; Query Match Best Local Similarity LDFSWL 10 1 LDFSWL 6 Matches g 3 K K S ઠે Q8bzu5 mus musculu Q91838 coturnix co P95247 mycobacteri Q55047 bhigella so Q98041 plesiomonas Q9f738 ehigella so Q84778 ehigella fas Q94240 oryza sativ Q9pej5 xylella fas Q85619 salmonella Q8450 salmonella Q8450 salmonella Q84970 helicobacte Q97xx helicobacte Q97xx helicobacte Q97xy neisseria m Q91rn9 neisseria m Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. February 18, 2004, 14:09:39; Search time 17.3684 Seconds (without alignments) 89.145 Million cell updates/sec Description GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. Total number of hits satisfying chosen parameters: 830525 seqs, 258052604 residues SUMMARIES Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM protein - protein search, using sw model 991838 995247 055047 095071 098738 0804K7 09750 09950 094950 09500 09500 097709 sp_cates sp_phage:* sp_phage:* sp_rodent:* sp_rodent:* sp_vartebrate:* sp_vartebrate:* Gapop 10.0 , Gapext 0.5 9p_humān:*
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	Eukaryota; Metazoa;	Metazo	a; Chordata;	dati		Craniata; Vertebrata; Eu	Euteleostomi	į,
	Mammalia; Eutheria;	utheri		nti		Sciurognathi, Muridae, N	Murinae; M	Mus.
	NCBI_TaxID=10090;	10000;						
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2 K	STRAIN=C57BL/6J; TISSUE=Colon; MEDIINE-22354683: D:: D:: Med-12466	L/6J; 54683:	TISSUE=Colon;	3 6	on; 466851.			
	The FANTOM Consortium.	Consor	tium.	1	, ,			
	the RIKEN G	enome	Explora	tion	n Research (the RIKEN Genome Exploration Research Group Phase I &	II Team;	
	"Analysis o	f the	mouse t	ran	of the mouse transcriptome ba	based on functional	nal annotation	tion of
E i	60,770 full	-lengt	full-length cDNAs.";	=.				
	Nature 420:	563-57	3 (2002)					

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Q91838 PRELLMINARY; PRT; Q91838; 01-OCT-2000 (TrEMBLrel. 15, Created)

RESULT 2 Q91838 ID Q918: AC Q918: DT 01-O

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                                                                                                                                                                                                                                                                                                                                                                "Sequence analysis of avian interferon regulatory factors (IRF) reveals close relation of the chicken and quail interferon induced transcriptional apparatus. Cytogenetic studies and sequence comparison of the avian IRF-1, ICSBP and a MRC class II gene reveals that the avian cell line C-32 is derived from quail."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=H37Rv;
MEDLINE=98295987; PubMed=9634230;
MEDLINE=98295987; PubMed=9634230;
Goldon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Romill T., Genlles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
                                                                                               Coturnix coturnix (Common quail), and
Coturnix coturnix; Japonica (Japanese quail).
Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                         SPECIES=C.coturnix;
Zoeller B., Mueller I., Nanda I., Guttenbach M., Dosch B., Schmid M.,
Jungwirth C.;
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SPECIES-C.coturnix japonica; STRAIN-BREED:FRANZOESISCHE MASTWACHTEL;
Soeller B., Ingrid R.M., Nanda I., Guttenbach M.;
"Sequence comparism of avian interferon regulatory factors and identification of the avian CEC-32 cell as a quail cell line.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJZ71052; CAC01088.1; -.
                           )1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
interferon regulatory factor 1 (Interferon regulatory factor-1)
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical 37.4 kDa protein (PPE family protein).
RV2352C OR MTCY98.2IC OR MT2419
01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
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PRINTS; PR00267; INTERNREGECT.
ProDom; PD002355; IRF; 1.
SWART; SM00348; IRF; 1.
PROSITE; PS00601; IRF; 1.
SEQUENCE 315 AA; 36257 MW; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
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                                                                                                                                                                                                                   NCBI_TaxID=9091, 93934;
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Best Local Similarity
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Matches
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     DDA RELEASE OF RELEASE OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF 
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SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland B., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genetic analysis and identification of an IS630 element in the form I
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                                                                                                                                                                                                                                                                                                           "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Form I operon ORF protein genes, insertion sequence IS630
                                                                                                                                                                                                                                                                                                                                        laboratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; Z83860; CAB06149.1; -. EMBL; AE007082; AAK46712.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U34305; AAA84874.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; Complete proteome.
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407 AA; 47980 MW; 23BFAF09EEBD55D7 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tuberculist, Rv2352c; -.
InterPro; IPR000030; Microbac_PPB.
Edm; PF00823; PPB; 1.
Hypothefical protein; Complete pro; SEQUENCE 391 AA; 37355 MW; 360)
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NCBI_TaxID=624;
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01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
ORFSP (WBGV) (ORFSG).
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STRAIN=53G;
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"Comparison of the O antigen gene clusters of Escherichia coli (Shigella) Sonnei and Plesiomonas shigelloides O17: Sonnei gained its current plasmid borne O antigen genes from Plesiomonas shigelloides in
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STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.P., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 415;
                                                                                                                                                                                  100.0%; Score 35; DB 2; Length 414; llarity 100.0%; Pred. No. 88; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE007082; AAK46715.1; -.
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                                                                                                                                           414 AA; 49034 MW; EA6CA44A19ACD8CD CRC64;
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Last annotation update)
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100.0%; Pred. No. 88;
iive 0; Mismatches 0;
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                                                               a recent event.";
Infect. Immun. 68:6056-6061(2000)
EMBL; AF285971; AAG17422.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2002 (TrEMBLrel. 22,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
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Matches 6; Conservative
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SEQUENCE 415 AA; 40
                                                                                                                                                                                                                                                                                                             175 LDFSWL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPE family protein.
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les 6; Conserv
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                                                                                                                          Plasmid
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Matches
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"Molecular cloning and characterization of the O-antigen gene cluster
of Shigalla sonnei: genetic etablitry, proposed biosynthetic pathway
and essential genes for expression of form I O polysaccharide in
Submitted (AGG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR025970; BAAG1712.1; --
EMBL, AF294823; AAK85169.1; --
                                                                                                                                                            Chida T., Okamura N., Yoshida Y., Ohtani K., Arakawa E., Watanabe H.; "Complete DNA sequence of the O-antigen (rfb) gene cluster in Plesiononas shigelloides serotype 017 having the same O-antigen as Shigella sonnei: comparison with that of S. sonnei."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                  "Genetic analysis of Shigelia sonnei form I antigen: idetification of novel IS630 as an essential element for the form I expression."; Microb. Pathog. 25:165-173(1998).
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                                          Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Shigella.
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  Plesiomonas shigelloides (Aeromonas shigelloides), and
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Last annotation update)
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                                                                                                                                       SPECIES-P. shigelloides; STRAIN-SEROTYPE 017;
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MEDLINE-99036814; PubMed-9817819;
Houng H.H., Venkatesan M.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 35; DB 100.0%; Pred. No. 88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=53G1;
MEDLINE=20448976; PubMed=10992522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shepherd J., Wang L., Reeves P.R.;
                                 Bacteria, Proteobacteria, Gammar
Enterobacteriaceae, Plesiomonas
NCBI_TaxID=703, 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                         Shigella sonnei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid Pinv.
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Salmonella typhimurium.
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084950
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SO KE KA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 35; DB 10; Length 1115; 100.0%; Pred. No. 2.4e+02; cive 0; Mismatches 0; Indels 0
                       Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0132; GLHVORLASEZ."
PROSTIE; PS00713; GLYCOSYL HYDROL F2 1; 1.
PROSTIE; PS00608; GLYCOSYL HYDROL F2 2; 1.
SEQUENCE 1115 AA, 126078 WW, TABERGAA305CARC5 CRC64;
                                                                                               the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Xf1033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AA
                                                                                                                                                             InterPro; IPR006101; Glyco hydro 2.
InterPro; IPR006102; Glyco hydro 21g.
InterPro; IPR006102; Glyco hydro 21g.
InterPro; IPR006104; Glyco hydro 21g.
InterPro; IPR006103; Glyco hydro 271M.
InterPro; IPR004200; Glyco hydro 42C.
InterPro; IPR004199; Glyco hydro 42C.
InterPro; IPR004199; Glyco hydro 42N.
Fram; PP02303; Bgal_small_C; 1.
Fram; PP02929; Bgal_small_N; 1.
Fram; PP02936; Glyco hydro 2; 1.
Fram; PP02837; Glyco hydro 2 C; 1.
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MEDLINE=20365717; PubMed=10910347;
                                                                                            Submitted (MAY-2001) to the EMBL; AP003683; BAB64698.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    697 LDFSWL 702
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                Gramene; Q942A0;
                                                                          clone: P0431G06."
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Q9PEJ5
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davise R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                                                                                                                               Gaps
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Enterobacteriaceae; Salmonella.
NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of a multiple drug resistant Salmonella
Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meidanis J., Setubal J.C.; "The genome sequence of the plant pathogen Xylella fastidiosa."; Nature 406:151-159(2000).
                                                                                                                                                                                                                                                                                         °;
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83.3%; Pred. No. 72;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                   Score 33; DB 16; Length 61;
Pred. No. 30;
                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l protein; Complete proteome.
144 AA; 16390 MW; ECOEDA7F0E325B08 CRC64;
                                                                                                                 EMBL, AE003940, AAF83843.1, -.
Hypothetical protein, Complete proteome.
SEQUENCE 61 AA, 6849 MW, 6CD0800BD7BAE107 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sentence update)
Putative pathogenicity island protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
SSCB (Secretion system chaparone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 AA
                                                                                                                                                                                                                                                                                               1; Mismatches
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MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                   94.3%;
83.3%;
                                                                                                                                                                                                     Query Match
Best Local Similarity 83.33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001440; TPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 413:848-852(2001)
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Gaps

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STRAIN=MC58 / Serogroup B;
MEDLINE-20175755; PubMed=10710307;
Tettelin H., Saunders N.J., Heldelberg J., Jeffries A.C., Nelson K.E.,
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Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C.,
Smith D.R., Moonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JHP0093.

Helicobacter pylori J99 (Campylobacter pylori J99).

Bacteria; Froteobacteria; Epsilonproteobacteria; Campylobacterales;

Helicobacteraceae; Helicobacter.

NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.3%; Score 33; DB 16; Length 253; 83.3%; Pred. No. 1.3e+02; ive 1; Mismatches 0; Indel8
                                                                                                                                                                                           Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trust T.J.;
"Genomic sequence comparison of two unrelated isolates of
                                                                                                                                                                                                                                      0; Indels
                                                                               InterPro; IPR002718; HP OMP.
Pfam; PF01856; HP OMP; I.
Hypothetical protein; Complete proteome,
SEQUENCE 253 AA; 29463 MW; C9A6BBEZCSA90003 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 AA; 29526 MW; SCSF5239737E90AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                       94.3%; Score 33; DB 16;
83.3%; Pred. No. 1.3e+02;
iive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  518 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                      253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gastric pathogen Helicobacter pylori.",
Nature 397:176-180(1999).
EMBL; AE001448; AAD05674:1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis (serogroup B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                        EMBL; AE000532; AAD07180.1; -. TIGR; HP0101; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein NMB1485.
NMB1485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                      Conservative
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pylori.";
Nature 388:539-547(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Best Local Similarity
5; Conserve
                                                                                                                                                                                                         Similarity
5, Conserva
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149 LDFSWI 154
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                                                                                                                                                                                                                                                                                 1 LDPSWL 6
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                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9ZMX2;
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                                                                                                                                                                                                                                    Matches
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                                 STRAIN-SL1344;
Cirillo D.M., Valdivia R.H., Monack D., Falkow S.;
"Macrophage-dependent induction of the Salmonella pathogenicity island
2 type III secretion system and its role in intracellular survival.";
Mol. Microbiol. 0:0-0(1998).
                                                                                                                                                                                                                                  Hensel M., Shea J.E., Waterman R., Mundy R., Nikolaus T., Banks G., Vazquez-Torres A., Gleeson C., Fang F.C., Holden D.W.; Genes encoding putative effector proteins of the type III secretion system of Salmonella pathogenicity island 2 are required for bacterial virulence and proliferation in macrophages.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=26695 / ATCC 700392;

MEDLINE=9739467; Pubmed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,

Nelson K., Quackenbush J., Zhou L., Kirkness B.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,

Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=1534946; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori (Campylobacter pylori).Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.3%; Score 33; DB 16; Length 144; larity 83.3%; Pred. No. 72; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 AA; 16375 MW; B60EDA7F0E325B0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 AA
                                                                                                                                                                                                           MEDLINE=99000132; PubMed=9786193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF020808; AAC28884.1; -. EMBL; AJ224892; CAA12190.1; -. EMBL; AE008761; AAL20327.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein HP0101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001440; TPR.
Pfam; PF00515; TPR; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 413:852-856(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 IDPSWL 50
                  SEQUENCE FROM N.A.
                                                                                                                                                                     SEQUENCE FROM N.A.
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SEQUENCE 144 AA
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Query Match

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RESULT 12

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Gaps

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Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey B.K.,
Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
Mason T., Clecko A., Parkesy D.S., Blair E., Cittone H., Clark B.B.,
Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;
"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Wajadream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; "Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                             94.3%; Score 33; DB 16; Length 518; 83.3%; Pred. No. 2.7e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.3%; Score 33; DB 16; Length 518; 83.3%; Pred. No. 2.7e+02; Arive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
NCBI_TaxID=65699;
                                                                                                                                                                                                                                                        Pfam; PF00571; CBS; 2.
Pfam; PF03471; CorC_HlyC; 1.
Pfam; PF03741; TerC; 1.
SW00116; TerC; 1.
Hypochetical protein; Complete proteome.
SEQUENCE 518 AA; 57342 MW; CFD9324DA672DC96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      518 AA; 57358 MW; 47FBC652664E38E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
CONSERVED hypothetical integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      518 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Z2491 / Serogroup A / Serotype 4A;
MEDLINE=20222556; PubMed=10761919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000644; CBS domain.
InterPro; IPR005170; Corc HlyC.
InterPro; IPR005496; TerC.
                                                                                                                                                                        EMBL; AE002498; AAF41841.1; -. TIGR; NMB1485; -.
                                                                                                                                                        Science 287:1809-1815(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00571; CBS; 2.
Pfam; PF03471; CorC HlyC; 1.
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 83.33
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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1 MDFSWL 6
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Search completed: February 18, 2004, 14:35:50 Job time : 19.3684 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM protein - protein search, using sw model Run on:

February 18, 2004, 13:39:39; Search time 3.55263 Seconds (without alignments) 79.423 Million cell updates/sec

US-09-643-260-11 35 1 LDFSWL 6 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		di			SUMMARIES		
Result		Ouery					
No.	Score	Match	Length	88	ΩI	Description	
1	35	100.0	313	-	IRF1 CHICK	76 ga	
~	33	94.3	868	н	NI80 YEAST	sacchai	
m	31	88.6	121	٦	YGD4_YEAST		
4	31	88.6	224	~	PDXH_MYCTU	006207 mycobacteri	
S	. 31	88.6	229	н	BCL2_BOVIN	_	
9	31	88.6	236	Н	BCL2_CRILO	Q9jjv8 cricetulus	
7	31	98.6	236	-	BCL2 MOUSE	P10417 mus musculu	
æ	31	88.6	236	-	BCL2_RAT	P49950 rattus norv	
Ø	31	98.6	239	н	BCL2_HUMAN	P10415 homo sapien	
10	31	88.6	444	-	GLGA_DEIRA	Q9rws1 deinococcus	
11	31	88.6	495	-	SYC_AQUAE	O67163 aquifex aeo	
12	31	88.6	612	-	YNB8 YEAST		
13	31	88.6	612	-	YND4 YEAST		
14	31	88.6	678	-	VID3_AGRRH	P13463 agrobacteri	
15	31	88.6	1343	-	VGR2_RAT		
91 .	30	85.7	438	-	E1BL_ADECT		
17	30	85.7	745	Н	IKKA_HUMAN		
18	30	85.7	745	-	IKKA_MOUSE	Q60680 m inhibitor	
19	30	85.7	756	~4	IKKB_HUMAN	O14920 homo sapien	
50	30	85.7	757	-	IKKB_MOUSE		
21	30	85.7	757	Н	IKKB_RAT		
22	30	85.7	926	Н	MAY3_SCHCO		
23	59	82.9		Н	BCL2 CHICK	Q00709 gallus gall	
24	53	82.9		٦	TRUA_BUCAP		
25	29	82.9		٦	YG78 PSEAE		
56	53	82.9		-	CITR_BACSU		
27	53	82.9	328	-	YCDU_ECOL1	P75910 escherichia	
	29	82.9		Н	SIA9 HUMAN	Q9unp4 homo sapien	
29	29	82.9		-	ARGJ_STAEP		
30	29	82.9		-	HISZ_SYNY3		
31	29	3		-	ADMR HUMAN	O15218 homo sapien	
32	53	82.9	477	٦	GLGA ECOLI	P08323 escherichia	
33	53	82.9	477	٦	GLGA_SALTI	Q8z232 salmonella	

P05416 salmonella P05416 salmonella P36195 gallus gall O02789 monodelphis P5165 rattus norv P0857 escherichia P07989 salmonella P40813 salmonella P47662 mycoplasma P75174 mycoplasma P4784 mycoplasma
GLGA_SALTY DPOM_HUMAN DPOM_HUMAN TDT_CHICK TDT_MONDO CPF4_RAT TIMK_ECOLI TIMK_ECOLI TIM SALTY TDT_MOUSE Y423_MYCGE Y423_MYCGE
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ALIGNMENTS

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                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                        SEQUENCE FROM N.A.
Schlenstedt G., Silver P.A.;
Submitted (MAY-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                     Silver P.A.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 CAP-GLY.
175 COLLED COLL (POTENTIAL).
375 COLLED COLL (POTENTIAL).
776 COLLED COLL (POTENTIAL).
1100289 MW; A72EA9E938845081 CRC64;
                                                                    P33420; Q08917;
01-FEB-1994 (Rel. 28, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
NIP80 protein (NIP100 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 1 CAP-Gly domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S65186; S65186.
SGD; S0006095; NIP100.
GC) GC:0005869; CGynactin complex; IDA.
GC); GC:000092; P:mitotic anaphase B; IGI.
InterPro; IPR000938; CAP-Gly.
                                                           PRT;
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
MEDLINE=97313271; PubMed=9169875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFGHI, PF01302; CAP GLY; 1. PROSITE; PS00845; CAP GLY 1; 1. PROSITE; PS50245; CAP GLY 2; 1. Cytoskeleton; Colled Goil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X72227; CAA51030.1; -. EMBL; Z73530; CAA97881.1; -.
                                                           STANDARD;
 295 LDFSWL 300
                                                           NI80_YEAST
                                                                                                                                                                                                                                                        REVISIONS
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SEQUENCE
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MEDLINE=98295987; PubWed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                    Gaps
                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, annotation update)
Pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5) (PNP/PMP oxidase)
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                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hypothetical 13.6 kDa protein in MIG1-AGA2 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31; DB 1; Length 121;
Pred. No. 17;
1; Mismatches 0; Indels
Score 33, DB 1; Length 868;
Pred. No. 54;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Hebling U., Hofmann B., Delius H.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; ATP-binding.
NP BIND 77 84 ATP (POTENTIAL).
SEQUENCE 121 AA; 13573 MW; 88D46FF50B67000F CRC64;
                                                                                                                                                                                      121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 AA.
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                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last seq
01-OCT-1996 (Rel. 34, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.6%;
83.3%;
 94.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z72556; CAA96735.1; -. PIR; S64036; S64036. SGD; S0003002; YGL034C.
                                                                                                                                                                                      STANDARD;
                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
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782 IDFSWL 787
 Query Match
Best Local Similarity
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                                                                  1 LDFSWL 6
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                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
                                                                                                                                                                                     YGD4 YEAST
P53186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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PDXH_MYCTU
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                                                                                                                                                                       YGD4_YEAST
                                   Matches
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DOMAIN
      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                              STRAIN=CDC 1551 / Oshkosh,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fletschmann R.D., Hickey E.,
Feterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                            "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                     laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OXIDIZE PNP AND PMP INTO PYRIDOXAL 5'-PHOSPHATE (PLP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: Pyridoxamine 5'-phosphate + H(2)O + O(2)
pyridoxal 5'-phosphate + NH(3) + H(2)O(2).
-!- COPACTOR: FWW (BY SIMILARITY).
-!- PATHWAY: De novo synthesis of pyridoxine (vitamin B6) and pyridoxal phosphate.
-!- SIMILARITY: BELONGS TO THE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Dectiphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMB; TIGRO0558; pdxH; 1.
PROSITE; PS01064; PYRIDOX OXIDASE; 1.
Pyridoxine blosynthesis; Öxidoreductase; Flavoprotein; PMN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.6%; Score 31; DB 1; Length 224; 83.3%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 AA; 25186 MW; 66ABC0AAACE90DC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-EBB-2003 (Rel. 41, Last annotation update)
Apoptosis regulator Bcl-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01243; Pyridox oxidase; 1.
ProDom; PD006312; Pyridox oxidase; 1.
TIGRFAMs; TIGR00558; pdxH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE007101; ARK46998.1; -
PIR; F70570; F70570.
HSSP; P28225; IDNL.
TIGR; MT2682;
Tuberculist; Rv2607; -
InterPro; IPR000659; Pyridox_oxi
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z95387; CAB08613.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                             (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDFDWL 37
                                                                                                     SEQUENCE FROM N.A.
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SEQUENCE 224 AA
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002718;
                                                                                                                                                                            Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                   -I-FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulares cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibite caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1) (By similarity).

-I-SUBUNI: Forms homodimers, and heterodimers with BAX, BAD, BAK and BCl-x(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity).

-I-SUBCELLUIAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
DOMAIN: The BH4 domain is required for anti-apoptotic activity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for interaction with RAF-1 (By similarity).

PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle (By similarity). In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTMILE Protective all y cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).

SIMILARITY: Contains 1 Bc1-2 homology 2 (BH2) domain.

SIMILARITY: Contains 1 Bc1-2 homology 2 (BH2) domain.

SIMILARITY: Contains 1 Bc1-2 homology 3 (BH3) domain.

SIMILARITY: Contains 1 Bc1-2 homology 4 (BH4) domain.
                                  STRAIN=Holstein; TISSUE=Thymus;
Reyer R.A., Cockerall G.L.;
"Bovine leukemia virus accidated-leukemogenesis is correlated
"Bovine leukemia virus programmed cell death and increased expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50062; BCL2 PAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01259; BH2; 1.
PROSITE; PS01259; BH4 1; 1.
PROSITE; PS01260; BH4 1; 1.
Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
                                                                                                                                                                                               of Bcl-2.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
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POLY-ALA.
BH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000712; Bc12 BH.
InterPro; IPR003093; Bc12 BH4.
InterPro; IPR004475; Bc12 family.
InterPro; IPR004725; Bc12 reg.
Pfam; PF00452; Bc1-2; 1.
Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
TIGRFAM8; TIGR00865; bc1-2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U92434; AAB53319.1; -.
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SEQUENCE FROM N.A.
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EMBL; AJ271720; CAB92245.1; -. PIR; JC7383; JC7383.
HSSP; Q07817; 1MAZ.
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01-MAR-1989 (Rel. 10, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26491 MW;
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PROSITE; PS01260; BH4_1; 1.
PROSITE; PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.6%;
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BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00337; BCL;
SMART; SM00265; BH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
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REVISIONS TO 221-222.
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90
133
184
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Librochem. Biophys. Res. Commun. 281:404-408 (2001).

Librochem. Biophys. Res. Commun. 281:404-408 (2001).

Librochem. Biophys. Res. Commun. 1940 (2001).

Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with Caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1) (By similarity).

Lesubulti. Forms homodimers, and heterodimers with BAX. BAD, BAK and Bcl.x(L). Heterodimerization with BAX requires intact BHI and BHI domains, and is necessary for anti-apoptotic activity (By commingratity). Also interacts with APAF-1 and RAF-1 (By similarity).

LesubcEllular LoCaTION: outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.

Cell DOMAIN: The BH4 domain is required for anti-apoptotic activity and cortive mitorial membrane of the nuclear envelope and the endoplasmic reticulum.

Cell DOMAIN: The BH4 domain is required for anti-apoptotic activity and cortive with RAF-1 (By similarity).

The apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by RC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle (By similarity). In the absence of growth factors, when the anti-apoptotic activity is by other protein kinases such as BRKs and stress-activated kinases and stress-activated whosphared and stress activity of Ray, and sinilarity).
                                                                                                                                                                                                        ö
                                      POTENTIAL.
LEARAMGE (BY CASPAGES) (BY SIMILARITY).
PHOSPHORYLATION (BY PKC) (BY SIMILARITY)
ADIDDOAF98FFFIID CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A)
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tomicic M.T., Kaina B.; "Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tomicic M.T., Christmann M., Kaina B.; "Cloning and functional analysis of cDNA encoding the hamster Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (By similarity).
PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity.
SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                        ö
                                                                                                                                                        DB 1; Length 229; 33;
                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Biophys. Res. Commun. 275:899-903(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND CLEAVAGE BY CASPASES.
MEDLINE=21092839; PubMed=11181062;
                                                                                                                                                                                                                                                                                                                                                                                                                236 AA.
                                                                                                                                                      88.6%; Score 31; DB 100.0%; Pred. No. 33; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Ovary;
MEDLINE=20431763; PubMed=10973819;
                                                                                     63 PF
25099 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apoptosis regulator Bcl-2.
                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                           229 AA;
                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                201 DFSWL 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and caspase-3.";
                                                                                                                                                                                                                                                                                                                                                                                                            CRILO
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                                                                                     MOD RES
SEQUENCE
                                          RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9JJVB;
                       DOMAIN
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BCL2_CRILO
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Matches
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CLEAVAGE (BY CASPASE-3 AND CASPASE-9).
PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECURNCE FROM N.A. (ISOFORMS ALPHA AND BETA).
STRAIN=BALB/c, TISSUE=Liver;
MEDLINE=87187643; PubMed=3032455;
Megrini M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.;
Molecular analysis of mbc1-2: structure and expression of the murine gene homologous to the human gene involved in follicular lymphoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
DOMAIN 10 30 BH4.
-!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
-!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
-!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
-!- SIMILARITY: BELONGS TO THE BcL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000712; BC12_BH.
InterPro; IPR003093; BC12_BH4.
InterPro; IPR00475; BC12_Eamlly.
InterPro; IPR004725; BC12_reg.
Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMS; TIGRO0865; bcl-2; 1.
SPOSITE; PS50062; BCL2 FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
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RESULT
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                                                                                                                                                                                                                                            MEDLINE-99069407; PubMed-9952076;
Deng X., Ito T., Carr B., Mumby M., May W.S. Jr.;
Treverseible phosphorylation of Bcl2 following interleukin 3 or mediated by direct interaction with protein phosphatase 2A*.";
Dryostatin 1 is mediated by direct interaction with protein phosphatase 2A*.";
J. Biol. Chem. 273:34157-34163(1998).

1. Biol. Chem. 273:34157-34163(1998).

2. Biol. Chem. 273:34157-34163(1998).

3. Biol. Chem. 273:34157-34163(1998).

3. Biol. Chem. 273:34157-34163(1998).

4. Biol. Chem. 273:34157-34163(1998).

5. Cherrol Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells.

Regulates cell death by controlling the mitochondrial membrane caspasses. Inhibits caspasse activity either by preventing the caspasses. Inhibits caspasse activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1).

3. Subultir: Forma homodimers, and hererodimers with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1.

5. SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.

6. HATERMATIVE POWDICTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute of Entry There are no restrictions on the European Bioinformatics Institute of the EMBL outstation on the European Bioinformatics Institute on a site content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibbsib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eguchi Y., Ewert D.L., Tsujimoto Y., "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dephosphorylated by protein phosphatese 24 (PP2A).

-1- PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptosic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity.

-1- SIMILARITY: Contains 1 BCl-2 homology 1 (BH1) domain.
-1- SIMILARITY: Contains 1 BCl-2 homology 3 (BH2) domain.
-1- SIMILARITY: Contains 1 BCl-2 homology 3 (BH3) domain.
-1- SIMILARITY: Contains 1 BCl-2 homology 4 (BH4) domain.
-1- SIMILARITY: Contains 1 BCl-2 homology 4 (BH4) domain.
                                                                                                                      PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES. MEDLINE=97277291; PubMed=9115213; Ito T., Deng X., Carr B., May W.S. Jr.; "Bcl-2 phosphorylation required for anti-apoptosis function."; J. Biol. Chem. 272:11671-11673 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P10417-1; Sequence=Displayed;
                                                                                      Nucleic Acids Res. 20:4187-4192(1992)
MEDLINE=92375724; PubMed=1508712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L31532; AAA37282.1; -.
EMBL; M16506; AAA37282.1; JOINED.
EMBL; M16506; AAA37281.1; -.
                                                                                                                                                                                                                                   DEPHOSPHORYLATION BY PP2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Beta;
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PIR; B25960; TVMSB1. HSSP; Q07817; 1MAZ. MGD; MGI:88138; BC12.

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DAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLGAYL
GHK -> VGACLVE (in isoform Beta).
/FIId=VSP_000513.
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MEDLINE=95129487; PubMed=7028536;
Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
"Expression of members of the bcl.2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
Endocrinology 136:232-241(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
CLEAVAGE (BY CASPASES) (BY SIMILARITY).
PHOSPHORYLATION (BY PKC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Brain;
MEDLINE=94193015; PubMed=8144041;
Sato T., Irie S., Krajewski S., Reed J.C.;
"Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
Gene 140:291-292(1994).
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                                                                                                                                                                                                                                                                                                               splicing; Transmembrane; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31; DB 1; Length 236;
Pred. No. 34;
0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 AA; 26425 MW; AA85EF6B0766BE0A CRC64;
GO; GO:0008189; F:apoptosis inhibitor activity; IDA. GO; GO:0005515; F:protein binding activity; IPI. GO; GO:0006915; P:apoptosis; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P49950; Q62837; Q64032;
01-0CT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
08-PEB-2003 (Rel. 41, Last annotation update)
                                             InterPro; IPR001712; B122 BH.
InterPro; IPR001712; B122 BH.
InterPro; IPR001725; B122 BH.
InterPro; IPR001725; B122 EHH.
InterPro; IPR001725; B122 EHH.
InterPro; IPR001725; B122 EHH.
InterPro; IPR001725; B122 FH.
INTERPRO; IPR00173; B12; I.
SWART; SW0037; B14; I.
FWOSITE; PS01080; BH; I.
FWOSITE; PS01080; BH; I.
FWOSITE; PS01289; BH2; I.
FWOSITE; PS01269; BH3; I.
FWOSITE; PS01269; BH3; I.
FWOSITE; PS01269; BH4]; I.
FWOSITE; PS01269; BH4]; I.
FWOSITE; PS01269; BH4]; I.
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100.0%; Pre
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Best Local Similarity 100.
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1152
1152
230
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236
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DOMAIN 10
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TRANSMEM
SITE
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VARSPLIC
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PS50063;

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                                                                                                                             reconstructions of the mode of the microbardian and the microbardian membrane including factor-dependent lymphohematopoietic and neural cells.

C -!- FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the microbardian membrane permeability. Appears to function in a feedback loop system with caspases. Inhibite caspase activity either by preventing the release of cytochrome c from the microhondria and/or by binding to the apoptosis-activating factor (APAF-1).

C -!- SUBNIT: Forms homodimers, and heterodimers with BAX mand belax(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with ABAF-1 and RAF-1 (By similarity).

C -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.

C -!- SUBCELLULAR LOCATION: Expressed in a variety of tissues, with highest levels in reproductive tissues. In the adult brain, dexpression is localized in mitral cells of the olfactory bulb, granule and pyramidal neurons of hippocampus, pontine nuclei, cerebellar granule neurons, and in ependymal cells. In prenatal and pyramidal neurons and in ependymal cells. In prenatal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drain, expression is inguist and incentered in the control plate.

C -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with Rak-1 (By similarity).

C -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates BC12 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bc12 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.

C growth factors, Bc12 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.

Dephosphorylated by protein phosphatases and similarity).

C -!- PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).

C -!- SIMILARITY: Contains 1 Bc1-2 homology 1 (BH1) domain.

C -!- SIMILARITY: Contains 1 Bc1-2 homology 4 (BH4) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                     "bcl-2 messenger RNA is localized in neurons of the developing and
MEDLINE=95059917; PubMed=7969891;
Castren E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H.,
Lindholm D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMARY, SMO0337, ECL; 1.
SMART, SMO0265, BH4; 1.
TIGRAMS, TIGROO865, bcl-2; 1.
PROSITE; PS0062; BCL2 FAMILY; 1.
PROSITE; PS01289; BH2; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01269; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; S74122; -; NOT ANNOTATED_CDS.
PIR; IS3744; IS3744.
PIR; IG7432; IG7432.
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Interpro; IPR00475; Bcl2_family.
Interpro; IPR00475; Bcl2_reg.
Pfam; PP00452; Bcl2_reg.
Pfam; PP02180; BH4; 1.
                                                                                          adult rat brain.";
Neuroscience 61:165-177(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000712; Bcl2_BH.
InterPro; IPR003093; Bcl2_BH4
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MEDIINE-52375724; PubMed=1508712;
Eguchi Y., Ewert D.L., Tsujimoto Y.;
"Isolation and characterization of the chicken bcl-2 gene: expression
in a variety of tissues including lymphoid and neuronal organs in
                                                                                          CLEAVAGE (BY CASPASES) (BY SIMILARITY). PHOSPHORYLATION (BY PKC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cleary M.L., Smith S.D., Sklar J.; "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin transcript resulting from the t(14,18)
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88196071; PubMed=2834197;
Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S.,
Goldman P., Korsmeyer S.J.;
"Alternative promoters and exons, somatic mutation and deregulation
of the Bcl-2-Ig fusion gene in lymphoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
MEDLINE=86259760; PubMed=3523487;
Tsujimoto Y., Croce C.M.,
Tsujimoto Y., Croce C.M.,
Tsujimoto Y., the structure, transcripts, and protein products of bcl-2, the gene involved in human follicular lymphoma.";
Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                          DB 1; Length 236; 34;
Mitochondrion; Phosphorylation.
                                                                                                                          A -> R (IN REF. 2).
E -> G (IN REF. 1).
S -> Y (IN REF. 2).
L -> Q (IN REF. 2).
H, E7688CB9071A872A CRC64;
                                                                                                                                                                                                                                                            0; Indels
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                    P10415; P10416; Q13842; Q16197; 01-MAR-1989 (Rel. 10, Created) 01-APR-1993 (Rel. 25, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                            Mismatches
                                           BH1.
BH2.
POTENTIAL.
                                                                                                                                                                                                                            Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adult and embryo.";
Nucleic Acids Res. 20:4187-4192(1992)
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                                                                                                                                                                                                                            88.00,
100.0%; Pre-
                                                                                                                                                                                              26622 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS TO 96; 110 AND 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apoptosis regulator Bcl-2.
                                                                                                                                                                                                           Query Match
Best Local Similarity 100...
-108 -109 -109
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBO J. 7:123-131(1988)
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                                                                                                                                                                                            236 AA;
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 Apoptosis;
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                                                                                                                                                          CONFLICT
CONFLICT
SEQUENCE
                                                                               TRANSMEM
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membrane of the nuclear envelope and the endoplasmic reticulum.

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Conservative
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                                                                    426 LDFSW 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                         ഹ
                                                                                                                                                                                                                                                                                                                                             CYSS OR AO 1068.
Aquifex aeolicus.
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                         1 LDFSW
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ID YNB8 YEAST
AC P53976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                              SYC_AQUAE
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0
                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- FUNCTION: Synthesizes alpha-1,4-glucan chains using ADP-glucose.
-!- CATALYTIC ACTIVITY: ADP-glucose + { (1,4)-alpha-D-glucosyl} (N) = ADP + { (1,4)-alpha-D-glucosyl} (N+1).
-!- PATHWAY: Glycogen biosynthesis; second step.
-!- SIMILARITY: Belongs to the glycosyltransferase family 1.
Bacterial/plant glycogen synthase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
MEDLINE=20036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Wonffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewki C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4 1; 1.
PROSITE; PS50063; BH4 2; 1.
PROSITE; PS50063; BH4—2; 1.
MILCOHONDATION; POPEDSIS; Alternative splicing; Transmembrane; Milcohondrion; Phosphorylation; Chromosomal translocation; Polymorphism; Disease mutation; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glycogen synthase (EC 2.4.1.21) (Starch [bacterial glycogen]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 444;
67;
                                                                                                                                                                                 Length 239,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deinococcus radiodurans.
Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
Deinococcaceae; Deinococcus.
                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF_00484; -; 1.
InterPror; TRR001296; Glyco_trans_1.
Pfam; PF00534; Glycos_transf_1; 1.
Glycogen biosynthesis; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP-GLUCOSE (BY SIMILARITY) 767605781A915302 CRC64;
                                                                                                                                                                                 DB 1;
35;
                                                                                                                                                                                                                                                                                                                                                                                                                                      444 AA
                                                                                                                                                                                                           100.0%; Pred. No. 35; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 100.0%; Pred. No. 67; 5; Conservative 0; Mismatches
                                                                                                                                                                                   88.6%; Score 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE001917; AAF10170.1; ALT_INIT.
TIGR; DR0594; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 A
48457 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 286:1571-1577(1999)
                                                                                                                                                                                                        Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444 AA;
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Best Local Similarity
Matches 5; Conserv
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211 DFSWL 215
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BINDING 15
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                                                                                                                                                                                                                                                                          2 DFSWL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GLGA DEIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                 Query Match
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GLGA DEIRA
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PROSITE; PS00178; AA TRNA LIGASE I; FALSE NEG.
Aminoacyl-tRNA synthetase; Proteïn biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
Strong, to methionyl-tRNA synthetase.
SYC AQUAE STANDARD; PRT; 495 AA.
067163;
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Cysteinyl-tRNA synthetase (EC 6.1.1.16) (Cysteine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 392:353-358(1998).
-!- CATALYTIC ACTIVITY: ATP + L-cysteine + tRNA(Cys) = AMP
diphosphate + L-cysteinyl-tRNA(Cys).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 495;
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                                                                                                                                                                                                                                                                                                                  Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
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266 270 "KMGKSK" REGION.
269 269 ATP (BY SIMILARITY).
495 AA; 57135 MW; A454658B2BBAEBA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.6%; Score 31; DB 1
100.0%; Pred. No. 75;
iive 0; Mismatches
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PIR, H70391, H70391.
HAMAP; MF 00041; -; 1.
InterPro; IPR002308; Cys tRNA-synt_la.
InterPro; IPR001412; FRNA-synt_l.
Pfan; PF01406; tRNA-synt_l.
PRINTS; PR00983; TRNASYNTHCYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98196666; PubMed=9537320;
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83.3%;

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5; Conservative
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       Best Local Similarity
                                                                                                                          LDFQWL 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pRiA4b.
                                                                                                                                                                                                                                                                                                                                                                            Protein virD3.
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                                                                                                                                                                                                                                                    VID3 AGRRH
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008775;
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VID3_AGRRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetacese; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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(Rel. 34, Last sequence update)
(Rel. 35, Last annocation update)
. 69.4 kDa protein in NCB3-HHT2 intergenic region.
(Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 36, Last annotation update)
1 69.6 kDa protein in HDAl-PUBl intergenic region.
                                                                                                                                                                                                                                                                      Andre B., Iraqui Houssaini I., Urrestarazu L.A., Vissers S.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO YEAST YNL034W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.6%; Score 31; DB 1; Length 612; 83.3%; Pred. No. 94; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duesterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D., Hilbert H., Moestl D., Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGD; S0004963; YNLO18C.
Hypothetical protein.
SEQUENCE 612 AA; 69551 MW; E655B2D96317FC62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ll protein.
612 AA; 69373 MW; E39B7080BBDE0285 CRC64;
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Matches 5, Conservative
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                                                                                                   rNL018C OR N2831.
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                                                                                                                                                                                            NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (
Hypothetical
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SEQUENCE 61
                                                                       Hypothetical
                                                  15-JUL-1998
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P53963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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DB 1; Length 612;

88.6%; Score 31;

Query Match

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16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
(VEGPR-2) (Protein-tyrosine kinase receptor flk-1) (Fetal liver kinase
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Mammalia; Eutheria; Rođentia; Sciurognathi; Muridae; Murinae; Rattus.
           Gapa
           ö
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Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
NCBI_TaxID=359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hirayama T., Muranaka T., Ohkawa H., Oka A.;
Coganizarion and characterization of the virCD genes from
Agrobacterium thizogenes ";
Mol. Gen. Genet. 213:229-237 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.6%; Score 31; DB 1; Length 678; 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels
     IndelB
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Wen Y., Edelman J.L., De Vries G.W., Sachs G.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               678 AA; 72777 MW; A5BCEBA58AC26532 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89039712; PubMed=3185501;
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SEQUENCE 678 AA; 72777
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FUNCTION: RECEPTOR FOR VEGF OR VEGF-C. HAS A TYROSINE-PROTEIN KINASE ACTIVITY. THE VEGF-KINASE LIGAND/RECEPTOR SIGNALING SYSTEM PLAYS A KEY ROLE IN VASCULAR DEVELOPMENT AND REGULATION OF VASCULAR PERMEABILITY (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                              tyrosine phosphate.
SUBCELLUALAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEAM; PRO0047; 197. PLANIABE.
PEAM; PRO0069; pkinase; 1.
Probom; PRO00001; prot. kinase; 2.
SMART; SM00409; IGC2; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PSS0035; IG LIKE; 5.
PROSITE; PSS0010; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00240; PRCEPTOR_TYR KIN 111; 1.
ANGIOGENESIS; Transferase; Tyrosine-protein kinase; Phosphorylation; ATP-binding; Receptor; Transmembrane; Signal; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
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(POTENTIAL).
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VASCULAR ENDOTHELIAL GROWTH FACTOR
RECEPTOR 2.
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IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 6.

IG-LIKE C2-TYPE 6.

IG-LIKE C2-TYPE 7.

IG-LIKE C2-TYPE 7.

IG-LIKE C2-TYPE 7.

ROTELIN KINASE.

ATP (BY SIMILARITY).

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EMBL, U93307; AAB97509.1; --
HSSP; P11362; 1FGK.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig-C2.
InterPro; IPR003598; Ig-C2.
InterPro; IPR001019; Prot kinase.
InterPro; IPR001185; RTKinaseIII.
InterPro; IPR001185; TYL_PKinase.
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1158
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SIGNAL
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DOMAIN
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CARBOHYD CARBOHYD CARBOHYD

CARBOHYD CARBOHYD

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Gaps
1055 1055 PHOSPHORYLATION (AUTO-) (BY SIMILARITY) 1343 AA; 150393 MW; AD7E509EB62D3FF4 CRC64;
                                                                                    6
                                                   Length 1343;
                                                 88.6%; Score 31; DB 1; Length 134 100.0%; Pred. No. 2.2e+02; Ative 0; Mismatches 0; Indels
                                                                                                                                                                                                   Search completed: February 18, 2004, 14:28:09
Job time : 4.55263 secs
                                                                                    5; Conservative
                                                             Local Similarity
                                                                                                                                                   256 LDFSW 260
                                                                                                                    1 LDFSW 5
   MOD RES
SEQUENCE
                                                     Query Match
                                                                                    Matches
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

February 18, 2004, 14:12:09; Search time 6.5921 Seconds (without alignments) 87.531 Million cell updates/sec Run on:

US-09-643-260-11 35 1 LDFSWL 6

Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	probable PPE prote	ical	_	ᇩ	hypothetical prote		- 12	conserved hypothet	NIP80 protein - ye	hypothetical prote			sodi	probable amino aci	probable membrane-	probable membrane	hypothetical prote			-	transforming prote	1-2 pr	B-cell lymphoma 2	transforming prote	unknown protein, 7	hypothetical prote		hypothetical prote	
SUM	ΩI	A70663	T44513	D82732	AI0698	D71975	E64532	A81865	C81077	865186	T21915	F69462	T04971	F83328	E95850	695953	S64036	S74754	F82836	T30439	F70570	TVMSA1	153744	JC7383	TVHUA1	C96594	865170	G72694	T31582	20200
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	Length	391	414) }	144	253	253	518	518	868	1214	208	371	449	467	490	121	150	199	219	224	236	236	236	239	247	253	262	296	331
de	Query	100.0	100.0	94.3	94.3	94.3	94.3	94.3	94.3	94.3	94.3	91.4	91.4	91.4	91.4	91.4	9.88	98.6	98.6	98.6		98.6		98.6	88.6	9.88	æ	88.6	88.6	ă
	Score	35	35	33	33	33	33	33	33	33	33	32	32	32	32	32	31	31	31	31	31	31	31	31	31	31	31	31	31	5
	Result No.	-	8	m	4	ហ	9	7	89	σ	10	11	12	13	14	15	16	17	18	19	20	21		23	24			27	28	5

hypothetical prote	protein T27B7.3 [i	probable emulsan r	hypothetical prote	probable transport	hypothetical prote	glycogen synthase	hypothetical prote	cysteine-tRNA liga	hypothetical prote	hypothetical prote	probable sodium/hy	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote
A82890	D88968	T44831	B71153	B83601	AE1892	B75501	T33504	H70391	AC1892	T45498	G83177	S62930	862956	AG2794	F97573
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30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

A70663
probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
probable PPE protein - Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: A70663
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamila, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 333, 537-544, 1989
A;Authors: Sqares, M.A.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70663
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: DA
A;Coss-references: GB:Z83860; GB:AL123456; NID:g3261681; PIDN:CAB06149.1; PID:e290759; A;Genetics:
A;Genetics:
A;Genetics:

ö Gaps ö Query Match 100.0%; Score 35; DB 2; Length 391; Best Local Similarity 100.0%; Pred. No. 21; Matches 6; Conservative 0; Mismatches 0; Indels Query Match

1 LDFSWL 6

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|||||| 3 LDFSWL 8 g

hypothetical protein 5P [imported] - Plesiomonas shigelloides C;Species: Plesiomonas shigelloides C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000 C;Accession: T44513 R;Chida, T.; Okamura, N.; Yoshida, Y.; Ohtani, K.; Arakawa, E.; Watanabe, H. Bubmitted to the BMBL Data Library, April 1999 A;Reference number: 222786

A,Accession: T44513
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DDA
A,Residues: 1-414 <CHI>A,CHSAA,Experimental source: EMBL:AB025970; PIDN:BAA85010.1
A,Experimental source: ATCC 14029

ö Gaps ö Query Match
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels ~

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hypothetical protein jhp0003 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: J2-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Accession: D71975
C;Accession: D71975
C;Accession: D71975
J1095, C; Gibson, R.; Merberg, D.; Mills, S.D.; Jang, Q.; Taylor, D.E.; Vovis, G.F.; Ives, C; Gibson, R.; Merberg, D.; Mills, S.D.; Jang, Q.; Taylor, D.E.; Vovis, G.F.; Jives, C; Gibson, R.; Merberg, D.; Mills, S.D.; Diang, Q.; Taylor, D.E.; Vovis, G.F.; A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: D71975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB:AE001439; NID:g4154594; PIDN:AAD05674.1; PID:g415460
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C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Accession: E64532

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne, son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: E64532
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C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: A81865
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Pred. No. 32;
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Pred. No. 32;
1; Mismatches
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83.3%;
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Best Local Similarity 83.5.
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Best Local Similarity
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                                                                                                 45 IDPSWL 50
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R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 4(66, 15:1157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MIID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Reterence number: A82515; MIID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Reterence number: A82515; MIID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Residues: 1-61 c&IM>
A;Residues: L-61 c&IM>
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CjAccession: A10698
R; Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R; Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wair, J.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Alathors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seroy A; Reference number: AB0502; MUID:21534947; PMID:11677608
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C;Genetics:
A;Gene: sscB
                                                                                                                                                                                                                                              hypothetical protein XF1033 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AI0698
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Pred. No. 17;
1; Mismatches 0; Indels
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Pred. No. 6.9;
1; Mismatches 0; Indels
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
                                                               175 LDPSWL 180
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A; Residues: 1-144 <PAR>
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MDFSWL
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Length 868; 0; Indels

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hypothetical protein F37D6.1 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans R; Accession: T21915 R; McMurray, A. Submitted to the EMBL Data Library, June 1996 A; Reference number: Z19487 A; Reference number: Z19487
        A;Residues: 169-429,'V',431-868 <SCH>
A;Cross-references: EMBL:X72227
C;Genetics:
A;Gene: SGD:NIP100; NIP80
A;Cross-references: MIPS:YPL174c; SGD:S0006095
A;Map position: 16L
C;Keywords: transmembrane protein
F;574-590/Domain: transmembrane #status predicted <TMM>
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83.3%; Pred. No. 1.2e+02;
iive 1; Mismatches 0;
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nes 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conserved hypothetical protein NMB1485 [imported] - Neisseria meningitidis (strain MC58 C; Species: Neisseria meningitidis (c) Species: Neisseria meningitidis (c) Species: Neisseria meningitidis (c) Species: 11-far-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Accession: C810.7 (c) Access
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A;Residues: 1-518 <TET>
A;Cross-references: GB:AE002498; GB:AE002098; NID:g7226724; PIDN:AAF41841.1; PID:g722672
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1485
Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000

Nature 404, 502-506, 2000

A;Title: Complete DNA Sequence of a serogroup A strain of Neisseria menigitidis Z2491.

A;Reference number: A81775; MUID:20222556; PMID:10761919

A;Recession: A81865

A;Retus: preliminary

A;Residues: 1-518 < PAR>

A;Residues: 1-518 < PAR>
A;Residues: 1-518 < PAR>
A;Residues: GB:AL15756; GB:AL157959; NID:g7380091; PIDN:CAB84922.1; PID:g738033

A;Reperimental source: serogroup A, strain Z2491

C;Genetics:
A;Gene: NMA1694
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A;Molecule type: DNA
A;Residues: 1-868 cBEN-
A;Residues: 1-868 cBEN-
A;Cross-references: EMBL:Z73530; NID:g1370366; PID:e246907; PID:g1370367; MIPS:YPL174c
A;Experimental source: strain S288C (AB972)
R;Schlenstedt, G.; Silver, P.A.
submitted to the EMBL Data Library, May 1993
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NiAlternate names: protein P2279; protein YPL174c
C;Species: Saccharomyces cerevisiae
C;Decies: 10-Dec-1994 #sequence_revision 31-May-1996 #text_change 05-Dec-1997
C;Accession: S65186; S34343
R;Benes, V.; Rechmann, S.; Nentwich, U.; Vobs, H.; Ansorge, W.
abubmitted to the Protein Sequence Database, May 1996
A;Reference number: S65183
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Pred. No. 70;
1; Mismatches 0; Indels
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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1 MDFSWL 6
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A;Molecule type: DNA
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hypothetical protein AF1703 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Fachaeoglobus fulgidus
C;Accession: F69462
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson.
T; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Scatus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-208 <KLE>
A;Cross-references: GB:AE000986; GB:AE000782; NID:92689309; PIDN:AAB89558:1; PID:926488
C;Superfamily: Methanobacterium thermoautotrophicum conserved hypothetical protein MTH1
                                                                                                                                                                                                                                                                                                             A;Map position: 1
A;Introns: 43/1; 59/3; 103/3; 149/2; 230/3; 278/3; 313/1; 439/2; 489/3; 571/1; 625/2; 6
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1214 <WIL>
A;Residues: 1-1214 <WIL>
A;Residues: 1-1214 <WIL>
C;Genetics: Clone F37D6
C;Genetics:
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A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: E95850
A;Status: preliminary
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83.3%;
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Best Local Similarity 83.3%;
Matches 5; Conservative
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A;Gene: expAl; SMb21319
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                                                                                               A; Molecule type: DNA
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                                                                                                                                                                         hypothetical protein T1611.30 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 23.Apr-1999 #sequence_revision 23.Apr-1999 #text_change 04-Mar-2000
C; Accession: T04971
R; Bevan, M.; Obermaier, B.; Deutschenbaur, S.; Piravandi, E.; Hoheisel, J.; Mewes, H.W.; Submitted to the Protein Sequence Database, November 1998
A; Reference number: Z15393
A; Accession: T04971
A; Molecule type: DNA
A; Residues: 1.371 < REV.>
A; Cross-references: EMBL: AL031394
A; Experimental source: cultivar Columbia; BAC clone T1611
C; Genetics:
A; Map position: 4
A; Introns: 69/1; 83/3; 123/3; 176/2; 201/2; 224/3; 275/3; 312/1; 333/1
A; Note: T1611.30
C; Superfamily: Arabidopsis thaliana hypothetical protein T1611.30
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Cipate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
Cipate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
Cipate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
Cipate: 15-Sep-2000
Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
J. Lory, S.; Olson, W.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc
A;Reference number: A82950; MUD:20437337; PMID:10984043
A;Accession: F83328
A;Accession: F83328
A;Molecule type: DNA
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A;Cross-references: GB:AE004681; GB:AE004091; NID:g9948587; PIDN:AAG05921.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
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C;Superfamily: sodium-dependent D-alanine/glycine transport protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 91.4%; Score 32; DB 2; Length 371; Best Local Similarity 83.3%; Pred. No. 77; Matches 5; Conservative 1; Mismatches 0; Indels
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LDFAWL 160
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A; Residues: 1-467 «KUR»
A; Cross-references: GB:ALS91985; PIDN:CAC48469.1; PID:g15139941; GSPDB:GN00167
A; Cross-references: GB:ALS91985; PIDN:CAC48469.1; PID:g15139941; GSPDB:GN00167
A; Experimental source: strain 10.1, megaplasmid by SymB
R; Galibert, F.; Finan, T.M.; Long, S.K.; Puller, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Rahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Reference number: As6039; MUID:21368234; PMID:11474104
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Cybacession: 095953

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar Proc. Natl. Acad. Sci. US.A. 98, 9889-9894, 2001

A;Title: The complete sequence of the 1,683-42 psymb megaplasmid from the N2-fixing endc. A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Recenter number: A95842; MUID:21396508; PMID:11481431

A;Residues: DAA

A;Residues: 1-490 «KUR»

A;Residues: 1-490 «KUR»

A;Residues: T.F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Chain, P.; Cowie, A.; Decano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, M.; Vorholter, F.U.; Weidner, S.; Weidner, S.; Wong, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.U.; Weidner, S.; Weidner, S.; Weng, C.; Lelaure, A;Title: The composite genome of the legume symbiont sinorhizobium meliloti.

A;Reference number: Askenserned annowation

A;Reference number: Ask6039; MUID:21368234; PMID:11474104
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C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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A;Genome: plasmid
C;Superfamily: sodium-dependent D-alanine/glycine transport protein
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Pred. No. 1e+02;
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Pred. No. 99;
1; Mismatches
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Sequence 11, Appl.
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Sequence 11, Application US/09847940B

Patent No. US20020156000A1

GENERAL INFORMATION:

APPLICANT: May, Michael J.

APPLICANT: Ghosh, Sankar

TITLE REFERENCE: PPI-117CP

CURRENT APPLICATION NUMBER: US/09/847,940B

CURRENT FILING DATE: 2001-05-02

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO !-
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US-10-369-493-22465
US-09-847-940B-12
US-09-847-946A-12
US-09-847-946A-99
US-09-847-946A-99
US-09-847-946A-90
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US-10-101-482-12
US-10-277-693A-10
US-10-072-693A-10
US-10-369-493-23432
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| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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; Sequence 42, Application US/09847946A
; Publication No. UG20030054999A1
GENERAL INFORMATION:
    APPLICANT: May, Michael J
    APPLICANT: Findeis, Mark A
    APPLICANT: Findeis, Mark A
    APPLICANT: Phillips, Kathryn
    APPLICANT: Hannig, Gerhard
    TITLE OF INVENTION: ANT-INFLAMMATORY COMPOUNDS AND USES THEREOF
    FILE REFERENCE: PPI-119
    CURRENT FILING DATE: 2000-05-02
    PRIOR PLILOR DATE: 2000-05-02
    PRIOR PLILOR DATE: 2000-05-02
    PRIOR PLILOR DATE: 2000-08-22
    NUMBER OF SEQ ID NOS: 160
    SOFTWARE: Patentin Ver. 2.0
    SEQ ID NO 42
    LENGTH: 6
    LENGTH: 6
    LENGTH: 6

APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
ITILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2010-105-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
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Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels
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Sequence 88, Application US/09847946A

Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: Way, Michael J

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Phillips, Kathryn

APPLICANT: Hannig, Gerhard

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REPERENT APPLICANTON NUMBER: US/09/847,946A

CURRENT PILING DATE: 2001-05-02

FRIOR PILING DATE: 2000-06-02

FRIOR FILING DATE: 2000-08-22

FRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SEQ ID NOS: 160

SEQ ID NO SE SEC ID NOS: 160

SEQ ID NOS: 160
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mathyn
APPLICANT: Findeis, Mathyn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR PLLING DATE: 2000-06-02
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
COTHER INFORMATION: sequence
US-09-847-946A-84
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US-09-847-946A-88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 100.0%; Score 35; DB 11; Length 6
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 6; Conservative
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| LDFSWL 6
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RESULT 6

US-09-847-946A-84; Sequence 84, Application US/09847946A; Publication No. US20030054999A1

US-09-847-946A-81

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1 LDFSWL 6
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Sequence 81, Application US/09847946A

Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Hannig, Gerhard

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REFERENCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT APPLICATION NUMBER: 60/201,261

PRIOR APPLICATION NUMBER: 60/201,261

PRIOR APPLICATION NUMBER: 60/201,261

PRIOR PILING DATE: 2000-05-02

PRIOR PILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 160

SOFTHARE: Patentin Ver: 2.0

LENGTH: 8
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; Publication No. US20030054999A1
; GENERAL INFORMATION:
    APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Phillips, Kathryn
; APPLICANT: Phillips, Kathryn
; APPLICANT: Phillips, Kathryn
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201.05-02
; PRIOR PPLING DATE: 2000-05-02
; PRIOR PPLING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 160
; SOFTHARE: Patentin Ver. 2.0
; SEQ ID NO 89
; LENGTH: B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h Similarity 100.0%; Score 35; DB 11; Length 8; Similarity 100.0%; Pred. No. 7e+05; 6; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAWMATORY COMPOUNDS AND USES THEREOF
TILE OF INVENTION NUMBER: US/09/847,946A
CURRENT APPLICATION NUMBER: 00/201,261
PRIOR APPLICATION NUMBER: 09/643,260,
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 83
SEQ ID NO 83
                                                                                                             APPLICANT: Ghosh, Sankar

APPLICANT: Ghosh, Mark A

APPLICANT: Pindeis, Mark A

APPLICANT: Pindeis, Mark A

APPLICANT: Pindig, Kathryn

APPLICANT: Hannig, Gerhard

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REFERENCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR FILING DATE: 2000-08-02

PRIOR FILING DATE: 2000-08-02

NUMBER OF SEQ ID NOS: 160

SOFTWARE: PatentIn Ver. 2.0
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US-09-847-946A-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Description of Artificial Sequence:NEMO binding; OTHER INFORMATION: sequence
US-09-847-946A-80
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Sequence 80, Application US/09847946A Publication No. US20030054999A1
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 6; Conservative
                                                           GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
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Indels

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APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Pindeis, Mark A
APPLICANT: Pindlips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
FILE REFERENCE: PPI-119
FILE REFERENCE: POI-05-02
FRIOR APPLICATION NUMBER: 09/201,261
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding; OTHER INFORMATION: sequence
US-09-847-946A-82
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100.0%; Pred. No. 7e+05; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                 Sequence 82, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
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APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Pindeis, Mark A
APPLICANT: Phillips, Kathry
APPLICANT: Phillips, Kathry
APPLICANT: Phillips, Kathry
APPLICANT: Phillips, Kathry
APPLICANT: Phillips, Kathry
APPLICANT: Phillips, Kathry
FILIR OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 86
LENGTH: 9
MANDER OF MARCH OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE OF THE TABLE
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Publication No. US20030054999A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Man's Michael J
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: AMITIINFLAMMATORY COMPOUNDS AND USES THEREOF
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CURRENT FILING DATE: 2001-05-02
PRIOR PLILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
SUFFWARE: PATCHTIN VOR: 160
SOFFWARE: PATCHTIN VEY. 2.0
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                                                                                                                                                                                                                                       Sequence 86, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 6; Conservative
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OTHER INFORMATION:
OTHER INFORMATION:
                                      1 LDFSWL 6
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                                                                                                                                                                                                                        US-09-847-946A-86
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ò 셤

Gaps

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Sequence 85, Application US/09847946A
; Bequence 85, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
 APPLICANT: May, Michael J
 APPLICANT: Ghosh, Sankar
 APPLICANT: Findeis, Mark A
 APPLICANT: Findeis, Mark A
 APPLICANT: Findeis, Mark A
 APPLICANT: Findeis, Mark A
 APPLICANT: Findeis, Mark A
 APPLICANT: Findeis, Mark A
 APPLICANT: Findeis, Mark A
 APPLICANT: Findeis, Mark A
 APPLICANT: Findeis, Mark A
 APPLICANT: MANTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
 FILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND
 CURRENT APPLICATION NUMBER: US/09/847,946A
 CURRENT FILING DATE: 2000-05-02
 PRIOR PILING DATE: 2000-05-02
 PRIOR PLICATION NUMBER: 09/43,260
 PRIOR FILING DATE: 2000-08-22
 NUMBER OF SEQ ID NOS: 160
 SOFTWARE: PALENTIN Ver. 2.0
 SEQ ID NO 85
 SEQ ID NO 85 FEATURE: OTHER INFORMATION: Description of Artificial Sequence:NEMO binding OTHER INFORMATION: sequence

Query Match

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161 LDFSWI 166
  US-09-881-752A-368
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Sequence 368, Application US/09881752A

Patent No. US20020115078A1

GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
APPLICANT: Tomb, Jean-Francois
APPLICANT: Tomb, Jean-Francois
APPLICANT: Tomb, Jean-Francois
APPLICANT: Tomb, Jean-Francois
APPLICANT: Oomen, Raymond P.
TITLE OF INVENTION: Encoding No. US20020115078A1el Helicobacter Polypeptides in the
TITLE OF INVENTION: Genome
TITLE OF INVENTION: Genome
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/041002
CURRENT APPLICATION NUMBER: US/09/881,752A
CURRENT APPLICATION NUMBER: US/09/881,752A
CURRENT FILING DATE: 1997-04-01

NUMBER OF SEQ ID NOS: 370

SEQ ID NO 368
LENGTH: 265
LENGTH: 265
LENGTH: 265
LENGTH: 265
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                                                                                                                                                                                                                                                                                          Sequence 79, Application US/09847946A

Fublication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REFERENCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2000-05-02

PRIOR PILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 79

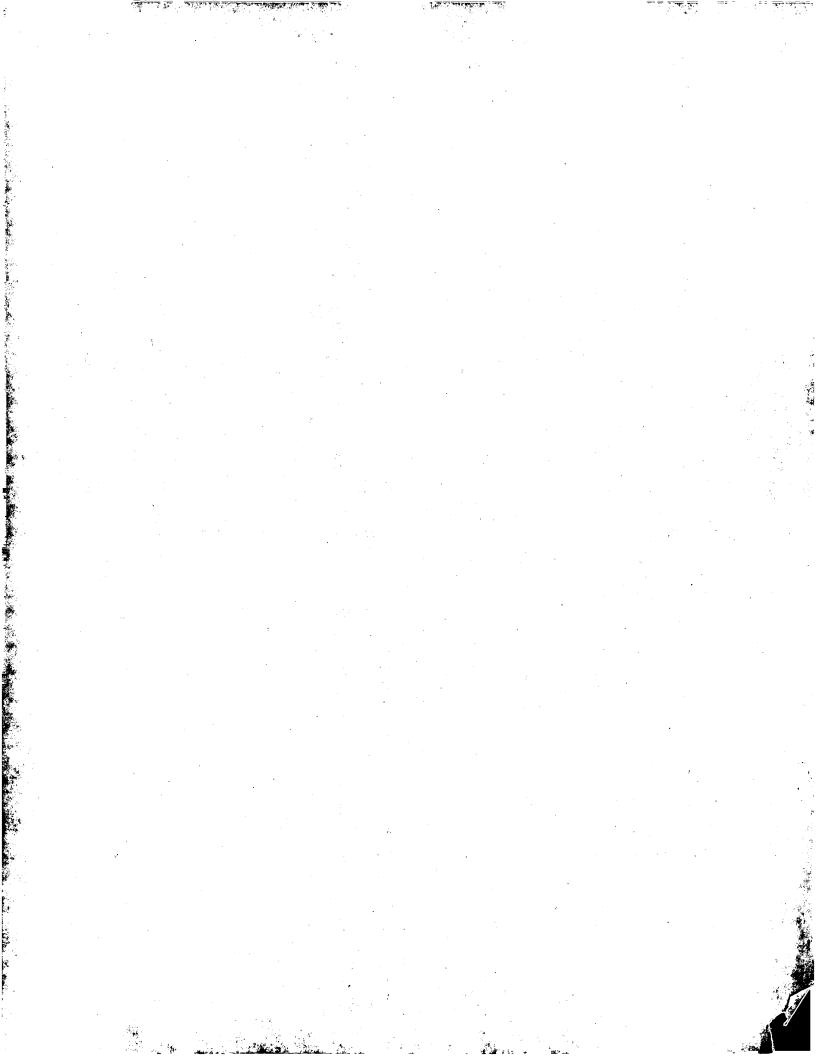
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
CTHER INFORMATION: Description of Artificial Sequence:NEMO binding
CTHER INFORMATION: sequence
US-09-847-946A-79
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                                            100.0%; Score 35; DB 11; Length 10; 100.0%; Pred. No. 10; cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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ORGANISM: Helicobacter pylori
                                         Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                       1 LDFSWL 6
                                                                                                                                                                                   3 LDFSWL 8
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                                                                                                                                                                                                                                                       RESULT 14
US-09-847-946A-79
US-09-847-946A-85
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Gapa ö Score 33; DB 10; Length 265; Pred. No. 3.7e+02; 1; Mismatches 0; Indels Query Match
Best Local Similarity 83.3
Matches 5; Conservative

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1 LDFSWL 6

Search completed: February 18, 2004, 15:41:58 Job time : 16.7529 secs



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February 18, 2004, 13:37:19; Search time 22.7763 Seconds (without alignments) 41.814 Million cell updates/sec
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| SIDS1/993data/geneseqf_geneseqp_enbl/AA1997.DAT:*
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1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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35
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length DB	DB	ΩI	Description
	35	100.0	9	23	ABB08733	Mutated IKKbeta NE
73	35	100.0	9	23	AAM48516	NBD mutant peptide
m	35	100.0	9	23	AAM48539	Anti-inflammatory
4	35	100.0	φ	23	AAM48581	Anti-inflammatory
ហ	35	100.0	9	24	ABU08426	Human NEMO binding
φ	35	100.0	7	23	AAM48585	Anti-inflammatory
7	35	100.0	80	23	AAM48578	Anti-inflammatory
80	35	100.0	œ	23	AAM48586	Anti-inflammatory
σ	35	100.0	σ	23	AAM48577	Anti-inflammatory

Anti-inflammatory	Anti-inflammatory	Anti-inflammatory	Anti-inflammatory	Anti-inflammatory	Anti-inflammatory	Human IKKbeta muta		H. pylori ORF 06ae	H. pylori GHPO 128	N. gonorrhoeae ami	Mutated IKKbeta NE	NBD mutant peptide	Anti-inflammatory	Anti-inflammatory	Human NEMO binding	Anti-inflammatory	Anti-inflammatory			Anti-inflammatory	Anti-inflammatory	Anti-inflammatory	Anti-inflammatory	Anti-inflammatory	Anti-inflammatory	eta	æ	ope #	aB	ø	Becrete	SSIII	SSIII	Novel human diagno	Human immune/haema
AAM48580	AAM48583	AAM48584	AAM48579	AAM48582	AAM48576	ABB77296	AAY70582	AAY11039	AAW98384	ABP79808	ABB08734	AAM48517	AAM48540	AAM48592	ABU08427	AAM48596	AAM48589	AAM48597	AAM48588	AAM48591	AAM48594	AAM48595	AAM48590	AAM48593	AAM48587	ABB77297	AAW87823	AAB74140	AAW87829	AAB74146	AAB34347	ABU07212	ABU07218	ABG10985	AAM88387
23	23	53	23	23	53	23	21	13	13	24	23	23	23	23	24	23	23	23	23	33	23	23	23	23	23	23	20	22	20	22	71	24	24	22	22
0	0	6	10	10	17	756	144	253	265	528	9	9	9	9	9	7	80	80	6	σ	O	6	10	10	11	756	23	23	25	25	42	46	46	87	106
100.0	100.0	100.0	100.0	100.0	100.0	100.0	94.3	94.3	94.3	94.3	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	9.88	9.88	9.88			8		88.6	
35	35	35	S	ŝ	ហ	'n	m	m	m		~	N		32	32	32	32	32	32	32	32	32	32	32	32	32	31	31	31	31	31	31	31	31	31
10	11	12	13	14	15	116	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 11. ABB08733 standard; peptide; 6 AA (first entry) 14-JUN-2002 ABB08733;

ALIGNMENTS

RESULT 1 ABB08733

kinase activation; leukocyte; inflammation; E-selectin; obteoclast; autoimmune disease; transplant rejection; osteoporosis; cancer; Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis; rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; antiinflammatory; immunosuppression; osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antisathmatic; antiallergic; dermatological; antibacterial; antibosoriatic; antirheumatic; antialredic; antialthritic; osteopathic; antiulcer; mutant; mutein. IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;

Key
Misc-difference 3
// note= "Wildtype Trp substituted by Phe" Synthetic.

ωФ

Homo sapiens.

WO200183547-A2

08-NOV-2001

antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallegic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKDeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

antiasthmatic; cytostatic;

autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.

```
The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB0725-ABB08725) comprising at least one NBMO binding domain (ABB773113). The compound has acts through selective inhibition of (ABB773113). The compound has acts through selective inhibition of Sylvahille (ABB773113). The compound has acts through selective inhibition of NBMO interaction results in inhibition of IKKOpeta kinase activation and subsequent decreased phosphorylation of IKKOpeta kinase activation and condition. The compound is useful in treating NF-kB mediated condition. Where compound is useful in treating NF-kB mediated conditions, where the condition is an inflammatory disorder. Alzaheimer's disease, transplant rejection, osteoporosis, cancer, Alzaheimer's disease, theorogeclerosis, a viral infection or ataxia telangiectasia. The inflammatory disorder is asthma, allergies, urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis, bowell disease, chronic obstructive pulmonary disease, visit and bursitis. The inflammatory disorder may also be dermatitis, osteoarthritis, psoriatic arthritis, lupus and bursitis. The inflammatory disease, ulcerative colitis, polymyalgia, scleroderma, Wegner's granulomary disease, ulcerative colitis, polymyalgia, scleroderma, Wegner's granulomatory viral infections cryoglobulinamena or multiple sclerosis. For chronic obstructive pulmonary disease, ulcerative anaphylaxis, drug and food sensitivity, contact dermatitis, crossed by Epstein-barr, cytomegalovirus or herpes simplex. Other diseases include HIV and influenza. The compound may also be dermatitied any application in which corticosteroids are used, including including including influenza and for dancer therapy. Also be dermatively or immunousppresession in th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiinflammatory compounds and for diagnosis of an inflammatory disorder. The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of a mutated NEMO binding domain of IKKOeta.
                                                                                                                                                                                                                                                                         Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting a cell with an anti-inflammatory compound comprising at least one NEMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 35; DB 23; Length 6; 100.0%; Pred. No. 9.3e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 23; Page 44; 82pp; English.
02-MAY-2001; 2001WO-US40654.
                                                                       22-AUG-2000; 2000US-0643260.
                                               02-MAY-2000; 2000US-201261P
                                                                                                                                                                                                                          WPI; 2002-179350/23
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Best Local Similarity
Matches 6; Conserv
                                                                                                                      (UYYA ) UNIV YALE.
                                                                                                                                                                           May MJ, Ghosh S;
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```

Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation.

Example 6; Page 47; 88pp; English.

psoriasis

Phillips K;

Findeis MA,

Ghosh S,

May MJ,

(UYYA) UNIV YALE

WPI; 2002-121889/16.

02-MAY-2001; 2001WO-US14346. 02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260. (PRAE-) PRAECIS PHARM INC.

WO200183554-A2. 08-NOV-2001.

Synthetic.

```
The invention relates to an antiinflammatory compound (especially AAM48648), comprising a membrane translocation domain (AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48649), comprising a membrane translocation domain card residues, fused to a NEWO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, antipacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of Cytokine-mediated NFKappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta kinase activation and subsequent decreased phosphorylation of IKAppaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psortasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, caranulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis, viral infections; and ataxia telegical compounds are also useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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100.0%; Pred. No. 9.3e+05;
"**emairches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM48539 standard; Peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LDFSWL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6. AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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AAM48539
ID AAM4
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Gaps

.; 0

Similarity 100.0%; 6; Conservative (

1 LDFSWL 6

LDFSWL

d ð

AAM48516 standard; Peptide; 6 AA

RESULT 2 AAM48516 NBD mutant peptide SEQ ID NO 11.

20-MAR-2002 (first entry)

AAM48516;

Anti-inflammatory peptide SEQ ID NO 84.

(first entry)

20-MAR-2002

AAM48581;

AAM48581 standard; Peptide; 6 AA

RESULT 4

AAM48539;

```
WPI; 2002-121889/16.
                                                         May MJ, Ghosh S,
                                                     UNIV YALE.
                                                                                                                       Sequence 6 AA;
                                  WO200183554-A2.
     20-MAR-2002
                                      08-NOV-2001
                               Synthetic
                                                                                                                   arthritie
                                                                      psoriasis
                                                     (UYYA)
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The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48628-AAM48645), comprising a membrane translocation domain (AAM48629-AAM48646). The AAM48646-AAM48651) which comporises from 6-15 annino acid residues, fused to a NEWO binding sequence (AAM48619). The antiinflammatory compounds have antiasthmatic, cytostactic, antipostriatic, antirheumatic, antiartitic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEWO binding domain that results in inhibition of IKKappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lumg inflammation or cancer, bowel disease, sepsis, vasculitis, osteoparchitis, inflammatory bowel disease, sepsis, vasculitis, osteopachitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomacosis, multiple sclerosis, transplant rejections, osteoporosis, telangiectasia. The compounds are also useful for treating telangisctasis, transplant rejections, and ataxia telangiectasis. The compounds are also useful for treating profit or screams, and profit architistic, disease; atherosclerosis, viral infections, osteoporosis, architist, end sensitivity, eczema, dermatitis, sunburn, aging and
                                                                                                                                                                                                         Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; definition of the manatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEWO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimar's disease; atherosclerosis; viral infection; ataxia telangiectasis; allergy; anaphylaxis; arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phillips K;
                                                                                                             Anti-inflammatory peptide SEQ ID NO 42.
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Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; anticheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                         Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an antiinflammatory compound (especially
                                                                                                                                                                                                                                                                                                                    Findeis MA, Phillips K;
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 62; 88pp; English.
                                                                                                                                                                                                                                    02-MAY-2001; 2001WO-US14346.
                                                                                                                                                                                                                                                       02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
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                                                                                                                                                                       Synthetic.
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Gaps ö

100.0%; Score 35; DB 23; Length 6; 100.0%; Pred. No. 9.3e+05; tive 0; Mismatches 0; Indels

6; Conservative

Query Match Best Local Similarity Matches 6; Conserv

6 AA;

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                                                                                                                                                                                                                                                                                                                                                                 IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB; muclear factor-kappaB induction; inflammatory disorder; autoimmune disease; osteoporosis; cancer; Alzheimer's disease; atherosclerosis; viral infection; Ataxia telangiectasia; transplantation detection; immunosuppressive; osteopathic; cytostatic; nootropic; neuroprotective; antiatherosclerotic; virucide; vasotropic; antirheumatic; antiatherosclerotic; virucide; vasotropic; antirheumatic; antiatherosclerotic; virucide;
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory disorders, autoimmune diseases, osteoporosis, cancer, Alzheimer's disease, atherosclerosis, viral infections, Ataxia telangiectasia, and for transplantation detection. The compounds of the invention block NF-kappaB induction by IKK but do not inhibit the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel antiinflammatory peptide compounds comprising NEMO binding domain, useful for modulating NF-kappaB induction in a cell and treating NF-kappaB-mediated inflammation disorders e.g., asthma,
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   Length 6;
                                   Indels
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                 9.3e+05;
 Score 35; DB 23;
Pred. No. 9.3e+05;
                                                                                                                                                                                                                                                                                                            Human NEMO binding site (NBD) mutant peptide #9.
                                   0; Mismatches
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                                                                                                                                                                                                  ABU08426 standard; peptide; 6 AA.
 100.0%;
100.0%;
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22-AUG-2000; 2000US-0643260.
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                                     6; Conservative
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Query Match
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Synthetic.
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DB 24; Length 6;

100.0%; Score 35;

Query Match

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The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48645), comprising a membrane translocation domain cham48620-AAM48645). The AAM48651 which comprises from 6-15 amino acid residues, tused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antiporiatic, antirheumatic, antiarthric, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, notropic, antiatherosclerotic, virucide and antiallergic activity. The compounds acr as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IrappaB kinase beta (IKKbeta kinase the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IKKbeta kinase activation and subsequent decreased phosphorylation of IKKbeta kinase compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psociasis, rheumatoid arthritis, osteoporosis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating anaphylaxis, pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
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                                                                                                                                                                                                                                                                                                                                                                                         Antinflammatory, antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEWO binding domain; ezzema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
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                                    Indels
                 Pred. No. 9.3e+05; Mismatches 0;
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100.08;
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or food sensitivity, eczema, dermatitis, sunburn, aging and
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                                                                                                                                                                                                                                                                                                                                                                          AAM48578 standard; Peptide; 8 AA.
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osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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100.0%; Pred. No. 9.3e+05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM48586 standard; Peptide; 8 AA.
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compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, autoimmune diseases such as lupus, polymyalgia, scleroderma, pursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis, Alzheiner's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain

Claim 6; Page 62; 88pp; English.

psoriasis

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(Gyrogatic, antipsoriatic, antilintenametry, compounds.)

(cytostatic, antipsoriatic, antilintenametry, cytostatic, antipsoriatic, dermatological, neuroprotective, concourage activity. The compounds act as selective inhibitors of cytokine-mediated NRkappaB activation by blocking inhibitors of IkappaB kinase beta (IKKbeta) at the NEWO binding domain that results in inhibition of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, inflammation or cancer, psoriasis, rheumatory disorders, e.g. asthma, lung inflammatory bowel disease, sepsis, vasculitis, osteonathritis, inflammatory bowel disease, such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease, atheroselezosis; viral infections; and atexia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, arcitical.
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(AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
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22-AUG-2000; 2000US-0643260.
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Matches
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us-09-643-260-11.rag

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The invention relates to an antiinflammatory compound (especially AM48629-AM48645), comprising a membrane translocation domain (AAM48629-AM48645), comprising a membrane translocation domain acid residues, tused to a NEMO binding sequence (AAM486519). The antiinflammatory compounds have antisathmatic, cytostatic, antipacratic, antiinflammatory compounds are antisathmatic, antibacterial, immunosuppressive, dermatological, neuroprotective, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappas activation by blocking interaction of Ikappas kinase beta (IKAbeta kinase activation and subsequent decreased phosphorylation of IKAppas The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoderma, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, grannlomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory resources.
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                                                                              Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
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100.0%; Pred. No. 9.3e+05;
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                                                                                                                                                                                                                    Claim 6; Page 62; 88pp; English.
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                                                                                         The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48629-AAM48645), comprising a membrane translocation domain (AAM48629-AAM48629). The AAM48651 which comprises from 6-15 amino acid residues, fused to a NEWO binding sequence (AAM48619). The antiinflammatory compounds have antiasthmatic, antibacterial, immunosuppressive, dermatological, neuroprotective, notropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFKappaB activation by blocking interaction of IkappaB kinase beta (IKKObeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, ung inflammation or cancer, psoriasis, rheumatoid arthritis, osteopartsis, inflammatory bowel disease, sepsis, vasculitis, decentable in the selection; osteoporosis; deranglacterial, and therosclerosis; transplant rejection; osteoporosis; Alzheimer's disease, abhorosclerosis, viral infections; and ataxia continuation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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                                               Claim 6; Page 62; 88pp; English.
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RESULT 11 AAM48583

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Length 9; 0; Indels Phillips K;

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AMM48620-AMM48645) comprising a membrane translocation domain (AAM48620-AMM4861) comprising a membrane translocation domain (AAM48620-AMM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antiposciatic, antirheumatic, antiarthritic, osteopathic, antiabacterial, immunosuppressive, dermacological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB compounds act as selective inhibitors of cytokine-mediated NFkappaB cutivation by blocking interaction of IkappaB kinase beta (IKKObeta) at the NEWO binding domain that results in inhibition of IKKOpeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatoin of IkappaB. The compounds are useful for treating inflammatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, constantial compounds are also useful for treating inflammatomic sections; and ataxia treating constant constant of the compounds are also useful for treating constant constant of the compounds are also useful for treating constant of the compounds are also useful for treating constant of the compounds are also useful for treating constant of the compounds are also useful for treating constant of the compounds are also useful for treating constant of the compounds are also useful for treating constant of the compounds are also useful for treating constant of the compounds are also useful for treating constant of the compounds are also useful for treating constant of the compounds are also useful for treating constant of the compounds are also useful for treating constant of the compounds are also useful for treating constant of the compounds are also useful for treating constant of the constant of the constant of the constant of the constant of the cons
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                                                                                                                                                                                                                                                                                                                                                                                   Findeis MA,
                                                                                                                                                                         02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.
                                                                                                        02-MAY-2001; 2001WO-US14346.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid residues, fused to a NEMO binding sequence (AAM488525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antinheumatic, antiartheumatic, antiartheumatic, osteopathic, antibacterial, immunosuppressive, dermacological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase
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                                                                                                                                                                         Phillips K;
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                                                                                                                                                                         May MJ, Ghosh S, Findeis MA,
22-AUG-2000; 2000US-0643260.
                                                                (PRAE-) PRAECIS PHARM INC.
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RESULT 13 AAM48579

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                                             Gaps
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100.0%; Score 35; DB 23; Length 10; 100.0%; Pred. No. 5.1;
                                           0; Indels
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                                                                                                                                                                                                                                         AAM48582 standard; Peptide; 10 AA.
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AMM48620-AMM48645), comprising a membrane translocation domain (AAM48620-AMM48645), comprising a membrane translocation domain (AAM48620-AMM48645), comprising a membrane translocation domain (AAM48620-AMM48619). The antiinflammatory compounds have antiasthmatic, ortostatic, antiaporiatic, antiinflammatory compounds have antiasthmatic, ortostatic, antiathersoclerotic, antiathersoclerotic, virucide and antiallargic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB compounds act as selective inhibitors of cytokine-mediated NFkappaB compounds act us selective inhibitors of cytokine-mediated NFkappaB compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatory disorders, e.g. asthma, compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatory disorders, e.g. asthma, costeoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's diseases atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, archivity, eczema, dermatitis, sunburn, aging and
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factor kappaB activation, and for treating asthma, lung inflammation,
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osteoporosis, Alzheimer's disease, atherosclerosis, viral infection, ataxia telangiectasia, allergy, anaphylaxis, arthritis.
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The invention relates to an antiinflammatory compound (especially AAM48629-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48620). Comprising a membrane translocation domain characteristic and residues, fused to a NEMO binding sequence (AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antiporalatic, antiheumatic, antiarthritic, osteopathic, contropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NRRappas compounds act as selective inhibitors of cytokine-mediated NRRappas compounds are useful for treating inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IKKbeta kinase activation and subsequent decreased phosphorylation of IKKppas The activation and subsequent decreased phosphorylation of IKKppas The activation and subsequent decreased phosphorylation of IKKppas (Inng inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; viral infection; osteoaporosis; celangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, are allergies, urticaria, anaphylaxis, are allergies, urticaria, anaphylaxis, are allergies, urticaria, anaphylaxis, are allergies, urticaria, anaphylaxis, are allergies, urticaria, anaphylaxis, are allergies, urticaria, anaphylaxis, are allergies, urticaria, anaphylaxis, are allergies, urticaria, anaphylaxis, and an activity, eczema, dermatitis, sunburn, aging and
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antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermacological; neuroprotective; antiatherosclerctic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimnune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
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14 30 90.9 261 4 Q9POIZ 19 30 90.9 261 10 Q9PKI3 19 30 90.9 261 11 Q99KI3 19 30 90.9 261 11 Q99KI3 20 20 2 Q9FZ38 20 30 90.9 290 2 Q9FBQZ 22 30 90.9 290 2 Q9FBQZ 23 30 90.9 307 11 Q9FRA3 26 30 90.9 316 16 Q9FRA3 28 30 90.9 344 11 Q9FRA3 29 30 90.9 442 10 Q9FX3 29 30 90.9 442 10 Q9FX3 29 30 90.9 461 10 Q9FX3 29 30 90.9 461 10 Q9FX3 29 30 90.9 461 10 Q9FX3 29 30 90.9 461 10 Q9FX3 29 461 10 Q9FX3 29 461 10 Q9FX3 29 461 10 Q9FX3 29 461 10 Q9FX3 29 461 10 Q9FX3 29 461 10 Q9FX 29 461 10	30 90.9 563 4 30 90.9 688 9 30 90.9 810 16 30 90.9 810 16 30 90.9 800 16 29 87.9 125 16 29 87.9 155 16 29 87.9 155 16 29 87.9 162 8 29 87.9 162 8 29 87.9 162 8 29 87.9 162 8	1 968Y8 PRELIMINARY; PRIGORY; 1-DEC-2001 (TERMELTEL 19, Creat 1-MAR-2003 (TERMELTEL 19, Last 1-MAR-2003 (TERMELTEL 19, Last 1-MAR-2003 (TERMELTEL 19, Last 1-MAR-2003 (TERMELTEL 19, Last 1-MAR-2003 (TERMELTEL 19, Last 1-MAR-2003 (TERMELTEL 19, Last 10 TERMILS elegans. Nearyota, Metazoa, Nematoda; Chr MANIARIA MARIAGA, Paloderinae; Caenort 11 12 12 13 14 15 16 17 18 18 18 18 18 18 18 18 18 18 18 18 18	STRAINBEITSCOL N2; Wilson R., Greco T., Sansone J.; Wilson R., Greco T. Sansone J.; Whe sequence of C. elegans cosmid T2884."; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases [3] SEQUENCE FROM N.A. STRAINBEITSCOL N2; Waterston N.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases EMBL, AF026206; AAK33908.1; WormPepp, T2884.1b; CE27216. InterPro; IPR001810; F-box. Fran, PF00646; F-box; 1. SWART; SM00256; FSDX; 1. SWART; SM0256; FSDX; 1. FROSITE; PSS0181; FBOX; 1. SEQUENCE 518 AA; 60125 MW; A8A30C911618ED47 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
High-affinity branched-chain amino acid transport system, permease
protein (High-affinity branched-chain amino acid ABC transport system membrane permease).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
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                                           Waterston R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF026206; AAK39309-1;
Wormbep; T28B4.1a; CE27215.
InterPro; IPR01810; F-box.
IPfam; PF00046; F-box; 1.
SMART; SM00256; FBOX; 1.
PROSITE; PS50181; FBOX; 1.
SEQUENCE 535 AA; 62557 MW; CFEA8794E188C104 CRC64;
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MEDINEE-22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Mature 420:563-573(2002).
Hypothetical protein.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                    Query Match
100.0%; Score 33; DB 5; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
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"The sequence of C. elegans cosmid T28B4.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein (Fragment).
Mus musculus (Mouse)
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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STRAIN=U152; Walker R.A., Higgins P., Payne D.J., Amyes S.G.; "A biochemical and molecular assessment of the heterogeneity of the metallo-beta-lactamases from clinical Stenotrophomonas maltophilia
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Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas
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Xanthomonadaceae; Stenotrophomonas.
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83.3%; Pred. No. 1e+03;
iive 1; Mismatches 0; Indel8
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83.3%; Pred. No. 3.7e+02;
tive 1; Mismatches 0; Indels
                       Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL049711; CAB41330.1; ...
InterPro; IPR001965; Znf PHD.
InterPro; IPR001841; Znf zring.
SWART; SM0249; PHD; 2.
SWART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                   PROSITE; PS50016; ZF_PHD_2; 1.
PROSITE; PS50018; ZF_RING_2; 1.
Hypothetical protein.
SEQUENCE 763 AA; 85199 WW; 92BB47843D5314F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 187
187 AA; 19931 MW; F07D49E4B4C88043 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Metallo-beta-lactamase 3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00753; lactamase_B; 1.
PROSITE; PS00743; BETA_LACTAMASE_B_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001018; Beta_lactamase_B.
InterPro; IPR001279; Blactmase-like_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metallo-beta-lactamase 2 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolates.";
Submitted (MAY-2000) to the
EMBL; AJ289083; CAB94702.1;
HSSP; P52700; ISML.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           613 LDASWI 618
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LDASWL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=40324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  maltophilia).
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Q9JRL8
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Q9JRL9
      SXADARABER
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MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftur B.,
Reich C.I., McKenly K., Badger J.H., Glodek A.,
Peterson S., Reich C.I., Weidman J.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Alcard. G., Cottet A., Mache R., Mewes H.W., Lemcke K., Alcard. J.P., Quetier F., Salanoubat M.; Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.9%; Score 31; DB 17; Length 535;
83.3%; Pred. No. 7.2e+02;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002585; Bac Ubq Cox.
InterPro; IPR000515; BPD transp.
Pfam; PF01654; Bac Ubq Cox; 1.
PROSITE; PS00402; BPD TRANSP INN MEMBR; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 535 AA; 57605 MW; 68C821D58A11EE96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
10-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypotherical 85.2 kDa protein.
                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Cytochrome oxidase, subunit I (CYDA-2).
                                                                                                                                                           535 AA
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                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                Archaeoglobaceae; Archaeoglobus
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                                                                                                                                                        PRELIMINARY;
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8 IDASWL 13
66 IDASWL 71
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Query Match

Best Loc Matches

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09SUZ5

RESULT 6 Q9SUZ5

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robar
Kanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas
maltophilia).
                                                                                                                                                                                                                                                                                                               Walker R.A., Higgins P., Payne D.J., Amyes S.G.; "A biochemical and molecular assessment of the heterogeneity of the metallo-beta-lactamases from clinical Stenotrophomonas maltophilia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malker R.A., Higgins P., Payne D.J., Amyes S.G.; "A biochemical and molecular assessment of the heterogeneity of the metallo-beta-lactamases from clinical Stenotrophomonas maltophilia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas
                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Stenotrophomonas.
NCBI_TaxID=40324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     maltophilia).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Stenotrophomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.9%; Score 30; DB 2; Length 18783.3%; Pred. No. 3.7e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ289081; CAB94700.1; -.
HSSP; P52700; ISML.
InterPro; IPR001018; Beta_lactamase_B.
InterPro; IRR001279; Blactmase-like.
Pfam; PF00753; lactamase_B; 1.
PROSTIE; PS00743; BETA_LACTAMASE_B_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ289084; CAB94703.1; --
HSSP; P52700; 1SML.

HRSPP-O; IPRO0118; Beta_lactamase_B.

InterPro; IPRO01279; Blactamase_like.

PRO0753; lactamase_B; 1.

PROSITE; PS00743; BETA_LACTAMASE_B_1; 1.

NON_TER 187

NON_TER 187

SEQUENCE 187 AA; 19900 MW; D3C749E4B60C3F18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 AA; 19901 MW; 72B8515412892A08 CRC64;
                                                                                       Last sequence update)
Last annotation update)
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Last annotation update)
                             187 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 AA
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01-OCT-2000 (TrEMBLrel. 15, Last seq
01-WAR-2002 (TrEMBLrel. 20, Last ann
Metallo-beta-lactamase 4 (Fragment).
                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
Metallo-beta-lactamase 1 (Fragment).
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                             PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                              isolates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isolates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                           Q9JRM0
                                                   Q9JRMO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9JRL7
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=511, and 37;
Walker R.A., Higgins P., Payne D.J., Amyes S.G.;
"A biochemical and molecular assessment of the heterogeneity of the metallo-beca-lactamases from clinical Stenotrophomonas maltophilia isolates.";
                                                                                                     STRAIN=0062; Walker R.A., Higgins P., Payne D.J., Amyes S.G.; Walker R.A., Higgins P., Payne D.J., Amyes S.G.; "A biochemical and molecular assessment of the heterogeneity of the metallo-beta-lactamases from clinical Stenotrophomonas maltophilia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Stenotrophomonas.
NCBL_TaxID=40324;
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Xanthomonadaceae, Stenotrophomonas.
NCBI_TaxID=40324;
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                                                                                                                                                                                                Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ289082; CAB94701.1; -.
HSSP; P52700; ISML.
InterPro; IPR001018; Beta_lactamase_B.
InterPro; IPR001018; Beta_lactamase_B.
Fam; PF00753; lactamase_B; 1.
PROSTIE; PS00743; BETA_LACTAMASE_B_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ289086; CAB94705.1; -.
EMBL; AJ289085; CAB94704.1; -.
                                                                                                                                                                                                                                                                                                                                                                          187 AA; 19960 MW; 877D49E4B4C898F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 AA; 19811 MW; 7A2B11372028E5FE CRC64;
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Last annotation update)
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InterPro; IFR001018; Beta lactamase B.
InterPro; IPR001279; Blactmase-like.
Pfam; PF00753; lactamase_B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metallo-beta-lactamase 511 (Fragment) MBL511 OR MBL5.
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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Best Local Similarity 83.3.
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12 VDASWL 17
                                                                                   SEQUENCE FROM N.A.
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12 VDASWL 17
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RESULT 9 Q9JRLS

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RESULT 10

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Gaps

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Length 187;

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EMBL, AE006509, AAK33511.1; -.
InterPro, IPR000415; Nitroreductase.
Pfam, PF00881; Nitroreductase; 1.
Complete proteome.
SEQUENCE 221 AA; 25283 MW; 724C1
                                                                                                                                                              Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity
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36 LDAAWL 41
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Q8TR10;
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QBTR10
ID QBTR1
AC QBTR1
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Q8P239
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MEDLINB=21192684; PubMed=11296296;
Ferretti J.J., McShan W.M., Ajdlc D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-2229686; PubMed=12368813; MEDLINE-2229686; PubMed=12368813; Melson K.E., Gaidos E.J., Nelson W.C., Read T.D., Elsen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daudherty S., DeBoy R.T., Dodson R.J., Umrkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wollf A.M., Vamathevan J., Weldman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales,
Alteromonadaceae, Shewanella.
NCBI_TaxID=70863;
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                                                Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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SEQUENCE 205 AA; 23686 MW; 3A301AC03E782334 CRC64;
                                                                                                                                                                                                                                                                                                  01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative NAD(P)H-flavin oxidoreductase.
Pred. No. 3.7e+02;
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                                              1; Mismatches
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EMBL; AE015792; AAN56548.1; -.
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                                                                                                                                                                                                                                                                                                                                                                            Conserved hypothetical protein.
                      83.3%;
                   Best Local Similarity 83.3
Matches 5; Conservative
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Matches 5; Conservative
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12 VDASWL 17
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Q9A120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIESES. pyogenes; STRAIN=MGAS315 / Serotype M3; MEDLINE=22133808; PubMed=12122206; Beres S.B., Sylva G.L., Barblan K.D., Lei B., Hoff J.S., Barblan K.D., Lei B., Hoff J.S., Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M., Schläevert P.M., Musser J.M.; "Genome sequence of a serotype M3 strain of group A Streptococcus: phyage-encoded toxins, the high-virulence phenotype, and clone emergence.";
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                                                           Score 30; DB 16; Length 221;
Pred. No. 4.4e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPYMI8 0570 OR SPYM3 0360.
Streptococcus pyogenes (serotype M18), and
Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000415; Nitroreductase.
Pfam; PF00881; Nitroreductase; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 221 AA; 25269 MW; A929A147EE0027D6 CRC64;
724C14E54FC72CB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Putative NAD(P)H-flavin oxidoreductase.
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EMBL; AE009993; AAL97264.1; -.
EMBL; AE014143; AAM78967.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                outbreaks.";
Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

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Adalgan J.E., Nuabaum C., Roy A., Endrizzi M.G., Macdonald P., Ralagan J.E., Nuabaum C., Roy A., Endrizzi M.G., Macdonald P., Ritzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Allan N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R., Linton L., McKernan K., Talamas J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M., Hedderich R., Indram-Smith C., Kucttner H.C., Krzycki J.A., Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., A Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., Mccalf W.W., Birren B.;
The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity.";
EMBL; ABO1807; AAM04790.1;
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                                                                                             Methanosarcina acetivorans.
Archaea; Buryarchaeota; Methanococci; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR005237; Cons hypoth289.
InterPro; IRR002761; DUFT1.
Pfam; PF01902; DUFT1. 1.
TIGRFAMS; TIGR00290; MJ0570 dom; 1.
TIGRFAMS; TIGR00289; TIGR00289; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 225 AA; 25146 MW; A573146D1DDPB9D1 CRC64;
                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C2A / ATCC 35395 / DSM 2834;
MEDLINE=21929760; PubMed=11932238;
                                                       Hypothetical protein MA1374. MA1374.
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Best Local Similarity 83.3
Matches 5; Conservative
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149 LDSSWL 154
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Search completed: February 18, 2004, 14:35:48 Job time : 19.3684 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

sw model OM protein - protein search, using February 18, 2004, 14:12:09; Search time 6.5921 Seconds (without alignments) 87.531 Million cell updates/sec Run on:

US-09-643-260-10 33

1 LDASWL 6 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Description	hypothetical prote	~	cytochrome oxidase	hypothetical prote	probable precorrin	beta-lactamase (EC	L1 metallo-beta-la	aminodeoxychrorism	hypothetical prote	probable homeodoma	bifunctional aspar	hypothetical prote	phosphoenolpyruvat	conserved hypothet	cytochrome c-L pre	hypothetical prote		⊣	hypothetical prote	VSF-	probable signal pe	probable transcrip	hypothetical prote	cell division prot	hypothetical prote				
ΩI	T32441	AF0463	A69537	T49089	T03533	T48880	S45349	T44437	T04815	D85312	AH0937	AG1957	QYFKG	C82994	B41377	G83450	C83837	G75626	F84612	D84504	A75397	E83444	T29979	H82759	E70890	A48399	A85739	0	A37209
DB	12	7	~	~	~	N	~	7	7	~	~	~	Н	~	H	~	~	~	~	~	7	~	7	~	~	~	~	~	Н
Length DB	419	£308	535	763	245	290	290	332	442	461	810	906	919	150	177	243	252	255	256	264	269	274	277	278	æ	286	æ	æ	289
* Query Match	0.	٥.	٥.	3.9	6.	6.0	6.0	6.0	6.0	٠	6.0	6.	6.0				6.				7.9	•	•	•	•	7.9	•		7.9
Query Match	1001	93	6	6	8		8	ŏ	8	9	9	8	8	60	87	60	87	œ	œ	æ	æ	æ	80	æ	80	œ	æ	œ	œ
Score	33	31	31	31	30	30	30	30	30	30	30	30	30	53	29	29	29	29	29	29	29	53	59	29	29	29	53	29	29
Result No.	1	7	ო	4	ß	9	7	60	6	10	11	12	13	14	15		17		19	20	21	22	23	24	25	56	27	28	53

thiosulfate sulfur	thiosulfate sulfur	hypothetical prote	thiosulfate sulfur	thiosulfate sulfur	thiosulfate sulfur	hypothetical prote	peptidoglycan hydr	thiosulfate sulfur	hypothetical prote	hypothetical prote	probable transposa	rfbG protein - Sal	CDPglucose 4,6-deh	hypothetical prote	Wnt-2 protein - Ca
\$15081	ROHU	AH2327	ROBO	JC4398	JC5286	G83182	F89791	T52663	B99790	A86300	F70678	S15305	AH0766	T26037	S32695
8	Н	~	-	~	7	7	~	~	~	7	~	7	7	~	7
295	296	296	297	297	297	301	316	318	326	329	333	359	359	360	360
87.9	87.9	87.9	87.9	87.9	87.9	87.9	87.9	87.9	87.9	87.9	87.9	87.9	87.9	87.9	87.9
29	53	53	59	29	59	59	53	53	29	53	29	53	53	29	29
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

hypothetical protein T28B4.1 - Caenorhabditis elegans

C'Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000

C, Accession: T32441
R;Wilson, R.; Greco, T.; Sansone, J.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid T28B4.
A;Reference number: Z21168

A,Accession: T32441 A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: DNA

A;Residues: 1-419 <WIL> A;Cross-references: EMBL:AF026206; PIDN:AAB71262.1; GSPDB:GN00028; CESP:T28B4.1 A;Experimental source: strain Bristol N2; clone T28B4

C;Genetics:

A;Gene: CESP:T28B4.1 A;Map position: X A;Introns: 47/3; 68/3; 102/3; 153/1; 207/1; 296/1

Gaps ö Query Match 100.0%; Score 33; DB 2; Length 419; Best Local Similarity 100.0%; Pred. No. 50; Matches 6; Conservative 0; Mismatches 0; Indels

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1 LDASWL 6

340 LDASWL 345

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AF0463
high-affinity branched-chain amino acid transport system, permease protein livH [import: C;Species resinia pestis
C;Species Versinia pestis
C;Species Versinia pestis
C;Date: 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AF0463
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. R;Dature 413, 523-527, 2001
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AF0463
A;Accession: AF0463
A;Accession: AF0463
A;Coss-references: DNA
A;Residues: 1-308 <KUR>
A;Coss-references: GB:ALS90842; PIDN:CAC93274.1; PID:g15981721; GSPDB:GN00175
C;Genetics:
A;Gene: livH
C;Superfamily: leucine transport protein livH

Query Match

93.9%; Score 31; DB 2; Length 308;

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R;Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M. Pocc. Natl. Acad. Sci. U. S.A. 94, 9384-9388, 1997.
A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003
A;Reference number: Z14955; MUID:97404404; PMID:9256491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Risanschagrin, F.; Dufresne, J.; Levesque, R.C. Antimicrob. Agents Chemother. 42, 1245-1248, 1998
Antimicrob. Agents Chemother. 42, 1245-1248, 1998
A;Title: Molecular heterogeneity of the L-1 metallo-beta-lactamase family from Stenotrop. A;Reference number: 224841; MUID:98253990; PMID:9593158
A;Accession: T48880
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S45349

S45349

Il metallo-beta-lactamase - Xanthomonas maltophilia

Cipsceises: Xanthomonas maltophilia

Cipsceises: Xanthomonas maltophilia

Cipate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997

Cipate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997

Cipate: 19-Mar-1997 #sequence 01-Aug-1997

Airtle: Sequence analysis of the L1 metallo-beta-lactamase from Xanthomonas maltophilia
Aireference number: 845349; MUID:94289479; PMID:8018721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Description: catalyzes the hydrolysis of an amide bond in the beta-lactam ring of the C;Keywords: antibiotic resistance; hydrolase
F;1-33/Domain: signal sequence #status predicted <SIG>F;34-290/Product: L-1 metallo-beta-lactamase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  beta-lactamase (EC 3.5.2.6) L-1 precursor [validated] - Pseudomonas maltophilia N;Alternate names: L-1 metallo-beta-lactamase C;Species: Pseudomonas maltophilia C;Species: Pseudomonas maltophilia C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000 C;Accession: T48880
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1.1.2e+02;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 245;
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A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Cross-references: EMBL:AF010282; PIDN:AAC21590.1
A;Experimental source: strain GN12873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30; DB 2
Pred. No. 1.2e+
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                       A;Map position: 1
C;Superfamily: precorrin-3 methylase
C;Keywords: methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.9%;
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity
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34 VDASWL 39
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C,Function:
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49089
R;Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Rudd, S.; Lemcke, Submitted to the Protein Sequence Database, April 2000
A;Reference number: Z25015
A;Accession: T49089
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-763 <ALC>
A;Cross-references: EMBL:ALO49711; GSPDB:GN00061; ATSP:F4F15.210
A;Experimental source: cultivar Columbia; BAC clone F4F15
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                                             Gaps
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C;Species: Archaeoglobus fulgidus
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Pred. No. 1.6e+02;
1; Mismatches 0; Indels
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93.9%; Score 31; DB 2; Length 763;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels
                                             Indels
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          Pred. No. 93;
1; Mismatches
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83.3%;
          83.3%;
Similarity 83.3
5, Conservative
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Best Local Similarity
Matches 5; Conserv
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8 IDASWL 13
                                                                                                                                                                             66 IDASWL 71
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C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
A;Note: this species has also been called Salmonella typhi
C;Accession: AH0937
B;Parkhill, J; Dougan, G;; James, K.D; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R;Parkhill, J; Dougan, G;; James, K.D; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, K.J. Connerton, P; Cronin, A; Davis, P; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parky, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A;Attle: Complete genome sequence of a multiple drug resistant Salmonella enterica seron, A;Reference number: AB0502; MUD:21534947; PMID:11677608
A;Accession: AH0937
A;Accession: AH0937
A;Accession: AH0937
A;Molecule type: DNA
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d;Note: Nostoc sp. etrain PCC 7120

c;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C;Accession: AG1957

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch¹
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An.
A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AG1957

A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bifunctional aspartokinase II/homoserine dehydrogenase IIcan I write [imported] - Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: STY3768
C;Superfamily: thrA bifunctional enzyme; aspartate kinase homology; homoserine dehydrog.
A; Reference and analysis of chromosome 4 of the plant Arabidopsis thaliana. A; Reference number: A85001; MUID:20083488; PMID:10617198
A; Accession: D85312
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-461 <STO>
                                                                                                                                                                                                                A;Cross-references: GB:NC_001268; NID:g7269545; PIDN:CAB79547.1; GSPDB:GN00140 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-810 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD09522.1; PID:g16504639; GSPDB:GN00176
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reaidues: 1-906 «KDR»
A;Cross-references: GB:BA000019; PIDN:BAB73167.1; PID:g17130557; GSPDB:GN00179
A;Cross-references: gtrain PCC 7120
C;Genetics:
A;Gene: all1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein all1210 [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30; DB 2; Length 810;
Pred. No. 3.9e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                          Score 30, DB 2; Length 461;
Pred. No. 2.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                       90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 83.3%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 VDASWL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 LDAAWL 151
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
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Matches 5, Conserv
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                                                                                                                                                                                                                                                                         A, Gene: AT4g26920
A, Map position: 4
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R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                                                                            C)percession: T44437

E)Accession: T44437

F) Tanaka, M.; Ohgiya, S.; Hoshino, T.; Kawasaki, K.; Yumoto, I.; Myorthe, N.; Ueno, A.; Tanaka, M.; Ohgiya, S.; Hoshino, T.; Kawasaki, K.; Yumoto, I.; Biotechnol. Lett. 21, 641-646, 1999

A;Title: Cloning and sequencing of clustered genes involved in fatty acid biosynthesis A;Reference number: Z22768

A;Accession: T44437

A;Accession: T44437

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-332 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F10M23.260 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23.4pr-1999 #text_change 11-Jun-1999
C;Accession: T04815
R;Bevan, M.; Lecharny, A.; Chefdor, F.; Krivitzky, M.; Kreis, M.; Hoheisel, J.; Mewes, Submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15385
A;Accession: T04815
A;Accession: T04815
A;Molecule type: DNA
A;Residues: 1-442 <BEV>A;Accession: Columbia; BAC clone F10M23
C;Genetics:
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb_2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                       Species: Moritella marina
Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
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Pred. No. 2.1e+02;
1; Mismatches 0; Indels
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Pred. No. 1.6e+02;
1; Mismatches 0; Indels
                                                                    Indels
                 Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: EMBL:AB021978; PIDN:BAA85259.1
A,Experimental source: ATCC 15381
C,Genetics:
A,Note: pabC
C,Superfamily: yceG protein
                                                                 1; Mismatches
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A;Introns: 140/3; 165/3; 236/1; 358/3
A;Note: F10M23.260
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Best Local Similarity 83.3%;
Matches 5; Conservative 1
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                                      Best Local Similarity 83.3
Matches 5; Conservative
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LDAAWL 192
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VDASWL 133
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                              : | | | | | |
34 VDASWL 39
                                                                                                                             1 LDASWL 6
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Search completed: February 18, 2004, 14:38:44
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   Query Match
Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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A; Residues: 1-177 < VAN>
                                                                                                                                                                                        DASWL 121
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                                                                                                                                   DASWL 6
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A.Molecule type: DNA
A.Residues: 1-606, KL', 609-799, FT', 802-914, L', 916-919 <ORE>
A.Residues: 1-606, KL', 609-799, FT', 802-914, L', 916-919 <ORE>
A.Residues: 1-606, KL', 609-799, FT', 802-914, L', 916-919 <ORE>
A.Ross-references: GB:MZ5819; NID:g144984; PIDN:AAA83537.1; PID:g144985
A.Rote: residues 2-15 were confirmed by protein sequencing
C.Comment: This enzyme catalyzes the carboxylation (by carbon dioxide) of phosphoenolpyz
C.Comment: The activity of this protein is not stimulated by acetyl-CoA in the absence c
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                           C)Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1999
C;Accession: S05512; JS0183
C;Accession: S05512; JS0183
C;Accession: S05512; JS0183
M.T.; Griot, M.U.; Sinskey, A.J.
Mol. Gen. Genet. 218, 330-339, 1989
A;Title: The phosphoenolpyruvate carboxylase gene of Corynebacterium glutamicum: molecul A;Reference number: S05511; MUID:89384460; PMID:2779518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: ppc

(S,Guperfamily: phosphoenolpyruvate carboxylase

C;Keywords: allosteric regulation; carbon dioxide fixation; carbon-carbon lyase; carboxy

C;Keywords: allosteric regulation; carboxylase #status predicted <MAT>

F;2-919/Product: phosphoenolpyruvate carboxylase #status predicted

F;611-624/Region: substrate binding #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-919 <EIK>
A;Cross-references: GB:X14234; NID:g48688; PIDN:CAA32450.1; PID:g48689
A;Cross-references: GB:X14234; NID:g48688; PIDN:CAA32450.1; PID:g48689
A;Note: the authors translated the codon ATT for residue 387 as Glu, AAA for residue 553
R;O'Regan, M.; Thierbach, G.; Bachmann, B.; Villeval, D.; Lepage, P.; Viret, J.F.; Lemoil Gene 77, 237-251, 1989
A;Title: Cloning and nucleotide sequence of the phosphoenolpyruvate carboxylase-coding gA;Reference number: JS0183; MJID:89326141; PMID:2666264
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A, Status: preliminary
A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-150 <STO>
A, Cross-references: GB. AE004934, GB. AE004091; NID: g9951515; PIDN. AAG08596.1; GSPDB: GN001
A, Experimental source: strain PA01
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                                                                        Gaps
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Pred. No. 4.4e+02;
1; Mismatches 0; Indels
   Length 906;
                                                                     Indels
Score 30; DB 2; Les
Pred. No. 4.4e+02;
1; Mismatches 0;
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Best Local Similarity 83.3%;
Matches 5; Conservative 1
   90.9%;
83.3%;
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                                                                     5; Conservative
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   Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                1 LDASWL 6
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A,Gene: PA5211
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Gaps

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C;Accession: B41377
R;Van Spanning, R.J.M.; Wansell, C.W.; De Boer, T.; Hazelaar, M.J.; Anazawa, H.; Harms, L. Bacteriol. 173, 6948-6961, 1991
A;Title: Isolation and characterization of the moxJ, moxG, moxI, and moxR genes of Parac A;Reference number: A41377; MUID:92041581; PMID:1657871
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S. Superfamily: cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochrome c-L; cytochro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amicyanir
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R;Chen, L.; Durley, R.C.E.; Matthews, F.S.; Davidson, V.L.
Science 264, 86-90, 1994
A;Title: Structure of an electron transfer complex: methylamine dehydrogenase, A;Reference number: A57995; MUID:94188715; PMID:8140419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Date: 28-May-1992 #sequence_revision 02-Jul-1996 #text_change 15-Sep-2000
                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytochrome c-L precursor [validated] - Paracoccus denitrificans N;Alternate names: cytochrome c5511; cytochrome c552; moxG protein C;Species: Paracoccus denitrificans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.9%; Score 29; DB 1; Length.177; 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels
                                                          Length 150
                                                                                                                                                                                      0; Indels
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                                    Score 29; DB 2; L. Pred. No. 1.16+02; 0; Mismatches 0;
87.9%; Scc...
100.0%; Pre
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Sequence 1, Appli Sequence 8, Appli Sequence 123, App Sequence 123, App Sequence 123, App Sequence 124, App Sequence 124, App Sequence 124, App Sequence 11783, A Sequence 11783, A Sequence 11783, A Sequence 12142, A Sequence 1213, App Sequence 12182, A Sequence 12182, A Sequence 12182, A Sequence 12182, A Sequence 12182, A Sequence 12182, A Sequence 12182, A Sequence 12182, A Sequence 12182, A Sequence 12182, A Sequence 12182, A Sequence 12182, A Sequence 12182, A Sequence 1217, App Sequence 1325, A Sequence 1325, A Sequence 1335, A Sequence 1347, App Sequence 1365, A Sequence 1365, A Sequence 1365, A Sequence 1365, A Sequence 1365, A Sequence 1365, A Sequence 1365, A Sequence 1365, A Sequence 1365, A

16 30 90.9 935 14 US-10-077-751-1 Sequence 17 30 90.9 935 15 US-10-315-023-3 Sequence 19 29 97.9 15 US-10-315-023-3 Sequence 20 29 87.9 136 10 US-09-738-973-123 Sequence 21 29 87.9 136 10 US-09-84-133-123 Sequence 22 29 87.9 136 15 US-01-144-649A-123 Sequence 23 29 87.9 269 12 US-10-108-260A-3740 Sequence 24 29 87.9 277 12 US-10-108-260A-3577 Sequence 25 29 87.9 277 12 US-10-369-493-592 Sequence 25 29 87.9 277 12 US-10-369-493-597 Sequence 25 29 87.9 278 12 US-10-369-493-867 Sequence	29 87.9 279 12 US-10-366-493-11783 29 87.9 279 12 US-10-369-493-11784 29 87.9 279 12 US-10-369-493-15142 29 87.9 285 12 US-10-369-493-7936 29 87.9 286 12 US-10-369-493-7936 29 87.9 293 12 US-10-369-493-21834 29 87.9 297 10 US-09-981-353-90 29 87.9 315 4 US-09-815-242-12482 29 87.9 315 9 US-09-815-242-12482 29 87.9 315 9 US-09-815-242-12482 29 87.9 315 9 US-09-815-242-12482	29 87.9 32.7 14 US-10-029-180-40 29 87.9 437 15 US-10-145-415-101 29 87.9 491 12 US-10-15-415-101 29 87.9 491 12 US-10-15-415-101 29 87.9 501 12 US-10-094-749-1887 29 87.9 512 US-10-094-749-1887 29 87.9 512 US-10-094-749-1887 29 87.9 512 US-10-306-93-305 29 87.9 512 US-10-306-93-305 29 87.9 854 11 US-10-369-493-347 29 87.9 854 11 US-09-770-172	ALIGNMENTS F. 1 847-940B-10 ALIGNMENTS ALIGNMENTS F. 1 847-940B-10 ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS F. 1	; SEQ ID NO 10 ; LENGTH: 6 ; TYPE: PRT ; ORGANISM: Artificial Sequence ; FRATURE: ; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants US-09-847-940B-10	Query Match 100.0%; Score 33; DB 10; Length 6; Best Local Similarity 100.0%; Pred. No. 7e+05; Matches 6; Conservative 0; Mismatches 0; Indels 0; Ga Qy
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM protein - protein search, using sw model Run on: February 18, 2004, 14:36:10; Search time 16.6974 Seconds 75.239 Million cell updates/sec	Title: US-09-643-260-10 Perfect score: 33 Sequence: 1 LDASWL 6 Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 801455 seqs, 209382283 residues	Total number of hits satisfying chosen parameters: 801455 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	e: Published Applications AA:* 1: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 2: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 3: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 4: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 5: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 6: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 7: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 8: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 9: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 10: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 11: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 12: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 13: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 13: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 13: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 16: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 16: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 17: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 16: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 17: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 18: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 18: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 18: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 10: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 10: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 10: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 10: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 10: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 10: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 10: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 10: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 10: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 10: \(\text{cgn2} = \(\text{ptodata} \) 1 \\ pubpaa/\pu \\ 10: \(\te	score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. \$ SUMMARIES Result Query No. Score Match Length DB ID	1 33 100.0 6 10 US-09-847-940B-10 Sequence 10, Appl 3 100.0 6 11 US-09-847-946A-10 Sequence 10, Appl 3 100.0 10.0 10.0 10.0 10.0 10.0 10.0 1

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Gaps

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US-10-291-265-782
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APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INPLAMMATORY COMPOUNDS AND USES THEREOF
ILLE REPERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR PAPLICATION NUMBER: 60/201,261
PRIOR PILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR PILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PATENTIN Ver. 2.0
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: NBD peptide
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Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NAKAGAWA, SAIUCHII
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: COCIIAL, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE REPERRNCE: 249-125
CURRENT FILIAG DATE: 2000-12-18
FRIOR APPLICATION NUMBER: UP 99/377484
FRIOR APPLICATION NUMBER: JP 99/377484
FRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 6278
LENGRIH: 105
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Publication No. US70020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Corynebacterium glutamicum
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1 LDASWL 6
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US-09-738-626-6278
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48 LDASWL 53

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JULIA APPLICANT: Hypeltation US/10291265

Publication No. US20030232054A1

GENERAL INFORMATION:

APPLICANT: Hypeq, Inc.

APPLICANT: Tang et al.

TITLE OF INVENTION: No. US20030232054A1e1 Nucleic Acids and Polypeptides

TITLE OF INVENTION: No. US20030232054A1e1 Nucleic Acids and Polypeptides

CURRENT APPLICATION NUMBER: US/10/291,265

CURRENT APPLICATION NUMBER: US/40/4

PRIOR APPLICATION NUMBER: 09/491,404

PRIOR APPLICATION NUMBER: 09/491,404

PRIOR APPLICATION NUMBER: 09/491,404

PRIOR APPLICATION NUMBER: 09/491,404

PRIOR PILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: 09/631,451

PRIOR PILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-09-15

NUMBER OF SEQ ID NOS: 944

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 782

LENGTH: 191
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Pred. No. 8.8e+02;
1; Mismatches 0;
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US-09-765-205-14
Sequence 14, Application US/09765205
Patent No. US20020034800A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Streptococcus pyogenes US-10-169-048-2
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CORGANISM: Homo sapiens
US-10-291-265-782
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APPLICANT: Roberg-Perez, Sharon
APPLICANT: Wadman, Shannon
APPLICANT: Wadman, Shannon
APPLICANT: Wadman, Shannon
TITLE OF INVENTION: FACTORS FOR ANGIOGENESIS, VASCULOGENESIS, CARTILAGE FORMATION,
TITLE OF INVENTION: BONE FORMATION, AND METHODS OF USE THEREOF
FILE REPERENCE: 3021.051062
CURRENT APPLICATION NUMBER: US 10/10/360,849A
CURRENT FILING DATE: 2003-02-07
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PATENTIN VERSION 3.2
ESEQ ID NO 15
LENGTH: 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BENER, JOÉÍFEY
APPLICANT: Clark, Karl
APPLICANT: Clark, Karl
APPLICANT: Larson, Jon
APPLICANT: Larson, Jon
APPLICANT: Exer. Stephen
APPLICANT: Roberg-Perez, Sharon
APPLICANT: Roberg-Perez, Sharon
APPLICANT: Roberg-Perez, Sharon
APPLICANT: Wadman, Shannon
APPLICANT: Wadman, Shannon
APPLICANT: Wadman, Shannon
APPLICANT: Benergerence: 3021.051032
TITLE OF INVENTION: FACTORS FORMATION, AND METHODS OF USE THEREOF
FILE REFERENCE: 3021.051032
CURRENT APPLICATION NUMBER: US 60/354,978
PRIOR APPLICATION NUMBER: US 60/354,978
PRIOR FILING DATE: 2002-07
PRIOR FILING DATE: 2002-07
PRIOR FILING DATE: 2002-07
PRIOR FILING DATE: 2002-07
PRIOR FILING DATE: 2002-07
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Pred. No. 1e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30; DB 12; Length 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 18, Application US/10360849A; Publication No. US20030220249A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 310, Application US/10291265; Publication No. US20030232054A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Discovery Genomics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hackett, Perry
Nasevicius, Aidas
Essner, Jeffrey
Clark, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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Matches 5; Conservative
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ORGANISM: home sapiens
                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 LDASWV 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 LDASWV 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/10360849A
; Sequence 12, Application US/10360849A
; Publication No. US2030220249A1
; GENERAL INFORMATION:
; APPLICANT: Discovery Genomics, Inc.;
; APPLICANT: Baser, Jeffrey
; APPLICANT: Earson, Jon
; APPLICANT: Larson, Jon
; APPLICANT: Wadman, Shannon
; APPLICANT: Wadman, Shannon
; APPLICANT: Wadman, Shannon
; TITLE OF INVENTION: FATTORS FOR ANGIOGENESIS, VASCULOGENESIS, CARTILAGE FORMATION,
; TITLE OF INVENTION: FATTORS FOR ANGIOGENESIS, VASCULOGENESIS, CARTILAGE FORMATION,
; TITLE OF INVENTION: PAUBER: US, 10,10,360,849A
; CURRENT FILING DATE: 2003-02-07
; PRIOR PAPLICATION NUMBER: US, 60/354,978
; MIMMED OF GEO, TA MOC. 27
                   APPLICANT: Cao, Li
TITLE OF INVENTION:
FILE REFERENCE: 1458.004/200130.449
CURRENT APPLICATION NUMBER: US/09/765,205
CURRENT FILING DATE: 2001-01-17
PRIOR FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FRAEKE
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Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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1; Mismatches
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Sequence 15, Application US/10360849A

Publication No. US2030220249A1;
GENERAL INFORMATION:
APPLICANT: Discovery Genomics, Inc.
APPLICANT: Hackett, Perry
APPLICANT: Basevicius, Aidas
APPLICANT: Essner, Jeffrey
APPLICANT: Clark, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin version 3.2
SEQ ID NO 12
LENCTH: 261
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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ORGANISM: danio rerio
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           ORGANISM: human
US-09-765-205-14
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LENGTH: 261
TYPE: PRT
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TYPE: PRT
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; TITLE OF INVENTION: No. US20030232054Alel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR PILING DATE: 2000-07-17
; PRIOR PLILNG DATE: 2000-07-17
; PRIOR PLILNG DATE: 2000-07-17
; PRIOR PLILNG DATE: 2000-09-13
; PRIOR PLILNG DATE: 2000-09-15
; RIOR PLILNG DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFOGRATION:
GENERAL INFOGRATION:
GENERAL INFOGRATION:
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: HAVASHI, MIXIRO
APPLICANT: COCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TEDAN, MASATO
APPLICANT: TEDAN, MASATO
APPLICANT: GZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US/99/738,626
CURRENT FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: US/99/738,626
CURRENT FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER: OF SEQ ID NOS: 7059
SOGTWARE: PATENTIN VET: 3.0
SEQ ID NO 6970
LENGTH: 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6970, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6970
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 90.9
Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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ORGANISM: Homo sapiens
US-10-291-265-310
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105 LDATWL 110
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RESULT 12 US-09-784-208-3

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Sequence 1, Application US/1007745

Sequence 1, Application US/1007745

Publication No. US20030172698A1

APPLICANT: NODA, TAKAYUKI

APPLICANT: SATO, KAZUHIRO

TITLE OF INVENTION: ORGANIC NITROGEN-CONTAINING COMPOSITION AND FERTILIZER COMPRISING

TITLE OF INVENTION: SAME

FILE REFERENCE: 2198433150

CURRENT FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: JP 2001-044137

PRIOR PILING DATE: 2001-02-20

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.1
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GENERAL INFORMATION:
APPLICANT: IZUI, Hiroshi
APPLICANT: ONO, Eiji
APPLICANT: MATSUI, Kazuhiko
APPLICANT: MATSUI, Kazuhiko
APPLICANT: MATSUI, Kazuhiko
APPLICANT: TO, Hisso
APPLICANT: TO, Hisso
APPLICANT: HARA, Yoshihiko
TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR
TITLE OF INVENTION: PRODUCING L-GLUTAMIC ACID
FILE REFERENCE: 0010-0989-0
CURRENT APPLICATION NUMBER: US/09/784,208
CURRENT FILING DATE: 1999-03-18
PRIOR PILING DATE: 1999-03-18
PRIOR PILING DATE: 1999-03-18
PRIOR PLILING DATE: 1998-03-18
PRIOR PLILING DATE: 1998-10-19
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 3
LENGTH: 935
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Pred. No. 3.1e+03;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Enterobacter agglomerans US-09-784-208-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Enterobacter agglomerans
US-10-077-745-1
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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NBD mutant peptide
Human NEMO binding
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                                                                                                                 February 18, 2004, 13:37:19; Search time 22.7763 Seconds (without alignments) 41.814 Million cell updates/sec
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
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| SIDSI/gcgdata/geneseqg-embl/AA1983.DAT:*
| SIDSI/gcgdata/geneseqg-embl/AA1985.DAT:*
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| SIDSI/gcgdata/geneseqg-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqg-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseqg/geneseqp-embl/AA1990.DAT:*
| SIDSI/gcgdata/geneseqg/geneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseqg/geneseqp-embl/AA1991.DAT:*
| SIDSI/gcgdata/geneseqg/geneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseqg/geneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseqg/geneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseqg/geneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseqg/geneseqp-embl/AA1992.DAT:*
| SIDSI/gcgdata/geneseqg/geneseqp-embl/AA1999.DAT:*
| SIDSI/gcgdata/geneseqg/gene
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                               1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                  OM protein - protein search, using sw model
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AAG92524
ABB77295
AAG32182
AAG32180
AAG32180
ABG20551
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match
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903.9
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Perfect score:
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Human ORFX ORF2370 Human gene 39 enco Human novel protei Streptococcus pyog Streptococcus pyog Streptococcus pyog Streptococcus pyog Streptococcus pyoly A bone marrow serr Human novel protei Novel human diagno Phosphoenolpyruvat Bacterial phosphoe Phosphoenolpyruvat C glutemicum prote Corynebacterium gl Alpha-ketoglutarat Succinate dehydrog Enterobacter agglo Enterobacter agglo Anino acid sequenc Enterobacter agglo Enterobacter agglo Enterobacter agglo Human secreted pro Human diagno Human immune/haema Human lung tumour Human lung tumour Human lung tumour Human lung tumour Human lung tumour Human lung tumour Human lung tumour Human lung tumour Human lung tumour Human lung tumour Human lung tumour Human lung tumour Human lung tumour Human phospholipas Bordetella pertuss Herbicidally activ Human protein SEQ Staphylococcus aur	ALIGNMENTS T. 1 ABB08732 standard; peptide; 6 AA. ABB08732; 14-JUN-2002 (first entry) Mutated IKKDeta NEMO binding domain peptide SEQ ID NO 10. IKKDeat; IKKalpha; NEMO; NEMO binding domain; NBD; NP-kBp; kinase activation; leukocyte; inflammation; E-selectin; osteoclast; altenmer's disease; transplant rejection; osteoprosis; cancer; altenmer's disease; transplant rejection; osteoprosis; ancer; rheumatoid arthritis; Orbh's disease; multiple sclerosis; HIV; altenmer's disease; viral; infection; asthma; anaphylaxis; psoriasis; rheumatoid arthritis; orbh's disease; multiple sclerosis; HIV; osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human; anti-arthritic; osteopathic; antiasthmatic; antialargic; dermatological; antibacterial; antiulcer; mutant; mutein. Homo sapiens Synthetic. Location/Qualifiers Misc-difference 3 Action/Qualifiers Misc-difference 3 Action-Mode = "Wildtype Trp substituted by Ala" WO200183547-A2.
AAB42606 AAE03936 AAU14439 AAU14439 AAU14439 AAU14203 AAV53628 AAV52638 AAV52634 AAV52634 AAV29634 AAV29634 AAV31987 AAV31987 AAV31987 AAV31987 AAV31987 AAV31987 AAV31987 AAV31987 AAV31987 AAV31987 AAV31987 AAV31987 AAV3189311 AAV3189311 AAV31987 AAV31988 AAV3189318 AAV3189318 AAV3189318 AAV3189318 AAV3189318 AAV3189318 AAV363119 AAV36333 AAV36833	ALIGNMENTS ry) nding domain peptide nding domain peptide NEMO binding domain coyet, inflammation; nosplant rejection; asth robn's disease; mult uppression; antimuli nootropic; neuropri nootropic; neuropri irucide; antiasthmat terial; antiasthmat terial; antiasthmat terial; antiasthmat incide; antiasthmat terial; antiasthmat incide; antiasthmat rerial; antiasthmat re
5551135551055153333350555064111555113555555	nntry) hbinding MO; NEM wikocyte wikocyte viral; Crobn' viral; viruci nocuppre viruci acteria athic;
11986 11986 11987	first entry) (first entry) ta NEMO binding dom ta NEMO binding dom ta NEMO; NEMO bi tansplant infe firstis; Crohn's di firstis; Crohn's di firmunosuppression cytostatic; noctrop cytostatic; virucide; firmunosuppression in antibacterial; anti costeopathic; antifice Location/Qualifi cos 3 /note= "wildtype 2.
88888888888888888888888888888888888888	standard; 002 (firsi IKKalpha; IKKalpha; IKGation; nc diseas;
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	7.1 ABB08732 St. ABB08732 St. 14-JUN-2002 Mutated IKKI IKKDeat; IKK IKIASE acti ALZheimer's ALZheimer'
01111111111111111111111111111111111111	RESULT 1 ABB08732 KX KX KX ABB0873 AC ABB0873 AC ABB0873 KW INCOEAT KW KINCOEAT KW ALCOEM KW ALC

Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Novel human diagno

C glutamicum prote Human IKKbeta muta

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antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NRkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                 Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Page 47; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAY-2001; 2001WO-US14346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-AUG-2000; 2000US-0643260.
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                                                                                                                                                                                                                                                                                                                                 Synthetic.
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   ceramplectasis. The intramancory disorder is ascense, allogises, cuticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis, cheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory bowel disease, vasculitis and bursitis. The inflammatory disorder may also be dermaticis, eccema, psoriasis, osteoarthritis, psoriatic arthritis, lupus and sporiasis, crowdylarthritis. Also for Crohn's disease, ulcerative colitis, polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis, cryoglobulinaemia or multiple sclerosis. For chronic viral infections caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral infections caused by Epstein-barr, cytomegalovirus or herpes simplex. Other infections cused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral infection anaphylaxis, drug and food sensitivity, contact dermatitis sumburn or aging. The compound may be used to replace corticosteroids in impunchangession in transplants and cancer therapy. Also for identifying antiinflammatory compounds and for diagnosis of an inflammatory disorder. The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of a mutated NEMO binding domain of IKKbeta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB08725-ABB08742) comprising at least one NEWO binding domain (ABB77313). The compound has acts through selective inhibition of cytokine-mediated NF-kB activation by blocking the interaction of NEMO with IKKbeta at the NEWO binding domain. Blockage of IKKbeta-NEWO interaction results in inhibition of IKKpeta kinase activation and subsequent decreased phosphorylation of IKAppaB. The compound may also act (directly or indirectly) by blocking the recruitment of leukocytes into sites of acute and chronic inflammation, by down-regulating the expression of E-selectin on leukocytes or by blocking osteoclast differentiation. The compound is useful in treating NF-kB mediated conditions, where the condition is an inflammatory disorder, an autoimmune disease, transplant rejection, osteoporosis, cancer, altabalmer's disease, atherosclerosis, a viral infection or ataxia telegals.
                                                                                                                                                                                                                                                                                                                          Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting a cell with an anti-inflammatory compound comprising at least one NEMO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 23; Page 44; 82pp; English.
02-MAY-2001; 2001WO-US40654.
                                                       02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
                                                                                                                                                                                                                                                                   WPI; 2002-179350/23.
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Best Local Similarity
                                                                                                                                              UYYA ) UNIV YALE.
                                                                                                                                                                                                        May MJ, Ghosh S;
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Phillips K;

Findeis MA,

Ghosh S,

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The invention relates to an antiinflammatory compound (especially AAM48629-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48620) comprising a membrane translocation domain (AAM48620-AAM48620). The AAM48651) which comprises from 6-15 amino acid residues, fused to a NEWO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, notropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NEKappa crivation by blocking interaction of Ikappas kinase beta (IKKbeta kinase activation and subsequent decreased phosphorylation of Ikappas. The compounds are useful for treating inflammation of Ikappas. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, britanian diseases such as lupus, polymylajdia, scleroderma, contropication and subsequent diseases such as lupus, polymylajdia, scleroderma, contropication and diseases such as lupus, polymylajdia, scleroderma, contropication and concer, psoriasis, polymylajdia, scleroderma, contropication and concernation and contropication and concernation and concernation and concernation and contropication and concernation concernation and concernation concernation concernation concernation concernation concernation concernation concernation concerna
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Alzheimer's disease; atherosclerosis; viral infections; and ataxia
telangiectasia. The compounds are also useful for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drug or food sensitivity, eczema, dermatitis, sunburn, aging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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ABU08425
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Gaps

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AAM48515 standard; Peptide; 6 AA

RESULT 2 AAM48515 NBD mutant peptide SEQ ID NO 10.

(first entry)

20-MAR-2002 AAM48515;

BXXXXX

ABU08425;

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sequences from the Corpusform bacterium Corpusbacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of corpuseform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from corpusform bacterium, corpusform bacterium, corpusform bacterium, corpusform bacterium, corpusform bacterium corpusform bacterium corpusform bacterium of a gene derived from corpusform bacterium, corpusform bacterium of a gene derived from corpusform bacterium, corpusform bacterium of panel for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of nucleotide and protein
                                                                                                                                     amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; SEQ ID NO: 6278; 246pp + Sequence Listing; English.
                                                                                        C glutamicum protein fragment SEQ ID NO: 6278.
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N. Ozaki A;
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                                                                                                                                                                                                                                                                                                                                                                                                 16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                       18-DEC-2000; 2000EP-0127688.
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                                                                                                                                                                                                             Corynebacterium glutamicum
                                            26-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakagawa S, Mizoguchi H,
Tateishi N, Senoh A, Ike
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                                                                                                                                     Coryneform bacterium; a organic acid synthesis.
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AAG92524;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to antiinflammatory compounds comprising NEMO binding domain (NBD) peptides. The NEMO binding domains are found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-beta (IKKbeta) and IkappaB kinase-beta (IKKbeta) and IkappaB kinase-beta (IKKB) publication are useful for modulating nuclear factor-kappaB (NF-kappaB) induction in a cell, where the compounds are capable of blocking the interaction between one or more IKKB such as IKKalpha or IKCbeta, and NEMO. The antiinflammatory compound further comprises at least one membrane translocation domain. The compounds are useful for treating inflammatory disorders, autoimmune diseases, osteoporosis, cancer, inflammatory disorders, autoimmune diseases, osteoporosis, ktaxia telangiectasis, and for transplantation detection. The compounds of the invention block NF-kappaB induction by IKK but do not inhibit the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
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                                                                                                                                                    Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta; IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB; nuclear factor-kappaB induction; inflammatory disorder; autoimmune disease; osteoporosis; cancer; Alzheimer's disease; ransplantation detection; Ataxia telangiectasia; transplantation detection; immunosuppressive; osteopathic; cytostatic; notoropic; neuroprotective; antiatherosclerotic; virucide; vasotropic; antirheumatic; antiatherosclerotic; virucide;
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                                                                                                            Human NEMO binding site (NBD) mutant peptide #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 22; Page 17; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAY-2001; 2001US-0847940.
                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        psoriasis, vasculitis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 A.
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                                                                12-JUN-2003
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Hayashi M, Ochiai K,

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Length 105;

22;

IKKbeat, IKKalpha, NEMO, NEMO binding domain, NBD, NF-kappaB, NF-kB, kinase activation; leukocyte; inflammation; E-selectin; osteoclast;

AAG92524 standard; Protein; 105 AA.

AAG92524

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Length 756; 0; Indels

100.0%; Score 33; DB 23; 100.0%; Pred. No. 7.9e+02; Mismatches

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6; Conservative

Matches

Query Match Best Local Similarity

756 AA;

Sequence

737 LDASWL 742

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derived from GenBank Accession No. 014920 (ABB77294)

us-09-643-260-10.rag

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The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB00725-ABB00742) comprising at least one NRMO binding domain (ABB07313). The compound has acts through selective inhibition of NEMO (STC) at the NEMO binding at least one NEMO binding domain. Blockage of IKKbeta-NEMO interaction results in inhibition of IKKbeta hisses activation and subsequent decreased phosphorylation of IKKbeta hisses activation and subsequent decreased phosphorylation of IKKbeta herocompound may also act (directly or indirectly) by blocking the recruitment of leukocytes into sites of acute and chronic inflammation, by down-regulating the expression of B-selectin on leukocytes or by blocking osteoclast differentiation. The compound is useful in treating NP-kB mediated conditions, where the condition is an inflammatory disorder, an autoimmune disease, transplant rejection, osteoporosis, cancer, alteriaria, anaphylaxis, cutaneous inflammatory disorder, and cuticaria, anaphylaxis, cutaneous inflammatory disease, vasculitis, boriasis, osteoarthritis, osteoarthritis, psoriatic arthritis, inflammatory conditions, where the inflammatory disorder is activative colitis, conditions, osteoarthritis, psoriatic arthritis, lupus and bursitis. The inflammatory disorder may also be dermatitis, inflammatory polymyladia, osteoarthritis, psoriatic arthritis, lupus and colymylarthritis. Also for Crohn's disease, ulcerative colitis, cryoglobulinaemia or multiple sclerosis. For chronic viral infections caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral classases include HIV and influence and solve ensettions are entitied cutaning anaphylaxis, drug and food sensitivity, contact dermatitis, may also be useful for traating anaphylaxis, drug and food sensitivity, contact dermatitis, may also be useful for in which corticosteroids are useful dermaticies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunosuppression in transplants and cancer therapy. Also for identifying antinflammatory compounds and for diagnosis of an inflammatory disorder. The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of an IKKbeta mutant, useful in examples of the invention.

Note: The present sequence is not given in the specification but is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting cell with an anti-inflammatory compound comprising at least one NEMO
                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAY-2001; 2001WO-US40654.
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autoimmune disease; transplant rejection; osteoporosis; cancer; Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis; rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; antiinflammatory; immunosuppressive; osteopathic; cytostatic; noctropic; neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antiasthmatic; antiallergic; dermatological; antibacterial; antipsoriatic; antirheumatic; /note= "Wildtype Trp substituted by Ala" antiarthritic; osteopathic; antiulcer; mutant; mutein.

Arabidopsis thaliana protein fragment SEQ ID NO: 38774.

17-OCT-2000 (first entry)

AAG32182;

AAG32182 standard; Protein; 618 AA.

RESULT 6

AAG32182

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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06-APR-1999;
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PR 06-AUG-1999; 99US-0147416.

PR 10-AUG-1999; 99US-014743.

PR 10-AUG-1999; 99US-014743.

PR 11-AUG-1999; 99US-014743.

PR 11-AUG-1999; 99US-0148171.

PR 11-AUG-1999; 99US-0148645.

PR 11-AUG-1999; 99US-0148646.

PR 11-AUG-1999; 99US-0148665.

PR 20-AUG-1999; 99US-0149922.

PR 20-AUG-1999; 99US-0149922.

PR 21-AUG-1999; 99US-0149922.

PR 21-AUG-1999; 99US-0149922.

PR 22-AUG-1999; 99US-0149922.

PR 22-AUG-1999; 99US-0151066.

PR 22-AUG-1999; 99US-0151066.

PR 22-AUG-1999; 99US-0151066.

PR 22-AUG-1999; 99US-015106.

PR 22-AUG-1999; 99US-015109.

PR 22-AUG-1999; 99US-015376.

PR 22-AUG-1999; 99US-015376.

PR 23-AUG-1999; 99US-015376.

PR 23-AUG-1999; 99US-015546.

PR 24-AUG-1999; 99US-015546.

PR 25-AUG-1999; 99US-015546.

PR 25-AUG-1999; 99US-015546.

PR 25-AUG-1999; 99US-015546.

PR 25-AUG-1999; 99US-015646.

PR 25-AUG-1999; 99US-01

Query Match 93.9%; Score 31; DB 21; Length 618; Best Local Similarity 83.3%; Pred. No. 1.5e+03; Matches 5; Conservative 1; Mismatches 0; Indels

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13-AUG-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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AAG32180

AAG32180 standard; Protein; 763 AA. X. X. AAG32180;

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Pred. No. 1.6e+03;
1; Mismatches 0; Indels
990S-0148684.
990S-0149368.
990S-0149368.
990S-0149425.
990S-0149722.
990S-0149923.
990S-0149923.
990S-0149923.
990S-0151086.
990S-0151086.
990S-0151086.
990S-0151080.
990S-0151080.
990S-0151033.
990S-0151438.
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990S-01514418.
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Best Local Similarity 83.3%;
Matches 5; Conservative
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|||||:
LDASWI 531
                         16-AUG-1999,
17-AUG-1999,
20-AUG-1999,
20-AUG-1999,
20-AUG-1999,
23-AUG-1999,
25-AUG-1999,
25-AUG-1999,
27-AUG-1999,
27-AUG-1999,
31-AUG-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-SEP-1999;
24-SEP-1999;
28-SEP-1999;
29-SEP-1999;
05-0CT-1999;
06-0CT-1999;
13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
15-0CT-1999;
16-0CT-1999;
17-0CT-1999;
17-0CT-1999;
18-0CT-1999;
18-0C
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15-SEP-1999;
16-SEP-1999;
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Score 31, DB 21; Length 763;
Pred. No. 1.8e+03;
1; Mismatches 0; Indels
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         9908 - 0.141930
9908 - 0.141930
9908 - 0.151068
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9908 - 0.151080
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Best Local Similarity 83.3%;
Matches 5; Conservative 1
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LDASWI 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDASWL 6
                                                                                             01-SEP-1999;
07-SEP-1999;
10-SEP-1999;
13-SEP-1999;
                                                                                                                                                                       22-SEP-1999
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ID ABG
XX
AC ABG
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990S - 013946 0

990S - 013946 1

990S - 013946 1

990S - 013946 3

990S - 013946 3

990S - 013976 3

990S - 01398 3

990S - 014035 3

990S - 014035 3

990S - 01423 7

990S - 01423 7

990S - 01423 7

990S - 01423 7

990S - 01423 7

990S - 01443 2

990S - 01443 2

990S - 01443 3

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990S - 0145 0

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990S - 0145 38

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99US-0147416.
99US-0147493.
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99US-0148319.
99US-0148341.
99US-0148684.
99US-0149178.
99US-0149172.
99US-0149723.
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20-AUG-1999;
20-AUG-1999;
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02-AUG-1999;
03-AUG-1999;
                                                     8-JUN-1999
                                                                          22-JUN-1999
23-JUN-1999
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24-JUN-1999
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04-AUG-19
05-AUG-19
05-AUG-19
                                                                                                                                        10-JUN-01
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Gaps

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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatorropic; vulnerary; antiparkinsonian; noctropic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; cosqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermator to, or preventing or treating the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating the proteins and nucleic acids may be used to treat cancers; proliferative disorders, neurodegenerative disorders, osteoarthritis, concliferative disorders, neurodegenerative disorders, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antilifiammatory disease; to enhance consultation; to inhibit thrombosis; and as a contraceptive.
Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppensant; cardiant; immunostimulant; thrombolytic; antiantentic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antidiabetic; antianaemic; gene therapy; cancer; proliferative disorder; hypotrension; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; eholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuia; burn; wound; bone damage; cartilage damage; antinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.9%; Score 30; DB 21; Length 119; 83.3%; Pred. No. 3.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 3920; 5507pp; English.
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99US-0127636.
99US-0127728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000WO-US08621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2000; 2000US-0540763
                                                                                                                                                                                                                                                                                                                                                               thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-602362/57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LDASWL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAC76815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200058473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-OCT-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, colymerase chair reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The color independence and sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as complement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymolectide sequences have applications in clasponstics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amine acid sequences and approach of the invention.

Note: The sequence data for this patent did not appear in the printed configuration, in for while and not expressive the energy of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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83.3%; Pred. No. 3.8e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ORFX ORF2370 polypeptide sequence SEQ ID NO:4740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID No 50910; 103pp; English.
     Novel human diagnostic protein #20542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB42606 standard; Protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT;
                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000US-0540217
                                                                                                                                                                                                                                                                                                                                                                                      23-AUG-2000; 2000US-0649167
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac RT, Liu C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS84738
                                                                                                                                                                                             WO200175067-A2
                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38
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RESULT 10 AAB42606

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ADD08345-AAD08394 represent cDNAs corresponding to 50 human secreted protein genes and AAE03898-AAE03947 represent the proteins they encode. C AAE03948-AAE03996 represent human secreted protein fragments or variants. C AAE03948-AAE03996 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions can be disapposed by determining the c amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 50 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abovementalities, haematopoietic disorders diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, C Parkinson's disease), cognitive disorders, schizophrenia, asthma, c satiovascular disorders angiogenic disorders, kidney disorders, skin disorders (e.g., psoriasis), sepsis, diabetes, and infections. The proteins can also be used to aid wound c healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell
                                                                                                                                                                                                    Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding 50 human secreted polypeptides, useful for preventing, diagnosing and/or treating diseases, e.g. Parkinson's disease, botulism, cancers and Scimitar syndrome -
                                                                                                                                                                   Human gene 39 encoded secreted protein HBMDM08, SEQ ID NO:99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Mature secreted protein"
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/label= signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                       AAE03936 standard; Protein; 156 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 547; 614pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                        binding partner identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0138629.
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                                                                                                                            (first entry)
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/note= "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                          09-AUG-2001
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                                                                                AAE03936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
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RESULT 11
                     AAE03936
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culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and immunosoratic immunosasys e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; ALDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer; s disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy;
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 50 human secreted polypeptides, useful for preventing, diagnosing and/or treating diseases, e.g. Parkinson's disease, botulism, cancers and Scimitar syndrome -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; proliferative disorder; cancer; tumour
                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human gene 39 encoded secreted protein fragment, SEQ ID NO:172.
                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                    Score 30; DB 22;
Pred. No. 5.2e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Komatsoulis GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 593; 614pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE03978 standard; Protein; 189 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 binding partner identification.
                                                                                                                                                                                                                        90.9%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2000; 2000WO-US15136.
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                                                                                                                                                                                                                                                               5; Conservative
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                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         LDASWV 61
                                                                                                                                                                                  156 AA;
                                                                                                                                                                                                                                                                                                    1 LDASWL 6
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                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE03978;
                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
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proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of creatment of amammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and fin gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, etem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the provise and function of alsorders and envised and osteoarthritis, an emana.

Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral or function or from any resulting from bacterial, viral or function or firm any resulting from bacterial, viral or firm any resulting from bacterial.

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Gaps

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Score 30; DB 22; Length 191; Pred. No. 6.4e+02; 1; Mismatches 0; Indels

90.98; 83.3%;

191 AA;

Sequence

Query Match
Best Local Similarity 83.3
Matches 5; Conservative

161 LDASWV 166

1 LDASWL 6

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AAU03119 standard; Protein; 221 AA.

RESULT 14

AAU03119

AAU03119;

tissue regeneration; immune disorder.

fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host disease, eczema, haemophila, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention.

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and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haemacopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, settofammation, calergies, neurological disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepais, diabetes, artherosclerosis, skin disorders, angiogenic disorders, kidney disorders, angiogenic disorders, kidney disorders, cardiovascular disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound challing and epithelial cell proliferation, to prevent skin aging due to subburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their contains or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked im diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISAA). The present sequence represents a human secreted protein fragment referred to in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; novel protein; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvolaemi; antiarthritic; cerebroprotective; antifungal; antiviral; antiboeterial; antiallergic; dermaclogical; haemostatic; antiathmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.9%; Score 30; DB 22; Length 189; 83.3%; Pred. No. 6.3e+02; live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU14439 standard; Protein; 191 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human novel protein #310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 LDASWV 169
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Virulence, attenuated microorganism; Streptococcal infection; Gram-positive bacteria; antimicrobial; impetigo; pneumonia.
                                                   Streptococcus pyogenes virulence protein #1.
                                                                                                                                                                                                99GB-0030463.
99GB-0030464.
99GB-0030466.
99GB-0030467.
99GB-0030471.
99GB-0030473.
                                                                                                                                                                                                                                                                                                                 2000GB-0003727.
2000GB-0003728.
2000GB-0003729.
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                                                                                                                                                                                                                                                                                                       2000GB-0003726
                                                                                                                                                                                                                                                                                                                                                 17-FEB-2000; 2000GB-0003730
                             23-OCT-2001 (first entry)
                                                                                                      Streptococcus pyogenes.
                                                                                                                          WO200148208-A2.
                                                                                                                                                                                                                                                                                                                   17-FEB-2000;
                                                                                                                                               05-JUL-2001
                                                                                                                                                                                                            23-DEC-1999
                                                                                                                                                                                                                      23-DEC-1999,
23-DEC-1999,
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23-DEC-1999,
                                                                                                                                                                                                                                                                          23-DEC-1999
                                                                                                                                                                                                                                                                                     23-DEC-1999
Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
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The invention relates to polynucleotides encoding novel human

Example 4; Page 816; 894pp; English.

Liu C, Drmanac RT;

Tang YT,

(HYSE-) HYSEQ INC.

WPI; 2001-451939/48.

N-PSDB; AAS22744

Isolated

25-JAN-2001; 2001WO-US02623 25-JAN-2000; 2000US-0491404

WO200155437-A2. Homo варіепв

02-AUG-2001

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Search completed: February 18, 2004, 14:26:22
Job time : 23.7763 secs
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Best Local Similarity
Matches 5; Conserv
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                                                    Telford J,
Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
  8
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                                                                                                                                                                                                                                                   AAU01119-AAU01149 represent novel Streptococcus pyogenes virulence proteins #1-31. The S. pyogenes virulence genes can be used to proteins #1-31. The S. pyogenes virulence genes can be used to produce attenuated microorganisms comprising a mutation that disrupt the expression of the virulence protein. The virulence genes, proteins or an attenuated microorganism or ordering; the proteins themselves, an attenuated microorganism or a vaccine comprising the virulence protein are useful for the manufacture of a medicament for use in the treatment or prevention of a condition associated with infection by Streptococcal or gram-positive bacteria, for veterinary treatment, and in a screening assay for the identification of an antimicrobial drug. Disorders which can be treated using S. pyogenes virulence polymolecities and polypeptide sequences include non-invasive infections and invasive infections etc. The virulence proteins are also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                          Novel peptide obtained from Streptococcus pyogenes useful for treating or preventing a condition associated with infection by Streptococcal or Gram-positive bacteria, preferably pneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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0
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83.3%; Pred. No. 7.5e+02;
Live 1; Mismatches 0; Indels
                                                                                                           Holden DW
                                                                                                           Feldman RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus polypeptide SEQ ID NO 4058.
                                                                                                                                                                                                                                Claim 4; Page 26-27; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP27441 standard; Protein; 221 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in the preparation of antibodies
                                                                                                           Shea JE,
17-FEB-2000, 2000GB-0003731.
17-FEB-2000, 2000GB-0003732.
17-FEB-2000, 2000GB-0003733.
02-MAY-2000, 2000GB-0010585.
02-MAY-2000, 2000GB-0010587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-OCT-2001; 2001WO-GB04789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                (MICR-) MICROSCIENCE LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes
                                                                                                                                   WPI; 2001-418285/44.
N-PSDB; AAS06351.
                                                                                                         Clarke EE, Zhou L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 LDAAWL 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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Gaps

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Score 30; DB 23; Length 221; Pred. No. 7.5e+02; 1; Mismatches 0; Indels

90.9%;

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Streptococcus/GBS (Streptococcus adalactise) or group A streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS), comprising one of 5483 sequences (S1), given in the specification. The proteins have entibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71256 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment to r prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactise and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biogical sample. (I) is used to detect Streptococcus in a biogical sample. (I) are used to detection or disease caused by the specific or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection
                                                                                                                                                                                                                                                                                                                                                                                                                                          New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a protein (ABP25413-ABP30895) from group B
                                                                                                                                                     Fraser C;
                                                                                                                                                Grandi G,
                                                                                                                                                Masignani V, Margarit Ros YI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 3561; 4525pp; English.
(CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus proteins.
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N-PSDB; ABN68072.
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OM protein - protein search, using sw model

Run on:

	16	35	37.5	σ	11	US-09-847-946A-29	Sequence 2
GenCore version 5.1.6	17	35 8	87.5	σ	11	US-09-847-946A-32	Sequence 3
Copyright (c) 1993 - 2004 Compugen Ltd.	18		87.5	6	11	US-09-847-946A-35	Sequence 3
	19		87.5	6	11	US-09-847-946A-36	Sequence 3
	20	35 8	37.5	10	11	US-09-847-946A-31	Sequence 3
otein search, using sw model	21	35	37.5	10	11	US-09-847-946A-34	Sequence 3
	22		87.5	11	11	US-09-847-946A-28	Sequence 2
February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds	23		37.5	11	11	US-09-847-946A-132	Sequence 1
(without alignments)	24		87.5	11	11	US-09-847-946A-140	Sequence 1
75.239 Million cell updates/sec	25		87.5	13	11	US-09-847-946A-143	Sequence 1
	56	35 E	37.5	13.	11	US-09-847-946A-144	Sequence 1
US-09-643-260-9	27		87.5	13	11	US-09-847-946A-145	Sequence 1
40	28		87.5	13	11	US-09-847-946A-148	Sequence 1
1 LNWSWL 6	29		87.5	17	11	US-09-847-946A-141	Sequence 1
	30		87.5	11	11	US-09-847-946A-142	Sequence 1
BLOSUM62	. 31		87.5	17	11	US-09-847-946A-146	Sequence 1
Gapop 10.0 , Gapext 0.5	32		87.5	17	11	US-09-847-946A-147	Sequence 1
	33		87.5	18	11	US-09-847-946A-131	Sequence 1
801455 segs, 209382283 residues	34		87.5	18	11	US-09-847-946A-135	Sequence 1
	35		87.5	18	11	US-09-847-946A-136	Sequence 1
hits satisfying chosen parameters: 801455	36		87.5	22	11	US-09-847-946A-133	Sequence 1
	37		87.5	22	11	US-09-847-946A-134	Sequence 1
length: 0	38	35	87.5	22	11	US-09-847-946A-137	Sequence 1
length: 2000000000	39		87.5	22	11	US-09-847-946A-138	Sequence 1
	40		87.5	22	11	US-09-847-946A-139	Sequence 1
3: Minimum Match 0%	41		87.5	28	10	US-09-847-940B-18	Sequence 1
Maximum Match 100%	42		87.5	28	11	US-09-847-946A-18	Sequence 1
Listing first 45 summaries	43		87.5	222	10	US-09-771-161A-141	Sequence 1
	44		87.5	745	D 6	US-09-796-872-2	Sequence 2,
Published Applications AA:*	45	35	37.5	745	10	US-09-844-908-10	Sequence 1
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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database

9: 10:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Scoring table:

Searched:

Perfect score:

Seguence:

Gaps OTHER INFORMATION: Description of Artificial Sequence:NBD mutants APPLICANT: Ghosh, Sankar
TITLE OF INVENTION: ANTI-INFLAWMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-117CP
CURRENT APPLICATION UNDER: US/09/847,940B
CURRENT FILING DATE: 2001-05-02
PRIOR PPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SEGTHARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 6 ö Length 6; IndelB ö 100.0%; Score 40; DB 10; 100.0%; Pred. No. 7e+05; ive 0; Mismatches 0; ; Sequence 9, Application US/09847940B ; Patent No. US20020156000A1 ; GENERAL INFORMATION: APPLICANT: May, Michael J. TYPE: PRT ORGANISM: Artificial Sequence 6; Conservative Query Match Best Local Similarity Matches 6; Conserv US-09-847-940B-9 US-09-847-940B-9 FEATURE:

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Sequence 9, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION: APPLICANT: May, Michael J

US-09-847-940B-9 US-09-887-1946A-9 US-09-882-171-360 US-09-882-171-360 US-09-815-242-10647 US-09-815-242-10647 US-09-815-242-10647 US-09-815-242-10647 US-09-817-946A-2 US-09-847-946B-2 US-09-847-946A-33 US-09-847-946A-30 US-09-847-946A-30 US-09-847-946A-30 US-09-847-946A-30

90.0 90.0 90.0 90.0 90.0 87.5 87.5

SUMMARIES

Query Match Length DB

Result Š

29, Appl 332, Appl 332, Appl 332, Appl 331, Appl 331, Appl 132, Appl 132, Appl 144, Appl 144, Appl 144, Appl 147, Appl 147, Appl 131, Ap ALIGNMENTS LINWSWL 6 1 LNWSWL 6 RESULT 2 US-09-847-946A-9 셤 ð Sequence 36, Appli Sequence 360, App Sequence 2983, App Sequence 1983, Ap Sequence 4997, Appli Sequence 29, Appl 2, Appl , Appli , Appli Appl Sequence 9, Appli Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution. Sequence 82, Sequence 2, Sequence 2, Sequence 3, Sequence Sequence Sequence Description '(gnz 6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
'(gnz 6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
'(gnz 6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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APPLICATION NUMBER: PCT/US98/04493
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PRIOR FILING DATE: 1998-00-06
PRIOR FILING DATE: 1997-03-07
PRIOR PLING DATE: 1997-03-07
PRIOR PLING DATE: 1997-03-07
PRIOR PLING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,626
PRIOR PLING DATE: 1997-03-07
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PRIOR PRICATION NUMBER: 60/047, 596
PRIOR PRICATION NUMBER: 60/047, 596
PRIOR PLING DATE: 1997-05-23
PRIOR PRICATION NUMBER: 60/047, 597
PRIOR PLING DATE: 1997-05-23
PRIOR PRICATION NUMBER: 60/047, 597
PRIOR PLING DATE: 1997-05-23
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PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,314
PRIOR PILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,569
PRIOR PILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,311
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,671
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,674
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APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
TITE.OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFRENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT APPLICATION NUMBER: US/09/847,946A
FRIOR PILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 160
SSCTYMARE: Patentin Ver. 2.0
TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 360, Application US/09803391
Publication No. US20030049618A1
GENERAL INFORMATION:
TITLE OF INVENTION: 186
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
CURRENT PFLING DATE: 2001-03-16
Prior application data removed - consult PALM or file wrapper
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
LENGTH: 117
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Publication No. US200301758581
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 09/809,391
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 09/149,476
PRIOR FILING DATE: 1998-09-08
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Homo sapiens
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US-09-882-171-360
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R APPLICATION NUMBER: 60/056,864
R APPLICATION NUMBER: 60/056,864
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,631
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,845
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,892
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R APPLICATION NUMBER: 60/056,892
R APPLICATION NUMBER: 60/057,761
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/043,669
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,312
RR FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,313
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,672
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,572
RR APPLICATION NUMBER: 60/043,572
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R APPLICATION NUMBER: 60/056,903

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,888

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,879

R APPLICATION NUMBER: 60/056,879

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R APPLICATION NUMBER: 60/056,893

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,630

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,878
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APPLICATION NUMBER: 60/056,877
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,889
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
PPLICATION NUMBER: 60/056,872
PILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,637
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,636
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,910
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,599
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APPLICATION NUMBER: 60/047,588
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,585
FILING DATE: 1997-05-23
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/056,886
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                                                                                                                                   FILING DATE: 1997-04-11
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Gaps Gapa ö Sequence 2983, Application US/10108260A
| Sequence 2983, Application US/20108260A
| Publication No. US20040005560A1
| GENERAL INFORMATION:
| APPLICANT: HELIX RESERVEH INSTITUTE
| TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
| FILE REFERENCE: H1-A0106
| CURRENT APPLICATION NUMBER: US/10/108,260A
| CURRENT FILING DATE: 2002-03-27
| NUMBER OF SEQ ID NOS: 5458
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 2983
| LENGTH: 117 90.0%; Score 36; DB 12; Length 117; 100.0%; Pred. No. 4.5e+02; ive 0; Mismatches 0; Indels 90.0%; Score 36; DB 12; Length 117; 100.0%; Pred. No. 4.5e+02; ive 0; Mismatches 0; Indels R PEFLICATION NUMBER: 60/047,014
R PILING DATE: 1997-06-23
R APPLICATION NUMBER: 60/043,578
R PILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,576
R PILING DATE: 1997-06-23
R APPLICATION NUMBER: 60/047,501
R PILING DATE: 1997-06-23
R APPLICATION NUMBER: 60/043,670
R PILING DATE: 1997-06-23
R APPLICATION NUMBER: 60/056,632
R APPLICATION NUMBER: 60/056,648
R PILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,816
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PRIOR FILING DATE: 1997-05-23
PRIOR PELING DATE: 1997-05-23
PRIOR PELING DATE: 1997-05-23
PRIOR PILING DATE: 1997-05-23
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PRIOR PELING DATE: 1997-05-23
PRIOR PELING DATE: 1997-04-11
PRIOR PELING DATE: 1997-04-11
PRIOR PELING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/05
PRIOR PELING DATE: 1997-06-22
PRIOR PELING DATE: 1997-06-22
PRIOR PELING DATE: 1997-08-22
Query Match
Best Local Similarity 100.
Matches 5; Conservative 5; Conservative TYPE: PRT
CORGANISM: Homo sapiens
US-10-108-260A-2983 Query Match Best Local Similarity 30 LNWSW 34 1 LNWSW 5 RESULT 5 US-10-108-260A-2983 Matches ò

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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
IIILE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: AND SPLICE VARIANTS THEREOF
FILE REFERENCE: DO262 NP
CURRENT APPLICATION NUMBER: U.S. 60/380,336
PRIOR APPLICATION NUMBER: U.S. 60/380,336
PRIOR FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 471
SOFTWARE: PATENTIN VERSION 3.2
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Pred. No. 1.3e+03;
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TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEI
TITLE OF INVENTION: AND SPLICE VARIANTS THEREOF
FILE REFERENCE: D0262 NP
CURRENT APPLICATION NUMBER: US.10/436,715
CURRENT FILING DATE: 2003-05-13
PRIOR APPLICATION NUMBER: US. 60/380,336
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-110-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
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PRIOR PILING DATE: 2001-02-16
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 29, Application US/10436715; Publication No. US20040018976A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT; ORGANISM: Enterococcus faecalis US-09-815-242-4997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.0
Best Local Similarity 100.
Matches 5, Conservative
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Matches 5; Conservative
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ORGANISM: Fugu rubripes
US-10-436-715-29
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APPLICANT: Oblean, Kari L.
APPLICANT: Oblean, Kari L.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, Judith W.
APPLICANT: Trawick, Judith D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
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APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert C.
BRIOR PILING DATE: 2000-05-28
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-10-22
PRIOR PILING DATE: 2000-10-22
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Vamanoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
FILE REFERENCE: ELITRA.011A
FILE REFERENCE: 2001-03-21
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 464;
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                                                                                                                                                                                                                                                                                        Sequence 10647, Application US/09815242
Parcent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4997, Application US/09815242
Patent No. US2002005156941
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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Best Local Similarity 100.
Matches 5; Conservative
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                                               2 NWSWL 6
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Gaps

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APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeas, Mark A
APPLICANT: Findeas, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
ITILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR PILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-847-946A-37

Sequence 37, Application US/08847946A

Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Phillips, Kathryn

APPLICANT: Hannig Gerhard

TITLE OF INVENTION NUMBER: US/09/847,946A

CURRENT APPLICATION NUMBER: 60/201,261

FRIOR APPLICATION NUMBER: 60/201,261

FRIOR PLING DATE: 2000-05-02

FRIOR FILING DATE: 2000-06-05

FRIOR FILING DATE: 2000-08-02

FRIOR FILING DATE: 2000-08-02

FRIOR FILING DATE: 2000-08-02

FRIOR FILING DATE: 2000-08-02

FRIOR FILING DATE: 2000-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTHER INFORMATION: Description of Artificial Sequence:NEMO binding; OTHER INFORMATION: sequence
US-09-847-946A-33
                                                ; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide US-09-847-946A-2
                                                                                                                  Score 35; DB 11; Length 6;
Pred. No. 7e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.5%; Score 35; DB 11; Length 6;
83.3%; Pred. No. 7e+05;
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                                                                                                                       87.5%;
83.3%;
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ORGANISM: Artificial Seguence
  ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                  Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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1 LDWSWL 6
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APPLICANT: Ghosh, Sankar
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
CURRENT FILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REPERBENCE: PPI-119
CURRENT FILING DATE: 2001-05-02
PRIOR PILING DATE: 2001-05-02
PRIOR PILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFFWARE: Patentin Ver. 2.0
SEQ ID NOS: 160
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-2
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APPLICANT: May, Michael J.
APPLICANT: Ghosh, Sankar
FILLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILLE REFERENCE: PPI-117CP
CURRENT APPLICATION NUMBER: US/09/847,940B
CURRENT FILING DATE: 2001-05-02
PRIOR PELICANTON NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
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                                                                                                                                                                                                                 Length 864;
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                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                               Score 36; DB 12;
Pred. No. 2.1e+03;
                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09847940B
Patent No. US20020156000A1
GENERAL INFORMATION:
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 471
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                          Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3'
Matches 5; Conservative
                                                                                                                TYPE: PRT

ORGANISM: Fugu rubripes

US-10-436-715-82
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                                                                    SEQ ID NO 82
LENGTH: 864
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LENGTH: 6
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Sequence 30, Application US/09847946A

Publication No. US2003005499A1

GENERAL INFORMATION:
APPLICANT: May, Michael J

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REFERENCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-06-22

NUMBER: O SEQ ID NOS: 160

SEQ ID NO 30

LENGTH: BATCH OF ID NOS: 160

SEQ ID NO 30

LENGTH: BATCH OF ID NOS: 160

SEQ ID NO 30

LENGTH: BATCH OF ID NOS: 160

SEQ ID NO 30
                                                             OTHER INFORMATION: Description of Artificial Sequence:NEMO binding OTHER INFORMATION: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
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APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark ar
APPLICANT: Findeis, Mark ar
APPLICANT: Findeis, Mark ar
APPLICANT: Findeis, Mark ar
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION UNDRER: US/09/847,946A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.5%; Score 35; DB 11; Length 8; 83.3%; Pred. No. 7e+05; 1: Mismatches 0; Indels
                                                                                                                                                      Score 35; DB 11; Length 7; Pred. No. 7e+05;
                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                   1; Mismatches
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PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 5; Conservative
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; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 8
; CRANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence:NEWO binding
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      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Mutated IKKbeta NE	NBD mutant peptide	Human NEMO binding	Drosophila melanod	Human IKKbeta muta	Human ovarian tumo	Human immune/haema	Macaca mulatta rha	Human novel secret
SUMMARIES	ABB08731	AAM48514	ABU08424	ABB62034	ABB77304	AAY76530		AAB53151	ABG95220
DB	23	23	24	22	23	20	22	21	23
% Query Match Length DB	9	9	Y	295	756	135	130	464	117
& Query Match	40 100.0	100.0	100.0	-1.00.0	100.0	95.0	92.5	92.5	90.0
Score	40	40	40	40	40	38	37	37	36
Result No.	ี	7	Ю	4	2	Q	7	80	σ

Briterococcus faeca	ABB08731 standard; peptide; 6 AA. ABB08731 standard; peptide; 6 AA. ABB08731 standard; peptide; 6 AA. ABB08731 14-JUN-2002 (first entry) Mutated IKKDeta NEWO binding domain peptide SEQ ID NO 9. IKKDeat; IKKAlpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB; kinase activation; leukocyte; inflammation; B-eelectin; osteoclast; autoimmune disease; transplant rejection; osteoporosis; cancer; althementoid arthritis; Crohn's disease; multiple sclerosis; HUV; corticosteroid; immunosuppression; antiinflammatory; immunosuppression; osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antiasthmatic; anti-HIV; human; antiarthritic; osteopathic; antiulcer; mutant; mutein. Homo sapiens. Synthetic. Location/Qualifiers Misc-difference 2 // note= "Wildtype Asp substituted by Asn" WO200183547-A2.
22222222222222222222222222222222222222	ide; 6 AA. ry) nding domain nding domain nding domain ry in Han nocyte; inflai robn's disea uppression; in nocrtopic; in nocrtopic; in nocrtopic; in not in in in in in in in in in in in in in
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	irst entry) NEMO binding domain NEMO binding domain Na, NEMO, NEMO bindia Na, Leansplant reje Ses, viral; infections, viral; infections, viral; infections obstatic, nootropic, votatic, viracide, antibacterial; antilo Location/Qualifiers 2 // note= "Wildtype As
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N N N N N N N N N N N N N N N N N N N	ABB08731 8t. ABB08731; 14-JUN-2002 Mutated IKK Kinase acti: autoimmune; Alzhaimer; Alzhaimer; autoimmune octicoster corticoster corticoster autiarterio antiarterio antiarterio antiarterio Alzhaimer; Key Key Misc-differ WO200183547
01111111111111111111111111111111111111	RESULT ABI NO SECONDARY AND SE

Antiinflammatory; antiasthmatic; cytostatic;

us-09-643-260-9.rag

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The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB08725-AB808742) comprising at least one NEWO binding domain (ABB77313). The compound has acts through selective inhibition of the compound has acts through selective inhibition of the compound in inhibition of IKCDeta kinase activation and subsequent decreased phosphorylation of IKCDeta kinase activation of NEWO interaction results in inhibition of IKCDeta kinase activation and subsequent decreased phosphorylation of IKCDeta kinase activation and creation treated to rindirectly) by blocking the interaction results in inhibition of IKCDeta kinase activation of NEWO interaction. The compound is useful in treating NR-KB mediated care differentiation. The compound is useful in treating observation to conditions, where the condition is an inflammatory disorder, an autoimmune disease, tatansplant rejection, osteoporosis, cancer, alto antoimmune disease, tatansplant rejection, osteoporosis, cancer, alto anaphylaxis, cutaneosclerosis, a viral infection or ataxia calmaged darbritis, outsneovel inflammatory disorder is asthma, alleagies, utilicaria, anaphylaxis, cutaneous inflammatory disease, vasculitis and bursitis. The inflammatory disease, vasculitis and chronic obstructive pulmonary disease, vasculitis and spondylatrhitis, psoriatis arthritis, psoriatis, psoriatic arthritis, psoriatis, crepobluinamia or multiple sclerosis. For chronic viral infections caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral colseases include HIV and influenza. The compound may also be useful for treating anaphylaxis, drug and food sensitivity, contact dermatitis, munosuppression in which orticosteroids are used, including inmunor aging. The compound may be used to replace corticosteroids in munical munical personal continuation of including domain of IKKDeta.

The compound may be administered alone or in combination is that of a mutated NEWO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting cell with an anti-inflammatory compound comprising at least one NEMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 23; Page 44; 82pp; English.
                                                                                          02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.
02-MAY-2001; 2001WO-US40654
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-179350/23
                                                                                                                                                                                                                                      (UYYA ) UNIV YALE.
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binding domain
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ABU08424 standard; peptide; 6 AA.
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                              arthritis
                                                          Sequence
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ID ABU(
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                             Gaps
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100.0%; Score 40; DB 23; Length 6; 100.0%; Pred. No. 9.3e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                      AAM48514 standard; Peptide; 6 AA
                                                                                                                                                                                                                                      NBD mutant peptide SEQ ID NO 9.
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                          6; Conservative
Query Match
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Matches 6; Conserv
                                                       1 LINWSWL 6
                                                                                1 LNWSWL 6
                                                                                                                                                                                                            20-MAR-2002
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RESULT 2 AAM48514

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The invention relates to an antiinflammatory compound (especially AAM48629-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48620). Comprising a membrane translocation domain (AAM48620-AAM48620). The AAM48651 which comprises from 6-15 amino acid residues, fused to a NEWO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NEKappaB crimate by blocking interaction of IkappaB kinase beta (IKKObeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, ung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, cannulatione and siseases such as lupus, polymyalgia, scleroderma, at telanulationed subsequent decreased processis; viral infections; and ataxia telanulations are also useful for treating compounds are also useful for treating compounds.
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                                antirheumaric; antiarthritis; osteopathis; antibacterial; virucide; immunosuppressive; dermacological; neuroprotective; antiarherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NRkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PRAE-) PRAECIS PHARM INC.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                08-NOV-2001.
                                                                                                                                                                                                                               Synthetic.
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ABU08424;

Synthetic

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
                                                                                                                                      developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 12894; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     discloses genomic DNA sequences (ABL16176-ABL30511), ey sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 12894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 40; DB 22;
100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myers EW;
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                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                               (first entry)
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                                                                                                                                                                                                                 Drosophila melanogaster.
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N-PSDB; ABL06137.
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                                                                                                                                                                    pharmaceutical
                                               26-MAR-2002
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                                                                                                                                           Drosophila;
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ABB62034;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to antiinflammatory compounds comprising NEMO binding domain (NBD) peptides. The NEWO binding domains are found on IkappaB kinase-beta (IKMCALs) and IkappaB kinase-beta (IKMCALs) and IkappaB kinase-alpha (IKMCALs) and IkappaB kinase-alpha (IKMCALs) are useful for modulating nuclear factor-kappaB (NF kappaB) induction in a cell, where the compounds are capable of blocking the interaction in a cell, where the compounds are sapable of blocking the interaction come in a si IKMCALsha or IKKObeta, and NEMO. The antiinflammatory compound further comprises at least one membrane translocation domain. The compounds are useful for treating inflammatory disorders, autoimmune diseases, osteoporosis, cancer, althamatory disorders, autoimmune diseases, osteoporosis, cancer, telangiectesia, and for transplantation detection. The compounds of the invention block NF-kappaB induction by IKK but do not inhibit the basal activity of NF-kappaB. ABU08412 represent human
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                                                                                                                                                                                   IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB; muclear factor-kappaB induction; inflammatory disorder; autoimmune disease; osteoporosis; cancer; Alzheimer"s disease; exteoporosis; cancer; Alzheimer"s disease; atherosclerosis; viral infection; Ataxia telangiectasia; transplantation detection; immunosuppressive; osteopathic; cytostatic; nooiropic; neuroprotective; antiatherosclerotic; virucide; vasotropic; antirheumatic; antiatheritic; mutant; mutein.
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                                                                                                                                                               antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel antiinflammatory peptide compounds comprising NEMO binding domain, useful for modulating NF-kappaB induction in a cell and for treating NF-kappaB-mediated inflammation disorders e.g., asthma,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 40; DB 24; 100.0%; Pred. No. 9.3e+05;
                                                                                                             Human NEMO binding site (NBD) mutant peptide #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 22; Page 17; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-2001; 2001US-0847940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ghosh S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAY M J.
GHOSH S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2002156000-A1.
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                                                                12-JUN-2003
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May MJ,

MAYM/) (/SOH5)

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Gape

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ABB62034 standard; Protein; 295 AA.

ABB62034 ID ABB6

a

Sequence

Length 295; 0; Indels

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Query Match
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DB 23; Length 756;

100.0%; Score 40;

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The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound C Comprises Comprising at least one NRMO binding domain (ABB0877313). The compound has acts through selective inhibition of Cytokine-mediated NF-kB activation by blocking the interaction of NEWO with IKKbeta at the NEWO binding domain. Blockage of IKKbeta-NEWO interaction results in inhibition of IkkappaB. The compound may also act (directly or indirectly) by blocking the recruitment of leukocytes into sites of acute and chronic inflammation, by down-regulating the expression of B-selectin on leukocytes or by blocking osteoclast of expression of B-selectin on leukocytes or by blocking osteoclast differentiation. The compound is useful in treating NF-kB mediated conditions, where the condition is an inflammatory disorder, an autoimmune disease, transplant rejection, osteoporosis, cancer, altachimer's disease, atherosclerosis, a viral infection or ataxia curticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis, curticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis, cremanic obstructive pulmonary disease, vasculitis and bursitis. The inflammatory disorder is athmitis, inflammatory conventivities, psoriatic arthritis, lupus and bursitis. Also for Crohn's disease, ulcerative colitis, cremay polymyapida, scleroderma, Wegner's granulomatosis, temporal arteritis, psoriatic arthritis, lupus and spondylarthritis, dand influenza. The compound may also be dermatitis, cremay polymyapida, cremayeria, drug and food sensitivity, contact dermatitis, cused by Epstein-barr, cytomegalovirus or herpes simplex, opter viral diseases include HIV and influenza. The compound may also be useful for treating anaphylaxis, drug and food sensitivity, contact dermatitis, may any any any any and any any and any any and any any and any any and any any any and any any and any any any and any any any and any any any and any any any any and any any any and any any any any and any any any an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunosuppression in transplants and cancer therapy. Also for identifying antiinflammatory compounds and for diagnosis of an inflammatory disorder. The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of an IKKbeta mutant, useful in examples of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting a cell with an anti-inflammatory compound comprising at least one NEMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The present sequence is not given in the specification but is derived from GenBank Accession No. 014920 (ABB77294).
antiarteriosclerotic; virucide; antiasthmatic; antiallergic; dermatological; antibacterial; antipsoriatic; antirheumatic; antiarthritic; osteopathic; antiulcer; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Wildtype Asp substituted by Asn"
                                                                                                                                                                                                                                                                                                                                Location/Qualifiers Misc-difference 738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-2000; 2000US-201261P
22-AUG-2000; 2000US-0643260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell with an an
binding domain
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                                                                                                                                                                                                            sapiens.
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                                                                                                                                                                                                                                                            Synthetic.
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tissue (and some also in testis and breast cancer tissue). The products tissue (and some also in testis and breast cancer tissue). The products of the invention can be used for gene therapy. (A) are used (i) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of ovarian cancer. (ii) directly for treating this form of cancer.

Cincluding expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling ESTS (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTS from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. AAY5605-Y76638 represent protein fragments encoded by the human ovarian tumor CDNA library derived EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid sequences expressed in ovarian, and some other, cancer tissues, and derived polypeptides, for treatment of ovarian cancer and identification of therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel nucleic acid (cDNA) sequences (A) which
                     Gaps
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                   Indels
                                                                                                                                                                                                                                                                               Human ovarian tumor EST fragment encoded protein 26.
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   100.0%; Pred. No. 3.8e+02; ive 0; Mismatches 0;
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                                                                                                                                                                           AAY76530 standard; Protein; 135 AA.
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Guery Match
Best Local Similarity 83.33,
Best Access Similarity 83.33,
                                                                                                                                                                                                                                             10-APR-2000 (first entry)
                     Conservative
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                                                                                                                                                                                                                                                                                                                                   gene therapy; treatment
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                                                                                   737 LNWSWL 742
Best Local Similarity
Matches 6; Conserv
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                                                     1 LNWSWL
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                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                           AAY76530;
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                                                                                                                                       RESULT 6
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2000US-0236327.
2000US-0236367.
2000US-0236368.
2000US-0236369.
2000US-0236370.
2000US-0237037.
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2000US-0246526
2000US-0246527
2000US-0246609
2000US-0246609
2000US-0246611
2000US-0246611
2000US-0246613
2000US-0249207
2000US-0249207
2000US-0249210
2000US-0249212
2000US-0249213
2000US-0249213
2000US-0249214
2000US-0249214
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2000US-0249216
2000US-0249216
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                          02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
13-0CT-2000;
13-0CT-2000;
20-0CT-2000;
  Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                      Human immune/haematopoietic antigen SEQ ID NO:12732.
                         AAM85139 standard; Protein; 130 AA
                                                                                                                                                                                                                                                  17-JAN-2001; 2001WO-US01354
                                                                             (first entry)
                                                                                                                                                                                              WO200157182-A2
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17-MAR-2000;

18-APR-2000;

19-MAY-2000;

28-JUN-2000;

20-JUN-2000;

11-JUL-2000;

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                                                                                                                                                                       Homo sapiens
                                                                            07-NOV-2001
                                                                                                                                                                                                                        09-AUG-2001
                                                   AAM85139;
RESULT 7
AAM85139
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The present invention describes a novel result macaque realizable tradition describes a novel realizable macada mulatta rhadinovirus 17577 (RRV). AAC64754 represents the called macada mulatta rhadinovirus 17577 (RRV). AAC64754 represents the encoded by the genome sequence. The present invention also specifically claims the individual open reading frame (ORF) nucleotide sequences from the genome which encode the individual proteins, but these sequences from the genome which encode the individual proteins, but these sequences are not given. A non-human animal infected with RRV can be used for testing the fficacy of drug in the treatment of condition associated with infection with RRV such as Kaposi's sarcoma, lymphopproliferative disorders, B-cell hyperplasia, lymphadenopathy, splenomegaly, hyperplasia, lymphadenopathy, splenomegaly, hypergammaglobinulinaemia or autcoimmune haemolytic anaemia, by administering the drug to a immuno-compromised non-human primate preferably Rhesus macaque monkey obtained by as a result of infection by Simian Immunodeficiency Virus (SIV). RRV is useful for producing non-human primate madel for testing potential treatments for conditions associated with RRV infection. It is also useful for testing the sesociated with RRV infection by administering the vaccine to the subject capable of infection with RRV incculating the subject with RRV and observing the effect of vaccine. AAC64755 to AAC64755 and AAB53205 to AAB53213 represent sequence used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; liver neoplasm cardiovascular disorder; cardiac arrest; skin aging; cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn; nervous system disorders; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; tissue regeneration; epithelial cell proliferation; organ transplantation; food additive; preservative; nutritional.
                                                                                                                                                                                                                                                                                                                                                                                                        New rhesus rhadino virus for producing non-human primate model useful for testing potential treatments and efficacy of the candidate vaccine for conditions associated with RRV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention describes a novel rhesus macaque rhadinovirus
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Pred. No. 6.3e+02;
L; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 128-129; 141pp; English.
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                                                                                                                                                                                                                                                                                                     Searles RP;
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                                                                                                                                                                                                                                               (UYOR-) UNIV OREGON HEALTH SCI.
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83.3%;
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98US-0109409.
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                                                                                                                                                                                                                                                                                                     Axthelm MK,
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Best Local Similarity
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WO200028040-A2
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20-NOV-1998;
                                                                                                           05-NOV-1999;
                                                     18-MAY-2000.
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amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
polynucleotides may be used to produce the secreted (I), by inserting
polynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic antigen genomic
sequences from the present invention. AAK64942 to AAK84950 and AAM82169
represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; SEQ ID NO 12732; 3071pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 22; Length 1.2. Pred. No. 1.7e+02;
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2000US-0256719.
2000US-0251479.
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                                                                                                     08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251989.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for preventing, metastasis -
                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-483426/52.
N-PSDB; AAKS7920.
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Best Local Similarity
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                            05-DEC-2000;
05-DEC-2000;
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Sequence

Matches

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Gaps

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28-FEB-2001

AAB53151;

RESULT 8 AAB5315

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(HUMA-) HUMAN GENOME SCI INC
  970S - 038621P

970S - 040161P

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970S - 040331P

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970S - 040331P

970S - 040331P

970S - 0403568P

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97US-055724P.
97US-056630P.
97US-056631P.
                                                                      98US-0149476
           Homo sapiens.
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22-AUG-1997;
22-AUG-1997;
                              US6420526-B1
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1-APR-1997;
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9703-05663699703-056642P9703-056642P9703-056642P9703-056845P9703-056847P9703-056874P9703-056874P9703-056874P9703-056874P9703-05681P9703-05681P9703-05681P9703-05681P9703-05681P9703-05681P9703-05681P9703-05681P9703-05681P9703-05681P9703-05681P9703-05681P9703-05681P9703-05681P9703-05681P9703-05681P-97US-056894P. 97US-056903P. 97US-056908P. 97US-056909P. 97US-056910P. 97US-056911P. 97US-057761P. 97US-057650P. 97US-057669P. 97US-058785P. 97US-061060P. 98WO-US04493 22-AUG-1997; 22-AUG-1997; 22-AUG-1997; 22-AUG-1997; 22-AUG-1997; 22-AUG-1997; 22-AUG-1997; 22-AUG-1997; 22-AUG-1997; 22-AUG-1997; 22-AUG-1997; 22-AUG-1997; 36-MAR-1998; 22-AUG-1997 22-AUG-1997 22-AUG-1997 22-AUG-1997 22-AUG-1997 05-SEP-1997

Bednarik DR; Ferrie AM; Carter KC, Bedi Greene JM, Feri R, Brewer LA; Kyaw H; Ruben SM, Rosen CA, Fischer CL, Soppet DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Ouan R, Hu J, Florence KA, Olsen HS, Ebner I Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z,

WPI; 2002-634796/68. N-PSDB; ABS73538.

New isolated human secreted protein for diagnosing, preventing, treating or ameliorating medical conditions and used as a food additive or preservative

Example 1; SEQ ID No 360; 129pp; English.

The invention relates to an isolated protein that is one of 186 human secreted proteins, given in the specification, encoded by one of 180 colors secreted proteins, given in the specification, encoded by one of in a pharmaceutical composition under treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, degs, chickens or sheep. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders and sogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypoptides can also be used to aid wound the maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypoptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents one of the novel human

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WO200170955-A2.
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                                                                                                                                                                                                                                        AAU33501;
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                                                             Sequence
                                                                                                         Matches
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                                                                                                         Gaps
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           Note: This sequence did not form part of the printed specification, but was obtained in electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID=6420526B1.
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                                                                                  Length 117;
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                                                                                                                                                                                                                                                                                     Enterococcus faecalis cellular proliferation protein #341.
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                                                                                                                                                                                                                                                                                                           Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                  DB 23; L
2.2e+02;
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                                                                               90.0%; Score 36; DB 100.0%; Pred. No. 2.2 ive 0; Mismatches
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 proteins of the invention.
                                                                                                                                                                                                                AAU35054 standard; Protein; 464 AA.
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2000US-253625P.
2000US-257931P.
2001US-269308P.
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                                                                              Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                               Enterococcus faecalis
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                                                          117 AA;
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26-MAY-2000;
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27-NOV-2000;
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16-FEB-2001;
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Yamamoto RT,
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                                                            Sequence
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella promoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to soreen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                         Length 464;
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                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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. 8.8e+02;
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                                                                                                                                                                                                                                                                                   Mismatches.
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                                                                                            ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                      Score 36;
Pred. No.
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Xu HH;
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100.0%; Pre
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26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-257931P.
16-FEB-2001; 2001US-269308P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus faecalis
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N-PSDB; AAS51360.
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Best Local Similarity
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                                                                                                                                                            464 AA;
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The present invention describes a polynuclectide (I) comprising a sequence of a Bifidobacterium genome selected from the nuclectide sequence given in ABQ81842 and ABQ81843, or a sequence given in ABQ81842 and ABQ81843, or a sequence sibribiting at least 90% identity or which hybridises with the sequences given in ABQ81843. Also described is a polynuclectide (II) encoding a fusion protein, comprising a sequence selected from 1097 sequences given in ABB65258 to ABB66354 ligated in frame to a polynuclectide adventing a heterologous polypeptide. (I) has antidiarrheic and antidiarchial activities, and can be used as an inhibitor of Salmonella. (I) (which is a probe) is useful for the detection and/or identification of Bifidobacterium longum in a blological sample. A carrier containing the lactic acid bacterium Bifidobacterium longum NCC2705 (CNCM 1-2618) can be used for preventing and/or treating diarrhoes brought about by pathogenic bacteria and/or rotavirus. The carrier is a food composition selected from milk, yogurt, curd, cheese, fermented milks, milk based fermented products, infant formula, per food or a pharmaceutical composition selected from tablets, liquid bacterial suspensions, dried oral cappensent, wet oral supplement, dry tube feeding or wet tube feeding. (I) is useful in DNA arrays or chips to carry out analysis of the expression of the Bifidobacterium gene. ABQ81844 to ABQ81850 represent Bifidobacterium related nucleotide sequences given in the Sequence
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                                                                                                                                                                                                                                                                                                                                                Gaps
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                 90.0%; Score 36; DB 22; Length 467;
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                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.00
Chas 5; Conservative
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                                                                                                                                                                                      467 AA;
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                             N.B. The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB; kinase activation; leukocyte; inflammation; E-selectin; osteoclast; autoimmune disease; transplant rejection; osteoporosis; cancer; Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis; rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; antiinflammatory; immunosuppressive; osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antiasthmatic; antiallergic; dermatological; antibacterial; antibsoriatic; antirheumatic; antirheumatic; antiarthritic; osteopathic; antiulcer.
not mentioned further within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting cell with an anti-inflammatory compound comprising at least one NEMO
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                                                                                                                                                    Score 36; DB 23; Length 767;
Pred. No. 1.5e+03;
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                                                                                                                                                              100.0%; Pred. ....
from the present invention but
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                                                                                                                                                                                                                                                                                                                                                                 ABB08725 standard; peptide; 6 AA.
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22-AUG-2000; 2000US-0643260.
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                                                                                                                                                                                          5; Conservative
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                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                               569 LNWSW 573
                                                                                                               767 AA;
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                                                                                                                                                                                                                            1 LNWSW 5
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                     specification.
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differentiation. The compound is useful in treating NF-kB mediated conditions, where the condition is an inflammatory disorder, an autoimmune disease, transplant rejection, osteoporosis, cancer, alizheimer's disease, atherosclerosis, a viral infection or ataxia talaries. Alizheimer's disease, atherosclerosis, a viral infection or ataxia telangiectasia. The inflammatory disorder is asthma, allergies, urticaria, anaphylaxis, osteoarthritis, psoriatic arthritis, inplammatory bowel disease, chronic obstructive pulmonary disease, vacculitis and bursitis. The inflammatory disorder may also be dermatitis, eczema, spondylarthritis, psoriatic arthritis, lupus and spondylarthritis. Also for Crohy Granulomatosis, temporal arteritis, polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis, cayoglobulinaemia or multiple sclerosis. For chronic viral infections caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral diseases include HIV and influenced. He used to replace corticosteroids in any application in which corticosteroids are used, including including liminamatory compounds and for diagnosis of an inflammatory disorder. The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of the NEWO binding domain of IKKDeta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.5%; Score 35; DB 23; Length 6; 83.3%; Pred. No. 9.3e+05;
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1; Mismatches Best Local Similarity 83.3 Matches 5; Conservative 1 LNWSWL 6 Query Match ઠે

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Gaps 0

0; Indels

Anti-inflammatory peptide SEQ ID NO 33. AAM48530 standard; Peptide; 6 AA. 20-MAR-2002 (first entry) RESULT 14 셤

Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic, antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoprosis; Alzheimer's disease, atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.

Synthetic.

WO200183554-A2.

08-NOV-2001

02-MAY-2001; 2001WO-US14346.

02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.

(PRAE-) PRAECIS PHARM INC. (UYYA) UNIV YALE.

May MJ, Ghosh S, Findeis MA, Phillips K;

WPI; 2002-121889/16

(AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antiphensatic, antiathmatory compounds have antiasthmatic, cytostatic, antiphensatic, antiathmitic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, compounds act as selective inhibitors of cytokine-mediated NFkappaB compounds act as selective inhibitors of cytokine-mediated NFkappaB compounds act as selective inhibitors of cytokine-mediated NFkappaB compounds act as selective inhibitors of cytokine-mediated NFkappaB compounds are useful for treating inhibition of IKappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lumg inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, osteoarthritis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; transplant rejection; osteoporosis; transplant rejections; and ataxia pro-inflammatory responses such as allergies, urticaria, anaphylaxis, dinger, election; osteoporosis; dinger food sensitivity, eczema, dermatitis, sunburn, aging and Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation, AAM48620-AAM48645), comprising a membrane translocation domain (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15 relates to an antiinflammatory compound (especially Claim 6; Page 61; 88pp; English. psoriasis arthritis

Score 35; DB 23; Length 6; Pred. No. 9.3e+05; 1; Mismatches 0; Indels 0; 87.5%; 83.3%; 5; Conservative Local Similarity 6 AA; Sequence Query Match Matches

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Gaps

1 LINWSWL 셤

RESULT 15

AAM48655 standard; Peptide; 6 AA. NBD mutant peptide SEQ ID NO 2. 20-MAR-2002 (first entry) AAM48655; AAM48655

antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NekappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis. Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;

WO200183554-A2.

08-NOV-2001.

02-MAY-2001; 2001WO-US14346.

02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.

(PRAE-) PRAECIS PHARM INC.

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The invention relates to an antiinflammatory compound (especially AAM48629-AAM48645), comprising a membrane translocation domain (AAM48629-AAM48651) which comprises from 6-15 and the Second of the Second of the Second of the Second of the Second of the Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Second of Sec
                                                                                                                                                                                                       Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                    Ghosh S, Findeis MA, Phillips K;
                                                                                                                                                                                                                                                                                                                                                                                        Example 6; Page 47; 88pp; English.
                                                                                                                                      WPI; 2002-121889/16.
(UYYA ) UNIV YALE.
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87.5%; Score 35; DB 23; Length 6; 83.3%; Pred. No. 9.3e+05; ive 1; Mismatches 0; Indels Search completed: February 18, 2004, 14:26:21 Job time : 23.7763 secs 5; Conservative |:|||| 1 LDWSWL 6 1 LNWSWL 6 Matches g

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	ion US/098477 5000A1 aael J. Sankar ANTI-INPLAM 117CP NUMBER: US/05-07 2010-05-07 2000-08-22 2000-08-22 2000-08-22 31 27 Ver. 2.0 Description Description 100.0%; y 100.0%; y 100.0%; rvative 0
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GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Findels, Mark A
APPLICANT: Findels, Mark A
APPLICANT: Findels, Mark A
APPLICANT: Findels, Mark A
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPL-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR PILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 100
SOFTHAME: PATENTIN UNIO: 2.0
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US-09-847-946A-33
                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide US-09-847-946A-2
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TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
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Pred. No. 7e+05;
1; Mismatches 0; Indels
                                     CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-847-946A-33; Sequence 33, Application US/09847946A; Publication No. US20030054999A1
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5, Conservative
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                 APPLICANT: Finder, Mark A
APPLICANT: Finder, Mark A
APPLICANT: Hannig, Kathryn
APPLICANT: Hannig, Gerhard
APPLICANT: Hannig, Gerhard
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: 108/109/847,946A
CURRENT APPLICATION NUMBER: 60/201,261
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
NUMBER OF SEQ ID NOS: 160
SCOTT NUMBER: Patentin Ver. 2.0
SEQ ID NOS: 160
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SEQ ID NOS: 160
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Patent No. US20020156000A1
GENERAL INFORMATION:
APPLICANT: May, Michael J.
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-117CP
CURRENT APPLICATION NUMBER: US/09/847,940B
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION WUMBER: 09/643,260
PRIOR PILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTHARE: Patentin Ver. 2.0
SEQ ID NO S
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US-09-847-940B-2
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ORGANISM: Artificial Sequence
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APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 6; Conservative
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Matches 5; Conservative
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US-09-847-940B-2
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US-09-847-946A-32
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APPLICANT: May, Michael J
APPLICANT: GRosh, Sankar
APPLICANT: Findels, Markar
APPLICANT: Findels, Mathry
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
TILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR PLILNG DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR PLILNG DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PREENT IN VET: 2.00
SEG ID NO 30
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence:NEMO binding OTHER INFORMATION: sequence
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                  APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-06-22
NUMBER OF SED ID NOS: 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 30, Application US/09847946A Publication No. US20030054999A1
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ORGANISM: Artificial Sequence
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Phillips, Kathryn
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Best Local Similarity 83.3
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Matches 5, Conservative
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3 LDWSWL 8
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Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

FILE REFRENCE: PLI119

CURRENT APPLICATION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REFRENCE: PLI10

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2001-05-02

PRIOR FILING DATE: 2000-06-02

PRIOR FILING DATE: 2000-06-22

PRIOR FILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 160

SEQ ID NOS: 160

SEQ ID NO 29
APPLICANT: Ghosh, Sankar
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathard
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAWMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR PLILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PALENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:NEMO binding OTHER INFORMATION: sequence US-09-847-946A-38
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.3
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Query Match
Best Local Similarity
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                                                                                                                      GENERAL INFORMATION:
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                                                        JS-09-847-946A-36
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                                                                  APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
ITILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
ITILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/641, 261
PRIOR APPLICATION NUMBER: 60/201, 261
PRIOR PILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 160
SEQ ID NOS: 160
SEQ ID NO 32
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Ghosh, Sankar
APPLICANT: Findeas, Mark A
APPLICANT: Pindeas, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
ITLE OF INVENTION: ANTT-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REPERBYCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
FRIOR APPLICATION NUMBER: 00/201,261
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence:NEMO binding OTHER INFORMATION: sequence US-09-847-946A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence:NEMO binding OTHER INFORMATION: sequence
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Pred. No. 7e+05;
1; Mismatches 0; Indels
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Sequence 32, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION:
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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LDWSWL 8
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LENGTH: 9
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                                                                                         APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PFI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR PELING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR PILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:NEMO binding OTHER INFORMATION: sequence
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Publication No. US20030054999A1
GENERAL INFORMITON:
APPLICANT: May, Michael J
APPLICANT: Hoosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REPERENCE: PPI-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 11; Length 9;
Pred. No. 7e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-05-02
PRIOR PEPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PATENTIN OF: 2.0
Sequence 36, Application US/09847946A Publication No. US20030054999A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.3%;
83.3%;
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Best Local Similarity 83.3%;
Matches 5; Conservative 1
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ORGANISM: Artificial Sequence
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                                                                      APPLICANT: May, Michael J
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                                                                                                                                     KESULT 14
US-09-847-946A-34
IS-09-847-946A-34

SEQUENCE 34, Application US/09847946A

PUDLICATION NO. US200300549991

GENERAL INFORMATION:
APPLICANT: Machael J
APPLICANT: Finders, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, Mannig, M
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APPLICANT: Ghosh, Sankar
APPLICANT: Ghosh, Sankar
APPLICANT: Ghosh, Sankar
APPLICANT: Pindeis, Mark A
APPLICANT: Pindeis, Mark A
APPLICANT: Hannig, Gerhard
ITIER OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR PILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PARENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
US-09-847-946A-34
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-28
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Pred. No. 68;
1; Mismatches 0; Indels
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. Sequence 28, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.3%;
Matches 5; Conservative
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LENGTH: 11
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Run on:	February 18,	2004,	13:37:19 { 4	; Search t without al 1.814 Mill	February 18, 2004, 13:37:19; Search time 22.7763 Seconds (without alignments) 41.814 Million cell updates/sec	
Title: Perfect score: Sequence:	US-09-643-260-8 39 1 LEWSWL 6	8 - 0				
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5	Gapext	0.5			
Searched:	1107863 seqs, 158726573 residues	, 15872	6573 resi	dues		
Total number of hits satisfying chosen parameters:	hits satisfy	ing cho	ısen param	eters:	1107863	
Minimum DB seq length: 0 Maximum DB seq length: 200000000	length: 0 length: 20000	00000				
Post-processing: Minimum Match 0% Maximum Match 10 Listing first 45	Minimum Match 0% Maximum Match 100% Listing first 45 st	ch 0% ch 100% Bt 45 8	Match 0% Match 100% first 45 summaries	·		
Database :	A Geneseq 19Jun03:* 1: /SIDSI/gcgdata/g	9Jun03: cgdata/	* geneseq/g	eneseqp-em	A_Geneseq_19Jun03:* 1: _/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:* 2: /circl/gradata/geneseq/geneseqp-embl/AA1980.DAT:*	

| SIDSI/gcgdata/geneseq_geneseqp_embl/AA1981_DAT:
| SIDSI/gcgdata/geneseqp_embl/AA1981_DAT:
| SIDSI/gcgdata/geneseqp_embl/AA1981_DAT:
| SIDSI/gcgdata/geneseqp_embl/AA1981_DAT:
| SIDSI/gcgdata/geneseqp_embl/AA1984_DAT:
| SIDSI/gcgdata/geneseqp_embl/AA1986_DAT:
| SIDSI/gcgdata/geneseqp_embl/AA1986_DAT:
| SIDSI/gcgdata/geneseqp_embl/AA1980_DAT:
| SIDSI/gcgdata/geneseqp_embl/AA1980_DAT:
| SIDSI/gcgdata/geneseqp_embl/AA1980_DAT:
| SIDSI/gcgdata/geneseqp_embl/AA1980_DAT:
| SIDSI/gcgdata/geneseqp_embl/AA1990_DAT:
| SIDSI/gcgdata/geneseqp_embl/AA2000_DAT:
| SIDSI/gcgdata/geneseqfygeneseqp_embl/AA2000_DAT: 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				
No.	Score	Match	Match Length DB ID	DB	ID	Description
-	39	100.0	9	23	ABB08730	Mutated IKKbeta NE
7	39	100.0	9	23	AAM48513	NBD mutant peptide
m	39	100.0	9	24	ABU08423	Human NEMO binding
4	39	100 0	756	23		Human IKKbeta muta
S	36	92.3	9	23	ABB08725	IKKbeta NEMO bindi
9	36	92.3	9	23	AAM48530	Anti-inflammatory
7	36	92.3	9	23	AAM48655	NBD mutant peptide
80	36	92.3	v	24	ABU08418	Human NEMO Dinding
6	36	92.3	7	23	AAM48534	Anti-inflammatory

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08-NOV-2001

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ABB08730 standard; peptide; 6 AA

ABB08730

ABB08730;

kinase activation; leukocyte; inflammation; E-selectin; Osteoclast; autoimmune disease; transplant rejection; osteoporosis; cancer; Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis; rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; antiinflammatory; immunosuppression; osteopothic; cytostatic; noctropic; neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antiashmatic; antiallergic; dermatological; antibacterial; antibsoriatic; antirheumatic; antiallergic; antiathritic; osteopathic; antiulcer; mutant; mutein. IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB; /note= "Wildtype Asp substituted by Glu" Mutated IXKbeta NEMO binding domain peptide SEQ ID NO 8. Location/Qualifiers 2 (first entry) Key Misc-difference WO200183547-A2 Homo sapiens 14-JUN-2002 Synthetic. 

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Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
ABU08423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                   The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB77313). The compound has acts through selective inhibition of (ABB77313). The compound has acts through selective inhibition of NEWO with Interaction results in inhibition of IXCDeta kinase activation and subsequent decreased phosphorylation of IXCDeta kinase activation and compound is useful in treating NP-KB mediated attifectly) or indirectly) by blocking the recruitment of leukocytes or by blocking osceoclast differentiation. The compound is useful in treating NP-KB mediated conditions, where the condition is an inflammatory disorder, an autoimmune disease, transplant rejection osteoporosis, cancer, altaheimer's disease, transplant rejection, osteoporosis, cancer, altaheimer's disease, transplant rejection, osteoporosis, cancer, anaphylaxis, cutaneous inflammatory disorder, an autoimmune disease, transplant proprieting pooriatic arthritis, inflammatory conditions and inflammatory disorder and activities, understing and burstits. The inflammatory disorder may also be dermatitie, obscrawi, pooriasis, osteoarthritis, psoriatic arthritis, lugus and spondylatthritis psoriatic arthritis, lugus and spondylatthritis psoriatic arthritis, lugus and spondylatthritis psoriatic arthritis, lugus and spondylatthritis also for Cromb edisease, ulcerative colitis, polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis, caused by Epstein-barr, cytomegalovirus or herpes simpled HIV and influenza. The compound may be useful for treating anaphylaxis, drug and food sensitivity, contact dermatitis mumunosuppression in transplants and care therespy. Also for identifying mumunosuppression in transplants ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                   Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting a cell with an anti-inflammatory compound comprising at least one NEMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 100.0%; Score 39; DB 23; Length 6; Similarity 100.0%; Pred. No. 9.3e+05; 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                              Claim 23; Page 44; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM48513 standard; Peptide; 6 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NBD mutant peptide SEQ ID NO 8.
02-MAY-2001; 2001WO-US40654.
                            02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAR-2002 (first entry)
                                                                                                                                      WPI; 2002-179350/23
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Best Local Similarity
Matches 6; Conserv
                                                                         (UYYA ) UNIV YALE.
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                                                                                                         May MJ, Ghosh S;
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                                                                                                                                                                                                   cell with an ar
binding domain
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antirheumatic; antiarthritic; osteópathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerolic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NRkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMM48628-AMM48645), comprising a membrane translocation domain.

(AAM48620-AMM48645), comprising a membrane translocation domain.

(AAM48620-AMM48645) or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEWO binding sequence.

(AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antiinflammatory compounds have antiasthmatic, antibsoriatic, antiinflammatory of compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEWO binding domain that results in inhibition of IKKbeta at curvation and subsequent decreased phosphorylation of IKKbeta kinase compounds are useful for treating inflammatory disorders, e.g. asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an antiinflammatory compound (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 39; DB 23; Length 6; 100.0%; Pred. No. 9.3e+05; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phillips
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 6; Page 47; 88pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Findeis MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAY-2001; 2001WO-US14346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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Human IKKbeta mutant D738E.

(first entry)

14-JUN-2002

ABB77305;

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The present invention relates to antiinflammatory compounds comprising NEMO binding domain (NBD) peptides. The NEWO binding domains are common on IkappaB kinase-beta (IKACALa) and IkappaB kinase-alpha from control on IkappaB kinase-beta (IKACALa) and IkappaB kinase-alpha are useful for modulating nuclear factor-kappaB (NF-kappaB) induction in a cell, where the compounds are capable of blocking the interaction that a cell, where the compounds are sixthera, and NEMO. The antiinflammatory compound further comprises at least one membrane translocation domain. The compounds are useful for treating inflammatory disorders, autoimnume diseases, osteoporosis, cancer, Alzheimer's disease, atherosclerosis, viral infections, Ataxia telangiectesia, and for transplantation detection. The compounds of the invention block NF-kappaB induction by IKK but do not inhibit the basal activity of NF-kappaB ABU08418 -ABU08432 represent human
                                                                                                                                                IkappaB kinase-bera; IkappaB kinase-alpha; IKKalpha; NF-kappaB; nuclear factor-kappaB induction; inflammatory disorder; autoimmune disease; osteoporosis; cancer; Alzheimer's disease; atherosclerosis; viral infection; Ataxia telangiectasia; transplantation detection; immunosuppressive; osteopathic; cytostatic; nootropic; neuroprotective; antiatherosclerotic; virucide; vasotropic; antirheumatic; antiathritic; mutant; mutein.
                                                                                                                                  Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antiinflammatory peptide compounds comprising NEMO binding domain, useful for modulating NF-kappaB induction in a cell and for treating NF-kappaB-mediated inflammation disorders e.g., asthma,
                                                                                          Human NEMO binding site (NBD) mutant peptide #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 22; Page 17; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.
                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAY-2001; 2001US-0847940
                                                       12-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  psoriasis, vasculitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the basal activity on NBD mutant peptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MAYM/) MAY M J. (GHOS/) GHOSH S.
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                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                            Synthetic.
                   ABU08423;
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The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB0877313). The comprising at least one NEWO binding domain (ABB0877313). The compound has acts through selective inhibition of cytokine-mediated NF-kB activation by blocking the interaction of NEWO cytokine-mediated NF-kB activation by blocking the interaction of NEWO control of IKADPAB in the NEWO CC cytokine sectivation and subsequent decreased phosphorylation of IKADPAB. The compound may also cat (directly or indirectly) by blocking the recruitement of leukocytes into sites of acute and chronic inflammation, by down-regulating the expression of E-selectin on leukocytes or by blocking osteoclast confidence of into sites of acute and chronic inflammatory disorder. Although the compound is useful in treating NF-kB mediated conditions, where the condition is an inflammatory disorder.

CC Altheimer's disease, transplant rejection, osteoporosis, cancer, autoimmune disease, transplant rejection, osteoporosis, cancer, conditions, where the inflammatory disorder is asthma, allergies, creaming the inflammatory disorder is asthma, allergies, creaming conditions and proposition or ataxia continued activities, osteoarthritis, psociatic arthritis, lupus and burshitis. The inflammatory disorder may also be dermatitis, conditions of psociasis, osteoarthritis, psociatic arthritis, lupus and spocial sistemed by Epstein-bark, crown's disorder may also be dermatitis, crown's disorder may also be dermatitis, crown's disorder may also be dermatitis, crown's disorder may also be dermatitis, crown's disorder may also be dermatitis, crown's disorder may also be dermatitis, crown's disorder may also be dermatitis, crown's disorder may also be dermatitis, crown's disorder may also be dermatitis, crowned by Epstein-bark, crown's disorder way also be dermatitis, crowned by Epstein-bark, crown's disorder way also be dermatitis, crowned by Epstein-bark, crowned by Epstein-bark, crowned by Epstein-bark
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                                                                                                                                           IKKDeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB; kinase activation; leukocyte; inflammation; B-selectin; osteoclast; autoimmune disease; transplant rejection; osteoporosis; cancer; Alzheimer's disease; viral; infection; osteoporosis; anaphylaxis; psoriasis; rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; antiinflammatory; immunosuppressive; osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antiashmatic; antiallergic; dermatological; antibacterial; antiboratio; antiallergic; antiallargic; antiallargic; antiarthritic; osteopathic; antiulcer; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Wildtype Asp substituted by Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 11; Page -; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAY-2001; 2001WO-US40654.
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22-AUG-2000; 2000US-0643260.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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Gaps

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100.0%; Score 39; DB 24; Length 6; 100.0%; Pred. No. 9.3e+05; ive 0; Mismatches 0; Indels

6; Conservative

1 LEWSWL 6

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Best Local Similarity Matches 6; Conserv

Query Match

ABB77305 standard; protein; 756 AA.

RESULT 4

subsequent decreased phosphorylation of IkappaB. The compound may also act (directly or indirectly) by blocking the recruitment of leukocytes inco sites of acute and chronic inflammation, by down-regulating the expression of E selectin on leukocytes or by blocking osteoclast differentiation. The compound is useful in treating NP-kB mediated conditions, where the condition is an inflammatory disorder, an autoimmune disease, transplant rejection, osteoporosis, cancer, Alzheimer's disease, transplant rejection, osteoporosis, cancer, Alzheimer's disease, atherosclerosis, a viral infection or ataxia telammatory disorder is asthma, allergies, utticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis, rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory disease, vasculitis and bursitis. The inflammatory disorder may also be dermatitis, espendylarthritis, psoriatic arthritis, lupus and poor boxel disease, chronic obstructive pulmonary disease, vasculitis, psoriatic arthritis, lupus and spondylarthritis. Also for Crohn's disease, ulcerative colitis, cryoglobulinaemia or multiple sclerosis. For chronic viral infections caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral diseases include HIV and influenza. The compound may also be useful for treating anaphylaxis, drug and food sensitivity, contact dermatitis, and suburn or aging. The compound may be used to replace corricosteroids in any application in which corricosteroids are used, including in the compound may be used to replace in a multiple sclerosis. The compound may be used in the compound may be used to replace corricosteroids in any application in which corricosteroids are used, including in the compound may be used to replace in a multiple sclerosis.

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immunosuppression in transplants and cancer therapy. Also for identifying antiinflammatory compounds and for diagnosis of an inflammatory disorder. The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of the NEMO binding domain of IKKbeta.

6 AA;

Sequence Query Match

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ö
sunburn or aging. The compound may be used to replace corticosteroids in any application in which corticosteroids are used, including immunosuppression in transplants and cancer therapy. Also for identifying antiinflammatory compounds and for diagnosis of an inflammatory disorder. The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of an IKKbeta mutant, useful in examples of the invention.

Note: The present sequence is not given in the specification but is derived from GenBank Accession No. 014920 (ABB77294).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IKKDeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB; kinase activation; leukocyte; inflammation; E-selectin; osteoclast; autoimmune disease; transplant rejection; osteoporosis; cancer; Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis; rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; antiinflammatory; immunosuppressive; osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antiasthmatic; antiallergic; dermatological; antibacterial; antipsoriatic; antiallergic; antiarthritic; osteopathic; antiulcer.
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                                                                                                                                                                                                                                                   Gaps
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0
                                                                                                                                                                                                             100.0%; Score 39; DB 23; Length 756; 100.0%; Pred. No. 4.8e+02; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IKKbeta NEMO binding domain peptide SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                            ABB08725 standard; peptide; 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAY-2000; 2000US-201261P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JUN-2002 (first entry)
                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                    737 LEWSWL 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-179350/23
                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                              756 AA;
                                                                                                                                                                                                                                                                                    1 LEWSWL 6
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                                                                                                                                                                              Sequence
                                                                                                                                                                                                               Query Match
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antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                       Antiinflammatory, antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
                                  Gaps
                                  ;
92.3%; Score 36; DB 23; Length 6; 83.3%; Pred. No. 9.3e+05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                         Anti-inflammatory peptide SEQ ID NO 33.
                                                                                                                                                                            AAM48530 standard; Peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
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                                                                                                                                                                                                                                          (first entry)
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                                 5; Conservative
                Local Similarity
                                                                1 LEWSWL 6
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                                                                                                                                                                                                                                          20-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                 Matches
                                                                                                                                             RESULT 6
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The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB08725-ABB08742) comprising at least one NEMO binding domain (ABB77313). The compound has acts through selective inhibition of cytokine-mediated NF-kB activation by blocking the interaction of NEMO with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO interaction results in inhibition of IKKbeta kinase activation and

Claim 23; Page 44; 82pp; English.

binding domain

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02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.
                                                                                                                                                                                          psoriasis
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                                             (PRAE-)
                                                          (UYYA)
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Matches
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(AAM48620-AMM48645), comprising a membrane translocation domain (AAM48620-AMM48645), comprising a membrane translocation domain acid residues, fueed to a NEWO binding sequence

(AAM48625-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antitheumatory compounds have antiasthmatic, antiabacterial, immunosuppressive, dermatological, neuroprotective, contropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IKAppaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoperosis, osteoathritis, inflammatory bowel disease, sepsis, vasculitis, useful multiple sclerosis; transplant rejection; osteoporosis; pro-inflammatory responses such as allergies, urticaria, and ataxia telangiactesia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antinflammatory; antiaethmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; deriarthritic; osteopathic; antiatherosclerotic; antiallergic; membrane translocation domain; NEWO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatorid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimmer's disease; atherosclerosis; viral infection;
                                                       Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                            The invention relates to an antiinflammatory compound (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.3%; Score 36; DB 23; Length 6; 83.3%; Pred. No. 9.3e+05; ive 1; Mismatches 0; Indels
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Phillips K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM48655 standard; Peptide; 6 AA
                                                                                                                            Claim 6; Page 61; 88pp; English
 Ghosh S, Findeis MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NBD mutant peptide SEQ ID NO 2.
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                              WPI; 2002-121889/16.
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1 LDWSWL 6
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                                                                                                   psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
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Matches
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The invention relates to an antiinflammatory compound (especially AAM48629-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48645). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antitheumatic, antiarthritic osteopathic, antiabacterial, immunosuppressive, dermatological, enuroprotective, notropic, antiatheroselerotic, virucide and antiallargic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappa8 activation by blocking interaction of Ikappa8 kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKAppa8. The compounds are useful for treating inflammatory disorders, e.g. asthma, inflammation or cancer, psoriasis, rheumatoid arthritis, osteoparthritis, inflammatory bowel disease, sepsis, vasculitis, osteoparthritis, inflammatory bowel disease, sepsis, vasculitis, osteoporosis, discinging autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis, transplant rejection; osteoporosis, all lareimer's disease, atherosclerosis, viral infections; and ataxia telangiactasia. The compounds are also useful for treating infections anaphylaxis, pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
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                                                                                                                                                                                                                                                                                                   Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
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Pred. No. 9.3e+05;
1; Mismatches 0; Indels
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                                                                                                                             Phillips K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Page 47; 88pp; English.
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                                                                                                                                 Findeis MA,
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83.3%;
PRAECIS PHARM INC.
UNIV YALE.
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Best Local Similarity
                                                                                                                                 May MJ, Ghosh S,
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AMM48620-AMM48645), comprising a membrane translocation domain (AAM48620-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48619). The antiinflammatory compounds have antiasthmatic, attipacterial, immunosuppressive, dermatological, neuroprotective, notropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB contropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB contropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of KappaB kinase beta (IKKbeta) at the NFWO binding domain that results in inhibition of IKkbeta at the NFWO binding domain that results in inhibition of IKkbeta in the of compounds are useful for treating inflammatory discorders, e.g. asthma, ung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoporosis, attoimmune diseases such as lupus, polymyalgia, scleroderma, burshilts, antoimmune diseases such as lupus, polymyalgia, scleroderma, compounds are also useful for treating the calcinos; and ataxia telangiectasia. The compounds are also useful for treating and traxia drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an antiinflammatory compound (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.3%; Score 36; DB 23; Length 7; 83.3%; Pred. No. 9.3e+05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                         Phillips K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 61; 88pp; English.
                                                                                                                                                                                                                                                                                                                                         Ghosh S, Findeis MA,
                                                                                                                                                                    02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
                                                                                                             02-MAY-2001; 2001WO-US14346.
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                                                                                                                                                                                                                                                        (PRAE-) PRAECIS PHARM INC.
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WO200183554-A2
                                                         08-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to antiinflammatory compounds comprising NEMO binding domain (NEMD) peptides. The NEMO binding domains are found on IkappaB kinase-bera (IKKbeta) and IkappaB kinase-lpha (IKKalpha) proteins. The antiinflammatory compounds of the invention are useful for modulating nuclear factor-kappaBB (NE-kappaB) induction in a cell, where the compounds are capable of blocking the interaction between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel antiinflammatory peptide compounds comprising NEMO binding domain, useful for modulating NF-kappaB induction in a cell and for treating NF-kappaB-mediated inflammation disorders e.g., asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiinflammatory compound further comprises at least one membrane transflocation domain. The compounds are useful for treating inflammatory disorders, autoimmune diseases, osteoporosis, cancer, Alzheimer's disease, atherosclerosis, viral infections, Ataxia telangiectasia, and for transplantetion detection. The compounds of the invention block NF-kappas induction by IKK but do not inhibit the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 24; Length 6; Pred. No. 9.3e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-inflammatory peptide SEQ ID NO 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 22; Page 17; 47pp; English.
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83.3%;
                                                                                                                                                                 02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
                                                                                                          02-MAY-2001; 2001US-0847940
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-209142/20.
N-PSDB; ABX94269, ABX94270.
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAR-2002 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    psoriasis, vasculitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NBD mutant peptides.
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                                                                                                                                                                                                                                                                                                                                      May MJ, Ghosh S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 AA;
                                                                                                                                                                                                                                                     (MAYM/) MAY M J. (GHOS/) GHOSH S.
  US2002156000-A1
                                                         24-OCT-2002
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Sequence

AAM48534;

RESULT 9 AAM48534

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Gaps

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Synthetic

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08-NOV-2001.
                                                                                                                              Synthetic.
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ID AAW9
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  à
                                                                                                                                                                                                                                                                                                                                                                              AMM48629. AAMM8645), comprising amenbramment constitution domain (Applead 20-AAMM8645), comprising amenbramment) comprises from 6-15 amino acid residues, fused to a NEWO binding sequence from 6-15 amino acid residues, fused to a NEWO binding sequence from 6-15 cytostatic, antiporiatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, notropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB compounds act as selective inhibitors of cytokine-mediated NFkappaB cativation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IkappaB. The compounds are useful for treating inflammenty disorders, e.g. asthma, lumg inflammation or cancer, posciasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, costeoarthritis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; callandariar's disease, atherocolerosis; viral infections; and ataxia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
                                                                                                                                                                                                                                                                             Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telanglectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                     invention relates to an antiinflammatory compound (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              food sensitivity, eczema, dermatitis, sunburn, aging and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.3%; Score 36; DB 23; Length 8; 83.3%; Pred, No. 9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                             Phillips K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM48535 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 61; 88pp; English
                                                                                                                                                                                                                            May MJ, Ghosh S, Findeis MA,
                                                                                                                                                  02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
                                                                                                                          02-MAY-2001; 2001WO-US14346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                       (PRAE-) PRAECIS PHARM INC. (UYYA ) UNIV YALE.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 AA;
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                                                                         WO200183554-A2.
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                                                  Synthetic.
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arthritis.
                                                                                                                                                                                                                                                                                                                   psoriasis
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(AAM48525-AAM48619). The antinflammatory compounds have antiasthmatic, cytostatic, antiporatatic, antirheumatory compounds have antiasthmatic, cytostatic, antiporatatic, antirheumatory compounds have antiasthmatic, cytostatic, antiporatatic, antirheumatic, antiarhitic, osteopathic, corpounds act as nelective, included and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB cortivation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IkappaB. The activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lum inflammation or cancer, psoriasis, rheumatoid arthitis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatomis, multiple sclerosis; viral infections; and ataxia
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antificumatic; antiatritute osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosolerotic; antialiergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKDeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to an antiinflammatory compound (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phillips K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 61; 88pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-2001; 2001WO-US14346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRAE-) PRAECIS PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-121889/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ghosh S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 AA;
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us-09-643-260-8.rag

AAM48526 standard; Peptide; 9 AA.

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RESULT 13
                                                                            AAM48526
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I-kappa-B kinase activity and I-kappa-B polypeptides (comprising a ix residue domain of I-kappa-B containing one of Ser33 and Ser36, and a candidate agent) can be used to screen for agents that cand activity of the modulation of the kinase activity of IKK-alpha forms a method for modulating signal transduction involving 1-kappa-B in a cell.

The IKK-alpha polypeptides are useful for generating oligonucleotide primers and probes for use in the isolation of natural IKK-alpha chroding nucleic acids. The nucleic acids are useful as transcripts, Mybridization probes, polymerase chain include IKK-alpha ableles and primers. Their diagnostic applications include IKK-alpha ableles in clinical and laboratory samples.

Therapeutic application includes the use of IKK-alpha nucleic acids for modulating callular expression or intracellular concentration/availability of active IKK-alpha.

Catalytically inactive IKK-alpha mutants suppress NF-kappa-B cativation induced by tissue necrosis factor (TRAF) and NF-kappa-B-inducing kinase (NIK) oversuppression. Polypeptides of IKK-appa-B-inducing kinase (NIK) oversuppression. Polypeptides of NF-kappa-B-inducing kinase (NIK) oversuppression. Polypeptides of Leu604, Thr679, Ser680, pro684, Thr686 or Ser687 of the full length of the invention of the invention of the invention.
                                                                                                                                                                                                                             I-kappa-B kinase; IKK-alpha; gene expression; modulation;
suppression; activation; tumour necrosis factor; TNF; interleukin-1;
IL-1; TNF receptor associated factor; TRAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprise at least one of these regions.
N.B. The present sequence is not given in the present specification
but is derived from the sequence given in AAW96157 as specified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Newly isolated human kinase IkappaB Kinase (IKK-^a) polypeptides - meeful in screening for agents that modulate the interaction of an IKK polypeptide to a binding target and for modulating signal transduction involving IkappaB in a cell
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                                                                                                                                                    IKK-alpha polypeptide with binding activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page -; 32pp; English.
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97US-0887115
                                                                            27-APR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-106044/09.
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9901541-A1.
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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AAW96182
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The invention relates to an antiinflammatory compound (especially AAM48645), comprising a membrane translocation domain (AAM48629-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48645), compounds for AAM48651) which comprises from 6-15 amino acid residues, fused to a NEWO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipacriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiafherosclerosic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NEKappaB activation by blocking interaction of IkappaB kinase beta (IKKOtca kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammation of IkappaB. The activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammation of IkappaB. The activation or cancer, psoriasis, rheumatoid arthritis, unflammatory bowel disease, sepsis, vasculitis, bursitis, unlimbactoria, all second as lupus, polymyladia, scleroderma, cannot activation and subsequent decreases such as lupus, polymyladia, scleroderma, cannot activation and subsequent diseases such as lupus, polymyladia, scleroderma, cannother activation and subsequent diseases, viral infections; and ataxia and ataxia and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activation and activ
                                                                                                                                                                                       Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEWO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
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                                                                                                                                      Anti-inflammatory peptide SEQ ID NO 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 61; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-2001; 2001WO-US14346.
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22-AUG-2000; 2000US-0643260.
                                                                                 (first entry)
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                                                                                 20-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                          AAM48526;
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Score 36; DB 23; Length 9; Pred. No. 9.3e+05;

92.3%; 83.3%;

Query Match Best Local Similarity

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Gaps

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arthritis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel antinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
    Gaps
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  Indels
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    Mismatches
                                                                                                                                                                                                                 Anti-inflammatory peptide SEQ ID NO 32.
                                                                                                                            AAM48529 standard; Peptide; 9 AA.
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22-AUG-2000; 2000US-0643260.
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                                                                                                                                                                                     20-MAR-2002 (first entry)
Conservative
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  Matches
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                                                                      Score 36; DB 23; Leural
Pred. No. 9.38+05;
O; Indels
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                                                                                                                                                              Best Local Similarity
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CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, cr granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; C Alzheimer's disease; atherosclerosis; viral infections; and ataxia cc Alzheimer's disease; atherosclerosis; viral infections; and ataxia cc relangiscrasia. The compounds are also useful for treating cc pro-inflammatory responses such as allergies, urticaria, anaphylaxis, cc drug or food sensitivity, eczema, dermatitis, sunburn, aging and cc arthritis.

XX SQ Sequence 9 AA;

Query Match

Best Local Similarity 83.3%; Score 36; DB 23; Length 9;
Best Local Similarity 83.3%; Pred. No. 9.3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps

Qy 1 LEWSWL 6

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2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 7, Appli	Sequence 7, Appli	20.	Sequence 2263, Ap	Sequence 120, App	Sequence 548, App	Sequence 3, Appli	Sequence 359, App	Sequence 359, App	Sequence 39808, A	Sequence 2210, Ap	Sequence 7842, Ap	Sequence 2, Appli	Sequence 17, Appl	Sequence 8, Appli
QI	US-09-847-940B-7	US-09-847-946A-7	US-10-369-493-20896	US-10-104-047-2263	US-10-080-170-120	US-10-080-170-548	US-09-759-667A-3	US-09-933-767-359	US-10-023-282-359	US-09-864-761-39808	US-10-104-047-2210	US-10-156-761-7842	US-10-147-324-2	US-10-257-378-17	US-10-067-668-8
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Score	38	38	38-	38	35	35	35	34	34	34	34	34	34	34	34
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Sequence 8, Appli Sequence 12634, A Sequence 7650, Ap Sequence 8, Appli Sequence 8, Appli Sequence 131, App Sequence 131, App Sequence 132, App Sequence 161, App Sequence 161, App Sequence 161, App Sequence 161, App Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli	32
115 US-10-175-696-8 112 US-10-369-493-12634 112 US-10-369-493-7850 113 US-09-847-9408-8 114 US-09-847-9468-8 115 US-10-106-698-8201 12 US-10-106-698-8201 13 US-09-820-893-73 11 US-09-810-893-131 12 US-10-264-237-1765 12 US-10-264-237-1765 13 US-10-193-002-80 12 US-10-193-002-80 12 US-10-193-002-80 13 US-10-193-002-80 14 US-10-193-22733 15 US-10-108-605-303 16 US-09-847-9468-9 17 US-09-847-9468-9 18 US-09-847-9468-3 18 US-09-847-9468-3 18 US-09-847-9468-3 18 US-09-847-9468-3 18 US-09-847-9468-3 18 US-09-847-9468-3 18 US-09-847-9468-3 18 US-09-847-9468-3 18 US-09-847-9468-3 18 US-09-847-9468-3 18 US-09-847-9468-3 18 US-09-847-9468-3	us-
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## ALIGNMENTS

Database :

Gaps Sequence 7, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
 APPLICANT: May, Michael J.
 APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR APPLICATION NUMBER: 09/643,260
; RIUMBER OF SEQ ID NOS: 27
; SOPTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 7 OTHER INFORMATION: Description of Artificial Sequence: NBD mutants ô 100.0%; Score 38; DB 10; Length 6; 100.0%; Pred. No. 7e+05; ive 0; Mismatches 0; Indels Sequence 7, Application US/09847946A; Publication No. US20030054999A1; GENERAL INFORMATION; APPLICANT: May, Michael J TYPE: PRT ORGANISM: Artificial Sequence 6; Conservative Best_Local Similarity Matches 6; Conserv LAWSWL 6 1 LAWSWL 6 US-09-847-940B-7 RESULT 2 US-09-847-946A-7 LENGTH: 6 Query Match ð g

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US-10-080-170-120
Sequence 120, Application US/10080170
Sequence 120, Application US/10080170
Sequence 120, Application No. USCO030129601A1
GENERAL INFORMATION:
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR TITLE OF INVENTION: TERATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495.0218
CURRENT APPLICATION NUMBER: US/10/080,170
FILE REPERENCE: DATE: 2002-06-10
PRIOR PELING DATE: 2002-06-10
PRIOR FILING DATE: 2001-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 548, Application US/10080170
Publication No. US20030129601A1
GENERAL INFORMATION:

APPLICANT: COLE, S.T.

TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR TITLE OF INVENTION: TEATHENTY OF MYCOBACTERIOSES
FILE REFERENCE: 03495.0218
CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT FILING DATE: 2002-06-10
PRIOR PPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
                                                                                                                                                                                                                                                                                Length 1217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DB 16; Length 196; . 9.3e+02;
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                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 38; DB 12; Best Local Similarity 100.0%; Pred. No. 1.5e+03; Matches 6; Conservative 0; Mismatches 0;
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Pred. No. 9.3e
1; Mismatches
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CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-080-170-120
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83.3%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 120
LENGTH: 196
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Best Local Similarity 83.3
Matches 5; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 548
LENGTH: 210
                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2263
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109 VAWSWL 114
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                                                                                                                                                          LENGTH: 1217
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US-10-360-493-20896
Sequence 20896, Application US/10369493
Fublication No. US20030233675A1
Sequence 20896, Application No. US20030233675A1
Sequence 20896, Application No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFEINS IN PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: DIANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (5205.) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
FRIOR FILING DATE: 2002-02-21
SRO ID NO 20896
LENGTH: 972
LENGTH: 972
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             APPLICANT: Findels, Mark A
APPLICANT: Findels, Mark A
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Cerhard
TILE REPERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT APPLICATION NUMBER: 60/201,261
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR PLILNG DATE: 2000-05-02
PRIOR PLILNG DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SEQ ID NOS: 160
SEQ ID NO 7
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
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Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels
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Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
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100.0%; Pred. No. 1.2e+03;
iive 0; Mismatches 0;
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US-10-369-493-20896
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Best Local Similarity 100.
Matches 6; Conservative
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Gaps

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PILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,877
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,878
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,949
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,974
FILING DATE: 1997-06-06
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FILING DATE: 1997-12-18
APPLICATION NUMBER: 60/068,053
FILING DATE: 1997-12-18
APPLICATION NUMBER: 60/070,923
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,917
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APPLICATION NUMBER: 60/048,898
FILING DATE: 1997-06-06
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APPLICATION UNDBER: 60/048,899
ALING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,893
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APPLICATION NUMBER: 60/048,900
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APPLICATION NUMBER: 60/048,901
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/049,019
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APPLICATION NUMBER: 60/048,970
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APPLICATION NUMBER: 60/048,916
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APPLICATION NUMBER: 60/049,373
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APPLICATION NUMBER: 60/048,875
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APPLICATION NUMBER: 60/048,963
                                                                                                                                                                                                                                                                                        FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,964
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APPLICATION NUMBER: 60/048,882
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Patent No. US20020064777A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mengiste, Tesaye
APPLICANT: Paszkowski, Jerzy
APPLICANT: Paszkowski, Jerzy
APPLICANT: Paszkowski, Jerzy
APPLICANTON: Recombination Repair Gene, MIM, from Arabidopsis thaliana
FILE REFERENCE: S-10568A
CURRENT APPLICATION NUMBER: US/09/759,667A
CURRENT FILING DATE: 1998-07-12
PRIOR APPLICATION NUMBER: 9915485.9
PRIOR APPLICATION NUMBER: 9900760.1
PRIOR PILING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 15
SOPTWARE: PatentIn version 3.0
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Pred. No. 3.3e+03;
1; Mismatches 0; Indels
Score 35; DB 16; Length 210;
Pred. No. 9.8e+02;
1; Mismatches 0; Indels
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Publication No. US20030181692A1

GENERAL INFORMATION:

APPLICANT: Ni et al.

TITLE OF INVENTION: 207 Human Secreted Proteins

FILE REFERENCE: PZ007P2

CURRENT APPLICATION NUMBER: US/09/933,767

CURRENT FILING DATE: 2001-08-22

PRIOR PILING DATE: 2001-02-21

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1000-03-29

PRIOR PLILNG DATE: 1000-03-29

PRIOR PLILNG DATE: 1998-10-04

PRIOR PLILNG DATE: 1998-06-04

PRIOR PLILNG DATE: 1998-06-06

PRIOR PLILNG DATE: 1997-06-06

PRIOR PRIOR PLING DATE: 1997-06-06

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: LENGTH: 1055
: TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-759-667A-3
   92.1%;
83.3%;
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Best Local Similarity 83.3%;
Matches 5; Conservative
                              Best Local Similarity 83.3
Matches 5; Conservative
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. 123 VAWSWL 128
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248 LAWSWV 253
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      Query Match
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EARLIER PRING DATE: 1997-06-06
EARLIER PRING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
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R PAPLICATION NUMBER: 60/048, 893
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048, 900
R PELING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048, 901
R FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R APPLICATION NUMBER: 60/048,915
RR FILING DATE: 1997-06-06
RR APPLICATION NUMBER: 60/049,019
RR FILING DATE: 1997-06-06
RR PELLING DATE: 1997-06-06
RR FILING DATE: 1997-06-06
RR FILING DATE: 1997-06-06
RR APPLICATION NUMBER: 60/048,970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,916
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,373
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/048,892
FILING DATE: 1997-06-06
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ORGANISM: Homo sapiens
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LOCATION: (56)
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NAME/KEY: SITE
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TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
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CURRENT FILING DATE: 2001-12-20
EARLIER FILING DATE: 1998-12-04
EARLIER FILING DATE: 1998-12-04
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
                              PRIOR APPLICATION UNDBER: 60/073,164
PRIOR FILING DATE: 1998-01-30
PRIOR FILING DATE: 1998-01-30
PRIOR PELING DATE: 1998-01-30
PRIOR PILING DATE: 1998-05-18
PRIOR PRILING DATE: 1998-05-18
PRIOR PILING DATE: 1998-05-18
PRIOR PILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
PRIOR PILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,922
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR PILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR PILING DATE: 1998-07-15
PRIOR PILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1245
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,884
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,894
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APPLICATION NUMBER: 60/048,971
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,020
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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Publication No. US20030092893A1
GENERAL INFORMATION:
FILING DATE: 1998-01-30
APPLICATION NUMBER: 60/073,164
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Best Local Similarity 100.
Matches 5, Conservative
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ORGANISM: Homo sapiens
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LENGTH: 56
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Gaps .. 0 Length 56; Indels Query Match

89.5%; Score 34; DB 15; I
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; ; LOCATION: (56)
i. TOTHER INFORMATION: Xaa equals stop translation
is-10-023-282-359

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Sequence 2210, Application US/1010447

Sequence 2210, Application US/1010447

Publication No. US2030328592A1

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVERTION: No. US2030236392A1e1 full length cDNA

FILE REFERENCE: H1-A0105

CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT FILING DATE: 2002-03-25

PRIOR FILING DATE:

NUMBER:

NUMBER:

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2210

LENGTH: 170
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Pred. No. 1.1e+03;
0; Mismatches 1; Indels
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Pred. No. 2.3e+03;
0; Mismatches 1; Indel8
                                  Indels
                                  0
   100.0%; Pred. No. 5.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATYORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2001-05-39
PRIOR APPLICATION NUMBER: JP 2001-27697
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-30
SPRIOR FILING DATE: 2001-06-30
SPRIOR FILING DATE: 2001-06-30
SPRIOR FILING DATE: 2001-08-02
SEQ ID NOS: 15109
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   Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                    33 LAWSW 37
                                                                                               1 LAWSW 5
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APPLICANT: Penn, Sarican G.

APPLICANT: Penn, Sarican G.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Hansel, David R.

APPLICANT: Hansel, David R.

TITLE OF INVESTION: GENE EXPRESSION ANLYSIS BY MICROARRAY

TITLE OF INVESTION: GENE EXPRESSION ANLYSIS BY MICROARRAY

TITLE OF INVESTION: GENE EXPRESSION ANLYSIS BY MICROARRAY

TITLE OF INVESTION: GENE EXPRESSION ANLYSIS BY MICROARRAY

TITLE OF INVESTION: GENE EXPRESSION ANLYSIS BY MICROARRAY

THEN APPLICATION WORDER: US 60/203, 366

PRIOR PLING DANE: 2000-023, 326

PRIOR PLING DANE: 2000-023, 426

PRIOR 
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN DUNG, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN BOUNE MARROW, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: SWISSPROT HIT: P14528, EVALUE 4.50e+00
                                                                                                                                                 Sequence 39808, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
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OTHER INFORMATION: MAP TO AC004596.1
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ORGANISM: Homo sapiens
9 LAWSW 13
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LENGTH: 64
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89.5%; Score 34; DB 9; Length 64;

Query Match

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               Sequence 2, Application US/10147324

Publication No. US20030215812A1

REMEMBAL INFORMATION:
APPLICANT: MA, YAN-HE
APPLICANT: MA, YAN-FEN

TITLE OF INVENTION: GENE ENCODING B-MANNANASE, ENZYME PREPARATION AND USES
TITLE OF INVENTION: THEREOF

TILE REPRENCE: 0304-0001

CURRENT APPLICATION UNMERR: US/10/147,324

CURRENT APPLICATION UNMERR: 2002-08-09

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 493

TYPE: PRT

CORANISM: Bacillus Sp.

US-10-147-324-2
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i Sequence 17, Application US/10257378

i Sequence 17, Application US/10257378

i Publication No. US20030190642A1

i GENERAL INFORMATION:

i APPLICANT: Jones, Glenville

i APPLICANT: Rambhaw, Heather A.

i APPLICANT: Rambhaw, Heather A.

i APPLICANT: Rambhaw, Heather A.

i APPLICANT: Stangle, Wayne A.

i TITLE OF INVENTION: A Thymus Expressed Human Cytochrome P450 (P450TEC)

i FILE REFERENCE: 11812-65

i CURRENT FILING DATE: 2001-04-20

i PRIOR PELING DATE: 2000-04-10

i PRIOR FILING DATE: 2000-04-20

i PRIOR FILING DATE: 2000-04-20

i NUMBER OF SEQ ID NOS: 56

i SOFTWARE: PatentIn Ver. 2.1

i SEQ ID NO 17

i LENGTH: S44
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Publication No. US20030022334A1
GREEAL INFORMATION:
APPLICANT: Glucksmann, Maria Alexandra
TITLE OF INVENTION: 33312, 33303, 32579, NOVEL HUMAN
TITLE OF INVENTION: CYTOCHROME P450 FAMILY MEMBERS AND USES THEREOF
FILE REFERENCE: 10448-136001
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Matches 5; Conservative
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US-10-067-668-8
US-10-147-324-2
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CURRENT APPLICATION NUMBER: US/10/067,668

CURRENT FILING DATE: 2002-02-04

PRIOR APPLICATION NUMBER: 60/266,140

PRIOR APPLICATION NUMBER: 60/266,140

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 544

CUBRY MATCH

SOCANISM: Homo sapiens

OUBRY MATCH

QUERY MATCH

Best Local Similarity 83.3%; Score 34; DB 15; Length 544;

Best Local Similarity 83.3%; Pred. No. 2.78+03;

MATCHES 5; Conservative 0; Mismatches 1; Indels 0; Gaps

OY 1 LAWSWL 6

CY 1 LAWSWL 51

Db 46 LGWSWL 51

Search completed: February 18, 2004, 15:41:56

Job time: 17.7529 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 18, 2004, 13:37:19; Search time 22.7763 Seconds (without alignments) 41.814 Million cell updates/sec Run on:

US-09-643-260-7 38

1 LAWSWL 6 Perfect score: Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

Searched:

1107863 seqs, 158726573 residues

1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A Geneseq 19Jun03:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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| SIDSI/gcgdata/geneseqy/geneseqp-embl/AA1999.DAT:*
| SIDSI/gcgdata/geneseqy

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Mutated IKKbeta NE	NBD mutant peptide	Human NEMO binding	Human IKKbeta muta	Propionibacterium	M. tuberculosis an	M. tuberculosis an	Drosophila melanoq	Drosophila melanog
SUMMAKIES	QI	ABB08729	AAM48512	-	-	-	ABU05469	ABU05897	ABB64219	ABB71850
	08	23	23	24	23	22	23	23	22	22
	Query Match Length DB ID	9	9	9	756 23	196	196	210	321	329
مد	Query Match	100.0	100.0	100.0	1,000	92.1	92.1	92.1	92.1	92.1
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## ALIGNMENTS

ABB08729 standard; peptide; 6 AA (first entry) 14-JUN-2002 ABB08729; ABB08729 

Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 7.

kinase activation; leukocyte; inflammation; B-selectin; obteoclast; autoimmune disease; transplant rejection; osteoporosis; cancer; alzimmune disease; viral; inflammation; osteoporosis; cancer; rheumatoid arthritis; croh; s disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; antiinflammatory; immunosuppressive; osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antiasthmatic; antiallergic; dermatological; antibacterial; antibsoriatic; antiallergic; antialredic; antialredic; antialredic; antialredic; osteopathic; antiulcer; mutant; mutein. IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;

Homo sapiens.

Synthetic.

Key Location/Qualifiers Misc-difference 2

/note= "Wildtype Asp substituted by Ala"

WO200183547-A2

08-NOV-2001.

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Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
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ABU08422
ID ABU0
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                                                                                                                                                                                                                                                                                                   The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB0773-ABB08742) comprising at least one NEMO binding domain (ABB077313). The compound has acts through selective inhibition of cytokine-mediated NF-kB activation by blocking the interaction of NEMO compound has acts through selective inhibition of new of interaction results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IKKbeta kinase activation and cat (directly or indirectly) by blocking the recruitment of leukocytes incompound may also cat (directly or indirectly) by blocking the recruitment of leukocytes incompound may also cat (directly or indirectly) by blocking the recruitment of leukocytes conditions, where the compound is useful in treating NF-kB mediated conditions, where the condition is an inflammatory disorder, an anticaria, anaphylaxis, cutaneous inflammatory disorder, and activated conditions and the inflammatory disorder is asthma, allergies, cuticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis, cremanical arthritis, sporiatic arthritis, luguas and bursitis. The inflammatory disorder may also be dermatitis, eczema, compound and issease, chronic obstructive pulmonary disease, vasculitis and spondylarthritis. Also for Crohn's granulomatosis, temporal arteritis, cryoglobulinaemia or multiple sclerosis, remporal arteritis, caryoglobulinaemia or multiple sclerosis. For chronic caryoglobulinaemia or multiple sclerosis. For chronic caryoglobulinaemia or multiple sclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        caused by Epstein-barr, cytomegalovitus or herpes simplex. Other viral diseases include HIV and influenza. The compound may also be useful for treating anaphylaxis, drug and food sensitivity, context dermatitis, surburn or aging. The compound may be used to replace corticosteroids in any application in which corticosteroids are used, including immunosuppression in transplants and cancer therapy. Also for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiinflammatory compounds and for diagnosis of an inflammatory disorder. The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of a mutated NEMO binding domain of IKKOeta.
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                                                                                                                                                                                      Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting cell with an anti-inflammatory compound comprising at least one NEMO
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                                                                                                                                                                                                                                                                           Claim 23; Page 44; 82pp; English.
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02-MAY-2001; 2001WO-US40654.
                                02-MAY-2000; 2000US-201261P
22-AUG-2000; 2000US-0643260
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antirheumatic; antiarthritic; oeteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosolerotic; antiallergic; membrane translocation domain, NEMO binding domain; eczema; cytokine; NekappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AM48645) comprises from 6-15 amino acid residues, fused to all membrane translocation domain (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antisheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosolerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKkbeta kinase activation and subsequent decreased phosphorylation of Ikkbeta kinase compounds are useful for treating inflammatory disorders, e.g. asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lung inflammation or cancer, psoriasis, rhematoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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telangiectasia. The compounds are also useful for treating
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22-AUG-2000; 2000US-0643260.
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Human IKKbeta mutant D738A.

(first entry)

14-JJN-2002

ABB77303;

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The present invention relates to antiinflammatory compounds comprising NEMO binding domain (NBD) peptides. The NEMO binding domains are found on IMappas kinase-beta (IKKDeta) and IKappas kinase-beta (IKKDeta) and IKappas kinase-alpha and IKASlpha) proteins. The antiinflammatory compounds of the invention are useful for modulating nuclear factor-kappas (NF-kappas) induction in a cell, where the compounds are capable of blocking the interaction between one or more IKKs such as IKKBalpha or IKKDeta, and NEMO. The antiinflammatory compound further comprises at least one membrane inflammatory disorders, autoimmung aleases, osteoporosis, cancer, inflammatory disorders, autoimmung diseases, osteoporosis, cancer, that all and for transplantation detection. The compounds of the invention block NF-kappas induction by IKK but do not inhibit the basal activity of NF-kappas. ABU08418-ABU08432 represent human are not inhibit.
                                                                                                                                                IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB; nuclear factor-kappaB induction; inflammatory disorder; autoimmune disease; osteoporceis; cancer, Alzheimer's disease; atherosclerosis; viral infection; Ataxia telangiectasia; transplantation detection; immunosuppressive; osteopathic; cytostatic; noorropic; neuroprotective; antiatherosclerotic; virucide; vasotropic; antiatherosclerotic; virucide;
                                                                                                                                Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel antiinflammatory peptide compounds comprising NEMO binding domain, useful for modulating NF-kappaB induction in a cell and for treating NF-kappaB-mediated inflammation disorders e.g., asthma,
                                                                                          Human NEMO binding site (NBD) mutant peptide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 22; Page 17; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-2001; 2001US-0847940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
                                                     12-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              psoriasis, vasculitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-209142/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          May MJ, Ghosh S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MAYM/) MAY M J. (GHOS/) GHOSH S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 AA;
                                                                                                                                                                                                                                                                                                                                                             US2002156000-A1.
                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                  24-OCT-2002
                                                                                                                                                                                                                                                                                                                         Synthetic
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                   ABU08422;
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The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound.

CABBOR723-ABBOR72) comprising at least one NEWO binding domain (ABBOR7313). The compound has acts through selective inhibition of cytokine-mediated NF-kB activation by blocking the interaction of NEWO binding domain. Blockage of IKKbeta-NEWO interaction results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IKKbeta kinase activation and chromic inflammatory by down-regulating the expression of E-selectin on leukocytes or by blocking osteoclast conditions, where the compound is useful in treating NF-kB mediated conditions, where the condition is an inflammatory disorder; an autoimmune disease, transplant rejection, osteoporosis, cancer, autoimmune disease, transplant rejection, osteoporosis, cancer, conditions, where the condition is an inflammatory disorder in an antiflammatory disease, atheroselerosis, a viral infection or ataxia telangiectasia. The inflammatory disorder is asthma, allergies, uritaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis, crecoarthritis, psoriatic arthritis, lupus and bursitis. The inflammatory disorder may also be dermatitis, conditions condylarthritis, also for Crohn's disease, ulcerative collitis, sporiasis, osteoarthritis, psoriatic arthritis, lupus and sporiations sporiations arthritis, raiso for Crohn's disease, ulcerative collitis, sporiatis or spondylarthritis. Also for Crohn's disease, ulcerative collitis, coleroderma, wegner's granulomatosis, temporal arteritis, caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral diseases include HIV and influence or herpes simplex, contact dermatitis, or treating anaphylaxis, drug and food sensitivity, contact dermatitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting a cell with an anti-inflammatory compound comprising at least one NEMO
                                                                                                                                      IXXDeat; IXXIpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB; kinase activation; leukocyte; inflammation; E-selectin; osteoclast; autoimmune disease; transplant rejection; osteoporosis; cancer; Alzheimer's disease; viral; infection; asthma; anaphylaxis; psortasis; rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; antiinflammatory; immunosuppressive; osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antiasthmatic; antiallergic; dermatological; antibacterial; antisorabic; antiallergic; antiallergic; antiarthritic; osteopathic; antiulcer; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Wildtype Asp substituted by Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key Location/Qualifiers
Misc-difference 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 11; Page -; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32-MAY-2001; 2001WO-US40654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
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binding domain
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                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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Indele

100.0%; Score 38; DB 24; Length 6; 100.0%; Pred, No. 9.3e+05;

0; Mismatches

6; Conservative

1 LAWSWL LAWSWL

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Query Match Best Local Similarity Matches 6; Conserv

ABB77303 standard; protein; 756 AA.

RESULT 4

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sunburn or aging. The compound may be used to replace corticosteroids in any application in which corticosteroids are used, including immunosuppression in transplants and cancer therapy. Also for identifying antiinflammatory compounds and for diagnosis of an inflammatory disorder. The compound may be administered alone or in combination with other known anti-inflammatory agents. The present sequence is that of an IKKbeta mutant, useful in examples of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endopthelmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                   he present sequence is not given in the specification but is from GenBank Accession No. 014920 (ABB77294).
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                                                                                                                                                                                                                             100.0%; Score 38; DB 23; Length 756; 100.0%; Pred. No. 6.7e+02;
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e J, Zhang Y, Jen S, Carter D;
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                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU62777 standard; Protein; 196 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                                                                                                                                                  6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes.
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N-PSDB; AAS59629.
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                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                          756 AA;
                                                                                                                                                                                                                                                                                                        1 LAWSWL 6
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                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                             Query Match
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polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (BLISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and alelecting a polymucleotide sequence that is highly conserved in both genomes with no counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. tuberculosis or M. leprae infection. The method reduces the number of potential new targets and protective antigens for new drugs and vaccine compositions to treat and prevent mycobacterial diseases, particularly tuberculosis and leprosy. The present sequence represents a marker protein from Mycobacterium tuberculosis and Mycobacterium leprae
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mycobacteria by a comparative genomic analysis of the sequences of Mycobacterium tuberculosis and M. leprae -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterioses; survival; virulence; protective antigen; vaccine; mycobacterial disease; tuberculosis; leprosy.
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                                                                                                                                                                                                                                       Score 35; DB 22; Length 196;
Pred. No. 4.6e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M. tuberculosis and M. leprae marker protein #120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 288-289; 874pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU05469 standard; Protein; 196 AA.
                                                                                                                                                                                                                                       92.1%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
Mycobacterium leprae.
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                                                                                                                                                                                                                                                                                5; Conservative
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                                                                                                                                                                                                                                                                                                                                                           102 VAWSWL 107
                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                     196 AA;
                                                                                                                                                                                                                                                                                                                      1 LAWSWL 6
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ABU05897;

RESULT 7 ABU05897

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ABBS7737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 19449; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.1%; Score 35; DB 22; Length 321; 83.3%; Pred. No. 7.6e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO 42342.
                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 19449.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB71850 standard; Protein; 329 AA.
    ABB64219 standard; Protein; 321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li PWD,
                                                                                                                                                                                                                                                                                                                                                   23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                              Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-656860/75.
N-PSDB; ABL08322.
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Matches 5; Conserv
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                                                                                                                                                                                     pharmaceutical
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                                                                                   26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and selecting a polynucleotide sequence that is highly conserved in both genomes with no counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. tuberculosis or M. leprae infection. The method reduces the number of potential new targets and protective antigens for new drugs and vaccine compositions to treat and prevent mycobacterial diseases, particularly tuberculosis and leprosy. The present sequence represents a marker
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                                          Gaps
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  Score 35; DB 23; Length 196; Pred. No. 4.6e+02; 1; Mismatches 0; Indels
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Pred. No. 4.9e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                 M. tuberculosis and M. leprae marker protein #548
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                                                                                                                                                                                                                            ABU05897 standard; Protein; 210 AA.
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83.3%;
Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                             (first entry)
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Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                    : | | | | |
109 VAWSWL 114
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123 VAWSWL 128
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                                                                               1 LAWSWL 6
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                                                                                                                                                                                                                                                                                                             08-APR-2003
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Cole S;

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Drosophila melanogaster.

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The present sequence is a MIM protein from Arabidopsis thaliana, which contributes to recombination repair of DNA damage in plant cells. The protein was tracked down with the help of a T-DNA tagged Arabidopsis mutant showing hypersensitivity to methyl methanesulphonate (MMS). It shows homology to a member of SNC (Structural Maintenance of Chromosomes) protein family and confers hypersensitivity to treatment with MMS, X-rays, UV light or mitomycin C. The present sequence is useful for DNA
     B type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                               New Arabidopsis polynucleotide encoding protein useful for assisting recombinant repair of DNA damage in plants -
/note= "conserved motif which harbours a Walker NTP binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human papillomavirus E7 protein inhibiting peptide SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; Length 1055; 2.6e+03; ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPV; E7 protein; inhibition; virucide; carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB:
Pred. No. 2.6e-
1; Mismatches
                                                                                                                                                                                                          (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Pages 22-25; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY78379 standard; peptide; 13 AA
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                                                                                                                        99WO-EP04984
                                                                                                                                                          98GB-0015485
                                                                                                                                                                        99GB-0000760
                                                                                                                                                                                                                                                                                         WPI; 2000-182437/16.
N-PSDB; AAZ50145, AAZ50146.
                                                                                                                                                                                                                                                           Mengiste T, Paszkowski J;
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Best Local Similarity 83.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repair in plant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus.
Synthetic.
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                                                      WO200004174-A1
                                                                                                                        14-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176 - ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; recombination; plant; DNA repair; hypersensitivity; SMC protein family; Structural Maintenance of Chromosomes; MIM; methyl methanesulphonate; irradiation; mitomycin C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.1%; Score 35; DB 22; Length 329;
83.3%; Pred. No. 7.8e+02;
.ive 1; Mismatches 0; Indels
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/label= Coiled_coil_region-II
/label= DA-box
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443..627
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/label= NTP_binding_domain
                                                                                                                                                                                                           Myers EW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY44787 standard; Protein; 1055 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                          Li PWD,
                                                                                                                      23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                     23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                          Adams M,
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Matches 5; Conserv
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17 LAWTWL 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 AA;
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                   WO200171042-A2
                                                                                                                                                                                                                                                                                                                               interactions -
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Binding-site
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                                                                                                                                                                                                          Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                             Human; secreted protein; fusion protein; gene therapy; protein therapy; disgnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system, asthma, lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schlock; Alzheimer's disease; restenosis; AIDS; osteoporosis, arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                               AAY78375 to AAY78415 represent peptides capable of inhibiting the human papillomavirus (HPV) B7 protein. The peptides have virucide activity. The peptides can be used in pharmaceutical compositions to inhibit HPV B7 protein, which allows the prevention and/or treatment of HPV associated diseases, which may comprise carcinomas.
       New peptides used for the prevention and treatment of human papilloma virus associated disease - \,
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                                                                                                                  89.5%; Score 34; DB 21; Length 13; 100.0%; Pred. No. 39;
                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                               Secreted protein encoded by gene 111 clone HTWBY29.
                                                                                                                                   0; Mismatches
                                                                                                                                                                                                             AAW88644 standard; Protein; 56 AA.
                                Claim 1; Page 22; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0048817
97US-0048819
97US-0048891
97US-0048895
97US-0048895
97US-0048915
97US-0048915
97US-0048949
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97US-0049375.
97US-0057628.
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97US-0057644.
97US-0057647.
97US-0057650.
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97US-0057667.
97US-0057761.
97US-0057764.
97US-0057764.
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                                                                                                                                    Conservative
                                                                                                                        Local Similarity
nes 5, Conserv
                                                                                                                                                  13 AA;
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06-JUN-1997;
06-JUN-1997;
06-JUN-1997;
06-JUN-1997;
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                                                                                                                                                                                                                             AAW88644;
                                                                                                  Sequence
                                                                                                                   Query Match
                                                                                                                            Best Loc
Matches
                                                                                                                                                                                           RESULT 12
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XFFX8X00000X8
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The invention relates to nucleic acid sequences (AAV84411 to AAV84633) encoding human secreted proteins (AAV88534 to AAV88756). The secreted protein gene sequences are deposited with the ATCC under deposit numbers ATCC 97979, 97974, 97975, 97977, 209007, 209008, 209009, 209010, 209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress GA; Fan P, Feng P, Ferrie AM, Fischer CL, Florence C; Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW; Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM; Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
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97US-0057775.
97US-0048872.
97US-0048882.
97US-0048882.
97US-0048882.
97US-0048891.
97US-0048891.
97US-0048910.
97US-0048910.
97US-00489173.
97US-00489173.
97US-00489173.
97US-0057651.
97US-0057651.
97US-0057651.
97US-0057661.
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97US-0057646.
97US-0057649.
97US-0057654.
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97US-0057760
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97US-0057769
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                05-SEP-1997

06-JUN-1997

06-JUN-1997

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06-JUN-1997;
05-SEP-1997;
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05-SEP-1997;
05-SEP-1997;
05-SEP-1997;
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05-SEP-1997;
05-SEP-1997;
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05-SEP-1997;
05-SEP-1997;
05-SEP-1997;
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06-JUN-1997;
06-JUN-1997;
06-JUN-1997;
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cells comprising recombinant vectors containing the nucleic acid
sequences are used for the recombinant production of the secreted
proteins. The polymucleotide and amino acid sequences are useful for are
useful for preventing, treating or ameliorating medical conditions e.g.
by protein or gene therapy. Pathological conditions can be also
diagnosed by determining the amount of the new polymeptides in a sample
or by determining the presence of mutations in the new polymucleotides.
Co by determining the presence of mutations in the new polymucleotides.
Co by determining the presence of mutations in the new polymucleotides.
Co by determining the amount of the polymucleotides in a sample
or by determining the presence of mutations in the new polymucleotides.
Co by determining the presence of mutations in the new polymucleotides.
Co by determining the presence of mutations in the new polymucleotides.
Co products for the diagnosis or treatment of cancer, neurodegenerative
disorders, developmental abnormalities and feetal deficiencies, blood
disorders, tumours, leukemias, disease of the immune system, autoimmune
cliseases, bhopatic and renal disease, lymphomas, inflammation, allergies,
clischemic shock, Alzheimer's and cognitive disorders involving osteoclasts
such as osteoporosis, arthritis or malignancies, diseases of testes,
lung or thymus, disestive/endocrine disorders, infections and AIDS. The
polypeptides are also useful for identifying their binding partners.
The present sequence represents human secreted protein (see descriptor.
The present sequence represents human secreted protein (see descriptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV; dermatological; immunosuppressive; antiinflammatory; immunostimulant; cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological; neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnerary; antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder; multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer; human immunodeficiency virus; hyperproliferative disorder; wound healing; caucher a disease; cardiovacular disease; Scimitar syndrome; chemotaxis; corneal graft neovascularisation; diabetic retinopathy; regeneration; neurological disorder; Huntington's chorea; Alzheimer's disease; Parkinson's disease; chromosome 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;
Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrie AM, Fan P;
Peng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;
Zeng Z, Greene JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8e+02;
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29-MAR-2000; 2000US-193170P.
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 AA;
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proteins (I) and polynucleotide (II) sequences. (I) and (II) have various activities based on the tissues and cells the genes are expressed in.

Example of these activities include: immunomodulatory; antisclerotic; dermatological; immunosuppressive, antiinflammatory; immunostimulant; antipartinsonian; immunosuppressive, antiinflammatory; immunostimulant; antiparkinsonian; antimicrobial; anticonvulsant; antialzheimers; vascular; antiparkinsonian; antimicrobial; and vulnerary. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) can be used in the prevention, diagnosis and treatment of immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immunodeficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease), cardiomyopathy and coronary arteriosclerosis; and openic disorders (e.g. corneal graft neovascularisation and diabetic retinopathy), neurological disorders (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), infectious diseases and/or for promoting wound healing, regeneration and/or chemotaxis. ABA813185 to ABA819193 and ABB50300 represent sequences used in the exemplification of
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                                                                                                                                                                            (II) have various
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                                                           Nucleic acids encoding 207 human secreted polypeptides, useful for preventing, diagnosing and/or treating, e.g. cancers, Parkinson's disease and diabetic retinopathy -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.5%; Score 34; DB 22; Length 56; 100.0%; Pred. No. 1.8e+02;
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                                                                                                                              Claim 11; Page 1140; 1533pp; English
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2000US-0207456.
2000US-0608408.
2000US-023356.
2000US-0234587.
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Best Local Similarity
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                              N-PSDB; ABA83304
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21-SEP-2000; 2
27-SEP-2000; 2
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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which human liver single exon encoded peptides of the invention.

Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; foetal liver; gene expression; single exon nucleic acid probe.
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                                                           Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human adult liver -
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                                                                                                         Claim 27; SEQ ID No 33771; 658pp; English
 Chen W, Rank DR;
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Best Local Similarity 100...
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Hanzel DK,
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27-SEP-2000;
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CC measuring human gene expression in a sample derived from human foetal
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CC liver. The single exon nucleic acid probes may be used for predicting,
CC maeauring and displaying gene expression in samples derived from human
CC moter the present sequence is a peptide encoded by a single exon
CC nucleic acid probe of the invention.
CN Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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SQ Sequence 64 AA;
Query Match
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Mismatches 0; Indels 0; Gaps 0;
CD 1 LAWSW 5
CO 1 LAWSW 5
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OM protein - protein search, using sw model
Run on: February 18, 2004, 14:36:10; Search time 16.6974 Seconds (without alignments) 75.239 Million cell updates/sec
Title: US-09-643-260-6 Perfect score: 40 Sequence: 1 ADWSWA 6
Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched: 801455 segs, 209382283 residues
Total number of hits satisfying chosen parameters: 801455
Minimum DB seq length: 0 Maximum DB seq length: 200000000
Post-processing: Minimum Match 10% . Maximum Match 100% . Listing first 45 summaries
Database: Published Applications AA:*  1: /cgn2_6/ptcdata/1/pubpaa/USO7_PUBCOMB.pep:*  2: /cgn2_6/ptcdata/1/pubpaa/USO7_WEW PUB.pep:*  3: /cgn2_6/ptcdata/1/pubpaa/USO6_PUBCOMB.pep:*  4: /cgn2_6/ptcdata/1/pubpaa/USO7_NEW PUB.pep:*  5: /cgn2_6/ptcdata/1/pubpaa/USO7_NEW PUB.pep:*  6: /cgn2_6/ptcdata/1/pubpaa/USO7_NEW PUB.pep:*  7: /cgn2_6/ptcdata/1/pubpaa/USO8_PUBCOMB.pep:*  8: /cgn2_6/ptcdata/1/pubpaa/USO8_PUBCOMB.pep:*  9: /cgn2_6/ptcdata/1/pubpaa/USO8_PUBCOMB.pep:*  11: /cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*  11: /cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*  12: /cgn2_6/ptcdata/1/pubpaa/USO9_NEW PUB.pep:*  13: /cgn2_6/ptcdata/1/pubpaa/USO9_NEW PUB.pep:*  14: /cgn2_6/ptcdata/1/pubpaa/USO9_NEW PUB.pep:*  15: /cgn2_6/ptcdata/1/pubpaa/USO0_NEW PUB.pep:*  16: /cgn2_6/ptcdata/1/pubpaa/USO0_NEW PUB.pep:*  17: /cgn2_6/ptcdata/1/pubpaa/USO0_NEW PUB.pep:*  18: /cgn2_6/ptcdata/1/pubpaa/USO0_NEW PUB.pep:*  18: /cgn2_6/ptcdata/1/pubpaa/USO0_NEW PUB.pep:*  18: /cgn2_6/ptcdata/1/pubpaa/USO0_NEW PUB.pep:*  18: /cgn2_6/ptcdata/1/pubpaa/USO0_NEW PUB.pep:*
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RESULT 1 US-09-847-946A-41 ; Sequence 41, Application US/09847946A ; Publication No. US20030054999A1	GENERAL INFOGRATION: GENERAL INFOGRATION: APPLICANT: May, Michael J APPLICANT: Ghosh, Sankar APPLICANT: Findeis, Mark A APPLICANT: Findeis, Mark A APPLICANT: Hannig, Gerhary APPLICANT: Hannig, Gerhary TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF FILE REFRENCE: PPI-119 CURRENT APPLICATION NUMBER: US/09/847,946A CURRENT FILING DATE: 2001-05-02 PRIOR FILING DATE: 2000-05-02/V PRIOR FILING DATE: 2000-05-02/V RIOR FILING DATE: 2000-05-02/V RIOR FILING DATE: 2000-05-02/V RIOR FILING DATE: 2000-05-02/V RIOR FILING DATE: 2000-05-02/V SEQ ID NOS: 160 SOFTWARE: Patentin Ver. 2.0	.; LENGTH: 6 : TYPE: PRT : ORGANISM: Artificial Sequence : FEATURE: : OTHER INFORMATION: Description of Artificial Sequence:NEMO binding : OTHER INFORMATION: sequence
RESULT 1 US-09-847; Sequenc; Publice	APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC AP	EBNGT  TYPE:  TYPE:  ORGAN  FEATT  OTHER  COTHER  US-09-847

ALIGNMENTS

Query Match 100.0%; Score 40; DB 11; Length 6; Best Local Similarity 100.0%; Pred. No. 7e+05; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps

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Sequence 78, Application US/09847946A

Sequence 78, Application US/09847946A

Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: Way, Michael J

APPLICANT: Ghosh, Sankar

APPLICANT: Pindeis, Mark A

APPLICANT: Pindeis, Mark A

APPLICANT: Hannig, Gerharbyn

APPLICANT: Hannig, Gerharbyn

APPLICANT: Hannig, Gerharbyn

APPLICANT: Hannig, Gerharbyn

APPLICANT: Hannig, Gerharbyn

APPLICANT: Hannig, Gerharbyn

APPLICANT: Hannig, Gerharbyn

APPLICANT: Pinles: 2001-05-02

FILE REFERENCE: PILLO NUMBER: 60/201,261

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-06-02

PRIOR FILING DATE: 2000-06-02

NUMBER OF SEQ ID NOS: 160

SOFTWARR: PatentIn Ver: 2.0

SEQ ID NO 78
                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Glosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Politips, Kathryn
APPLICANT: NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-02
SPRIOR FILING DATE: 2000-08-02
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
COTHER INFORMATION: sequence
US-09-847-946A-78
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ORGANISM: Artificial Sequence
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Best Local Similarity
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US-09-847-946A-70
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Sequence 77, Application US/09847946A

Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Hannig, Gerhard

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

CURRENT FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 05/021,261

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR PLING DATE: 2000-05-02

PRIOR PLING DATE: 2000-08-22

PRIOR PLING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTMARE: PatentIn Ver. 2.0
                                                                                                                     APPLICANT: May, Michael J
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
ITILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
ITILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 160
SEQ ID NOS: 160
SEQ ID NO 73
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
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                                              Sequence 73, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100."
Matches 6; Conservative
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1 ADWSWA 6
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LENGTH: 7
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US-09-847-9464-75

US-09-847-9464-75

SQUEENCE 75, Application US/09847946A

PUBLICATION NO. US20030054999A1

GENERAL INFORMATION:

APPLICANT: Ghosh, Sankar

APPLICANT: Findeis, Mark A

APPLICANT: Phillips, Kathryn

APPLICANT: Phillips, Kathryn

APPLICANT: Phillips, Kathryn

APPLICANT: Phillips, Kathryn

APPLICANT: Phillips, Kathryn

APPLICANT: Phillips, Kathryn

APPLICANT: Phillips, Kathryn

APPLICANT: Phillips Rathryn

FILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2000-05-02

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR FILING DATE: 2000-08-02

NUMBER OF SEO ID NOS: 160

SOFTWARE: PatentIn Ver. 2.0

SEO ID NO 75

INNOTEN: 0
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APPLICANT: Ghosh, Sankar
APPLICANT: Ghosh, Sankar
APPLICANT: Pindeish, Mark A
APPLICANT: Pindeish, Mark A
APPLICANT: Pindeish, Mark A
APPLICANT: Pindeish, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAWMATORY COMPOUNDS AND USES THEREOF
FILE REPERENCE: PPI-119
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:NEMO binding; OTHER INFORMATION: sequence
US-09-847-946A-75
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Similarity 100.0%; Score 40; DB 11; Length 9; Similarity 100.0%; Pred. No. 7e+05; 6; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 6; Conserv
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US-09-847-946A-72

Sequence 72, Application US/09847946A

Publication No. US20030054999A1

GENERAL INFORMATION:
APPLICANT: Ghosh, Sankar
APPLICANT: Findels Mark A
APPLICANT: Findels Mark A
APPLICANT: Findels Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Rathryn
APPLICANT: Phillips, Sankar
APPLICANT: Phillips, Sankar
APPLICANT: Phillips, Rathryn
APPLICANT: Phillips, Rathryn
APPLICANT: NUMBER: US/09/847,946A
CURRENT APPLICATION NUMBER: 2000-05-02

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-06-05

PRIOR FILING DATE: 2000-08-22

NUMBER: OS/643,260

SOFTWARE: PatentIn Ver. 2.0

LEWGTH: 9

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LEWGTH: 9
                                                                                                                                                                                                                                                                         APPLICANT: May, Michael J
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Pindeis, Mark A
APPLICANT: Pindeis, Mark A
APPLICANT: Pindeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
ITILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: 08/091,261
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 160
SOFTHARE: Patentin Ver. 2.0
SEQ ID NO 69
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                                                                                                                                                                                                      Sequence 69, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
Matches 6; Conserv
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Squence 17, Application US/1041626

Fublication No. US20030186418A1

GENERAL INFORMATION:

APPLICANT: Gualfetti, Peter

APPLICANT: Mitchinson, Colin

APPLICANT: Phillips, Jay Ian

TITLE OF INVENTION: No. US20030186418A1e1 Variant EGIII-Like Cellulase

TITLE OF INVENTION: No. US20030186418A1e1 Variant EGIII-Like Cellulase

TITLE OF INVENTION: No. US20030186418A1e1 Variant EGIII-Like Cellulase

TITLE REFERENCE: GG631

CURRENT PAPLICATION NUMBER: US/10/441,626

CURRENT FILING DATE: 2003-05-19

NUMBER OF SEQ ID NOS: 64

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17

LENGTH: 236
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 68 Application US/09847946A

Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Ghosh, Sankar

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Phillips, Kathryn

APPLICANT: Phillips, Kathryn

APPLICANT: Phillips, Kathryn

APPLICANT: Phillips, Kathryn

APPLICANT: Phillips, Kathryn

CURRENT PLING DATE: 2001-05-02

PRIOR PLING DATE: 2000-05-02

PRIOR PLING DATE: 2000-06-02

PRIOR PLING DATE: 2000-06-02

PRIOR PLING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: PatentIn Ver. 2.0
                                         ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding ; OTHER INFORMATION: sequence US-09-847-946A-74
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                                                                                                                                                    100.0%; Score 40; DB 11; Length 10; 100.0%; Pred. No. 11; tive 0; Mismatches 0; Indels
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; ORGANISM: Gliocladium roseum (3)
US-10-441-626-17
  ORGANISM: Artificial Sequence FEATURE:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 6; Conservative
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US-10-441-626-17
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Sublication No. US20030054999A1

GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Pindeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Rathryn
APPLICANT: Phillips, Carhard
FILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REPERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT APPLICATION NUMBER: 06/201,261
PRIOR PLING DATE: 2000-05-02
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 71
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Description of Artificial Sequence:NEWO binding ; OTHER INFORMATION: sequence US-09-847-946A-71
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Publication No. US200300549991
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
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100.0%; Score 40; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                             Score 40; DB 11; Length 9;
Pred. No. 7e+05;
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CURRENT FILING DATE: 2001-05-02
PRIOR PELLING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
SOFTWARE: PATENTIN VET. 2.0
SOFTWARE: PATENTIN VET. 2.0
TYPE: PRI
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; OTHER INFORMATION: sequence US-09-847-946A-76
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Best Local Similarity 100.
Matches 6; Conservative
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Patent No. US20020156000A1
CARBERAL INFORMATION:
APPLICANT: May, Michael J.
APPLICANT: Ghosh, Sankar
TILLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-1170P;
CURRENT APPLICATION NUMBER: US/09/847,940B
FURRENT FILING DATE: 2001-05-02
PRIOR PELING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
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Score 37; DB 12; Length 236;
Pred. No. 3.5e+02;
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Sequence 5090, Application US/09815242

Sequence 5090, Application US/09815242

SEQUENCE INCRATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Trawick, John D.

APPLICANT: Trawick, John D.

APPLICANT: Xu, H. Howard

ITILE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION NUMBER: 60/201, 078

PRIOR APPLICATION NUMBER: 60/206, 848

PRIOR PILING DATE: 2000-03-21

PRIOR PELING DATE: 2000-05-28

PRIOR PELING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253, 625

PRIOR APPLICATION NUMBER: 60/253, 625

PRIOR PELING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/269, 308

PRIOR PELING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: 60/269, 308

PRIOR PELING DATE: 2000-02-16

PRIOR PELING DATE: 2000-02-16

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PRIOR DATE: 2000-02-20-16

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                                                                                1; Mismatches
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; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-5090
    Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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563 ADWAWA 568
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; SOFTWARE: Patentin Ver. 2.0
; SRO ID NO 4
; LENGTH: 6
; TYPE: PRT
; OGGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-4

Query Match
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps

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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory	
SUMMARIES	AAM48538 AAM48570 AAM48574 AAM48567 AAM48575 AAM48560 AAM48572 AAM48573	
DB	8888888888	
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& Query Match	0.000000000000000000000000000000000000	
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Result No.	1464666	

	Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory Anti-inflammatory
AAM48568 AAM48571 AAW48571 AAW21305 AAV21305 AAV20333 AAN40332 AAN403394 AAB08727 AAM48510 AAM48537 AAM48548 AAM48548 AAM48548 AAM48548 AAM48553 AAM48553 AAM48553 AAM48553 AAM48553 AAM48553 AAM48553 AAM48553 AAM48553 AAM48553	AAM48564 AAM48541 AAM48550 AAM48551 AAM48555 AAM48555 AAM48558
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ALIGNMENTS

Anti-inflammatory peptide SEQ ID NO 41. AAM48538 standard; Peptide; 6 AA. (first entry) 20-MAR-2002 AAM48538; RESULT 1

antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NPkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis. Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;

02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260. 02-MAY-2001; 2001WO-US14346. WO200183554-A2. 08-NOV-2001. Synthetic. 

(PRAE-) PRAECIS PHARM INC.

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The invention relates to an antiinflammatory compound (especially AMM48628-AMM48627) comprising a membrane translocation domain (AAM48628-AMM48627) comprising a membrane translocation domain canno acid residues, fused to a NEMO binding sequence (AAM48625-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB compounds are as selective inhibitors of cytokine-mediated NFkappaB cortivation by blocking interaction of IkappaB kinase beta (IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, osteoarthritis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoprorais; and ataxia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            telangiectasia. The compounds are also useful for treating
pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
                                                                                                                             Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
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                                            Ghosh S, Findeis MA, Phillips K;
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                                                                                                                                                                                                                                         Claim 6; Page 61; 88pp; English.
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                                                                                WPI; 2002-121889/16.
(UYYA ) UNIV YALE.
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                                            Мау МЈ,
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AMM48620-AMM48645), comprising a membrane translocation domain (AAM48620-AMM48627) or AAM486651 which comprises from 6-15 amino acid residues, fused to a NEWO binding sequence (Cytostatic, antiporiatic, antiinflammatory compounds have antiasthmatic, cytostatic, antiporessive, dermatological, neuroprotective, onotropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NRkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IKkbeta kinase compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoporosis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, grannlomicosis, multiple sclerosis; transplant rejection; osteoporosis; grannlomicosis, multiple sclerosis; transplant rejection; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermacological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
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                                                                                                                                                                                                                                                 Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
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                                       02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.
02-MAY-2001; 2001WO-US14346.
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                                                                                                       (PRAE-) PRAECIS PHARM INC.
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                                                                                                                             (UYYA ) UNIV YALE.
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                                                                                                                                                                    May MJ,
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WPI; 2002-121889/16.
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Best Local Similarity
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                                                                                               Synthetic.
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AMM48620-AMM48645). Comportsing a membrane translocation domain
(AAM48620-AMM48645). The AMM48646-AAM48651) which comprises from 6-15
anino acid residues, fused to a NEWO binding sequence
(AAM48625-AAM48619). The antiinflammatory compounds have antiasthmatic,
(VLOStatic, antiabooriatic, antiinflammatory compounds have antiasthmatic,
ontropic, antiatherosclerotic, virucide and antiallergic activity. The
compounds act as selective inhibitors of cytokine-mediated NFkappaB
activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
the NEWO binding domain that results in inhibition of IKkbeta kinase
activation and subsequent decreased phosphorylation of IKkpeta kinase
activation and subsequent decreasis, rhemmatory disorders, e.g. asthma,
lung inflammatory bowel disease, sepsis, vasculitis,
osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
osteoathritis, inflammatory bowel disease, sepsis, vasculitis,
drandlomatosis, multiple sclerosis, transplant rejection, osteoporosis,
drandlomatosis, multiple sclerosis, transplant rejection, and ataxia
telanglectasis. The compounds are also useful for treating
drandlomatosis, multiple sclerosis, urticaria, anaphylaxis,
drandlomatosis, multiple sclerosis, urticaria, anaphylaxis,
drandlomatosis, uniticaria, anaphylaxis,
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                                                                                                                                                                                                                                                                                  Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to an antiinflammatory compound (especially
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                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 62; 88pp; English.
                                                                                                                                                                                                                      May MJ, Ghosh S, Findeis MA,
                                                                                          02-MAY-2001; 2001WO-US14346.
                                                                                                                        02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
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                             WO200183554-A2.
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Synthetic.
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The invention relates to an antiinflammatory compound (especially AM48628-AAM48645), comprising a membrane translocation domain (AAM48628-AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEWO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antisthmatic, cytostatic, antiporiatic, antirheumatic, antiarthiz, osteogathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NRAappaB compounds act as selective inhibitors of cytokine-mediated NRAappaB cortivation by blocking interaction of IkappaB kinase beta (IKKbeta kinase the NEWO binding domain that results in inhibition of IKKbeta kinase compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, or bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis, transplant rejection, osteoporosis, allocations, and ataxia
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cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
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                                                                                                                                                                                 ataxia telangiectasia; allergy; anaphylaxis; arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phillips K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Findeis MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
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Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.

Anti-inflammatory peptide SEQ ID NO 69.

(first entry)

20-MAR-2002

AAM48566;

AAM48566 standard, Peptide, 9 AA.

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antirheumatic; antiarrhitis; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antialergic; membrane translocation domain; NRO binding domain; eczema; cytokine; NRkappaB; IkappaB kinase beta; IKKOeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                          Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                       Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                        May MJ, Ghosh S, Findeis MA, Phillips K;
Anti-inflammatory peptide SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 62; 88pp; English.
                                                                                                                                                                                                                                   02-MAY-2001; 2001WO-US14346.
                                                                                                                                                                                                                                                           02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 AA;
                                                                                                                                                                                WO200183554-A2
                                                                                                                                                                                                           08-NOV-2001
                                                                                                                                                        Synthetic
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AMM48620-AAM48645), comprising a membrane translocation domain.

(AAM48620-AAM48645), comprising a membrane translocation domain.

(AAM48620-AAM48619). The antiinflammatory comprises from 6-15
amino acid residues, fused to a NEWO binding sequence

(AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
cytostatic, antiposoriatic, antirheumatic, antiarthritic, osteopathic,
antibacterial, immunosuppressive, dermatological, neuroprotective,
compounds act as selective inhibitors of cytokine-mediated NFkappaB

compounds act as selective inhibitors of cytokine-mediated NFkappaB

compounds act as selective inhibitors of trappaB kinase beta (IKKbeta) at
the NEMO binding domain that results in inhibition of IKAppaB. The
compounds are useful for traction inhibition of IKAppaB. The
compounds are useful for tracting inflammatory disorders, e.g. asthma,
lum inflammation or cancer, psoriasis, rheumatodid arthritis,
osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
dursitis, autoimmune diseases such as lupus, polymyalgia, sclercoderma,
granulomatosis, multiple sclerosis, transplant rejection; osteoporosis,
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The invention relates to an antiinflammatory compound (especially
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CAMMA8525-AAW48619). The antinflammatory compounds have antiasthmatic, cytostatic, antiportatic, antinflammatory compounds have antiasthmatic, cytostatic, antiportatic, antinflammatory compounds have antiasthmatic, cytostatic, antiportatic, antinflammatic, antiathatic, osteopathic, antibaterial, immunosuppressive, dermatological, neuroprotective, contropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB compounds are useful for treating inhibition of IKAppaB. The activation and subsequent decreased phosphorylation of IKAppaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, ung inflammation or cancer, psortasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vaculitis, dranal autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; clandiscensis, and ataxia are largametory responses such as allergies, urciating and ataxia pro-inflammatory responses such as allergies, unburn, aging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM48628-AAM48645), comprising a membrane translocation domain
(AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to an antiinflammatory compound (especially
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Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,

Claim 6; Page 62; 88pp; English.

psoriasis

Phillips K;

Findeis MA,

Ghosh S,

May MJ,

WPI; 2002-121889/16.

(PRAE-) PRAECIS PHARM INC. (UYYA ) UNIV YALE.

02-MAY-2001; 2001WO-US14346. 02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.

WO200183554-A2.

Synthetic.

08-NOV-2001

Gaps ö Length 9; Indels 100.0%; Score 40; DB 23; Similarity 100.0%; Pred. No. 9.3e+05; 6; Conservative 0; Mismatches 0; Query Match Best Local Similarity 1 ADWSWA 6 Matches ð

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Gaps

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100.0%; Score 40, DB 23; Length 8; 100.0%; Pred. No. 9.3e+05; ive 0; Mismatches 0; Indels

6; Conservative

1 ADWSWA 6 ADWSWA 6

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Query Match Best Local Similarity

Best Loc Matches

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RESULT 6

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ADWSWA
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AAM48569 standard; Peptide; 9 AA.
     (first entry)
     20-MAR-2002
   AAM48569;
AAM48569
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Anti-inflammatory peptide SEQ ID NO 72.

antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; defined antiatherosclerotic; antiallerotic; membrane translocation domain; NEWO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; ataxia telangiectasia; allergy; anaphylaxis; arthritis,

Synthetic.

WO200183554-A2.

08-NOV-2001

02-MAY-2001; 2001WO-US14346.

02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.

(PRAE-) PRAECIS PHARM INC.

(UYYA ) UNIV YALE

Phillips K; Findeis MA, Ghosh S, May MJ,

WPI; 2002-121889/16.

Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation, psoriasis

Claim 6; Page 62; 88pp; English.

The invention relates to an antilninammatory compound (especially AMM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48646), comprising a membrane translocation domain (AAM48620-AAM48646). The AMM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEWO binding sequence (AAM486525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antiatherselectric, antiatherselectric, virtuide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkapab activation by blocking interaction of Ikapab kinase beta (IKKbeta kinase activation and subsequent decreased phosphorylation of IKApapa The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis, viral infections; and ataxia telangisctasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, child and screen, dermatitis, unburn, aging and invention relates to an antiinflammatory compound (especially arthritis.

9 AA; Sequence

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                                                       Gaps
                                                       ö
Length 9;
                                                    Indels
100.0%; Score 40; DB 23;
100.0%; Pred. No. 9.3e+05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                             AAM48572 standard; Peptide; 9 AA
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                                                       6; Conservative
                    Local Similarity
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     Query Match
                                Best Loca
Matches
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WO200183554-A2.

Synthetic.

08-NOV-2001.

02-MAY-2001; 2001WO-US14346.

02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.

(PRAE-) PRAECIS PHARM INC. (UYYA ) UNIV YALE. Findeis MA, Phillips K; May MJ, Ghosh S,

WPI; 2002-121889/16.

Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation. psoriasis

Claim 6; Page 62; 88pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM48629-AAM88645), comprising a membrane transflocation domain.

(AAM48620-AAM48645), comprising a membrane transflocation domain

(AAM48820-AMM48627) or AAM48646-AAM48651) which comprises from 6-15

amino acid residues, fused to a NEWO binding sequence

(AAM48825-AAM48619). The antiinflammatory compounds have antiasthmatic,

cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,

antibacterial, immunosuppressive, dermatological, neuroprotective,

nootropic, antiatheroscleroic, virucide and antiallergic activity. The

compounds act as selective inhibitors of cytokine-mediated NFkappaB

activation by blocking interaction of ItspapaB kinase beta (IKKObeta) at

the NEWO binding domain that results in inhibition of IKKObeta kinase

activation and subsequent decreased phosphorylation of IkkappaB. The
                                                                                                                                                                                                                                                                                                                                                       Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                           Gaps
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                                                                                            100.0%; Score 40; DB 23;
100.0%; Pred. No. 9.3e+05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                           Anti-inflammatory peptide SEQ ID NO 76.
                                                                                                                                                                                                                                              AAM48573 standard; Peptide; 9 AA.
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22-AUG-2000; 2000US-0643260.
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                                                                                                                        6; Conservative
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                                                                                                       Best Local Similarity Matches 6; Conserv
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                                                                                                                                                   1 ADWSWA 6
                                                                    9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           psoriasis
                                                                    Sequence
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AAM48573
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compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursatis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections, and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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100.0%; Pred. No. 9.3e+05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-inflammatory peptide SEQ ID NO 71.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM48568 standard; Peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Findeis MA,
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antibacterial, immunosuppressive, dermatological, neuroprotective, noctropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NRkapaB cetivation by blocking interaction of IkapaB kinase beta (IKKDeta) at the NEWO binding domain that results in inhibition of IKKDeta kinase activation and subsequent decreased phosphorylation of IKKapaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, costeoarthritis, inflammatory bowel disease, sepsis, vasculitis, costeoarthritis, intible sclerosis, transplant rejection; osteoporosis, caranulomatosis, multiple sclerosis, transplant rejection; osteoporosis, clangiener's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, unticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirhemmatory; antiarthatic; osteopathic; antibacterial; virucide; immunosuppressive; definition of the manatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEWO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKOeta; cancer; psoriasis; cytokine; NFkappaB; IkappaB kinase beta; IKKOeta; cancer; psoriasis; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
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22-AUG-2000; 2000US-0643260.
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(AAAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipacatory compounds have antiasthmatic, antibacterial, immunosuppressive, dermatological, neuroprotective, antiatherosaclerotic, antiatherosaclerotic, virucide and antiallergic activity.

Compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IxappaB kinase beta (IXAbeta kinase activation by blocking interaction of IxappaB kinase beta (IXAbeta kinase activation and subsequent decreased phosphorylation of IXAppaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, or seconthitis, inflammatory bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; irransplant rejection; osteoporosis; Alzheimer's disease; atheroscalerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, pro-inflammatory responses such as allergies; urticaria, anaphylaxis,
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                 AAM48620-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
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Novel antiinflammatory compound comprising membrane translocation

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2000US-0217496
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14-AUG-2000;
14-AUG-2000;
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             The invention relates to an antiinflammatory compound (especially AAM48629-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48645), comprising a membrane translocation domain acid residues, fused to a NEMO binding sequence (AAM48625-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antiinflammatic, antiathritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NEKapaB activation by blocking interaction of IkapaB kinase beta (IKKDeta kinase activation by blocking interaction of IkapaB kinase beta (IKKDeta kinase activation and subsequent decreased phosphorylation of IkApaB . The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoporosis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis, transplant rejection; osteoporosis, Alzheimer's diseases intherosclerosis, viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, arthritis, arthritis, surburn, aging and
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domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation, psoriasis
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                                                                                               Claim 6; Page 62; 88pp; English.
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2000US-0184664.
2000US-0186350.
2000US-0189874.
2000US-0190076.
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02-MAR-2000; 2
16-MAR-2000; 2
17-MAR-2000; 2
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04-FEB-2000;
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           THE SECOND SECTION OF THE SECOND SECTION OF THE SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SEC
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antigens. The nucleic acids and proteins are used to prevent, treat (e.g. by gene therapy) or ameliorate a medical condition in e.g. humans, mice, cabbits, goates, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. The antibodies to the antigens can also diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (BLISA). Disorders which are diagnosed or treated immunosorbent assays (BLISA). Disorders which are diagnosed or treated immunosorbent assays (BLISA). Disorders which are diagnosed or treated immunosorbent assays (BLISA). Disorders which are diagnosed or treated cardiovascular disorders e.g. cardioarast, cerebrovascular disorders e.g. cardioarast, cerebrovascular disorders e.g. cardioarast, nervous system disorders e.g. cardioarast, infections caused by bacteria, viruses and fungicand ocular disorders e.g. corneal infection. The polypeptides and sloop be used to aid wound healing and epithelial cell proliferation, to transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present polypeptide represents a partial sequence of a novel BGIII-like callulase of Gliocladium roseum. It was deduced from a partial gene sequence isolated from genomic DNA using PCR primers (see AAX59180-91) based on conserved motifs (see AAY06325-29) of Trichoderma resets EGIII callulase and related enzymes. PCR has been used to identify novel EGIII-like enzymes, including the present polypeptide, from bacterial and fungal sources (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                     capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, coffactors and other nutritional components. Numerous examples of diseases and disorders treated by the nucleic acids and proteins are given in the specification. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cellulase; endoglucanase; EGIII; textile; feed additive; baking;
food processing; grain wet milling; pulp; paper.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 22; Length 33; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; SEQ ID No 1549; 642pp; English
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N-PSDB; AAS34125.
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05-JAN-2001;
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The invention relates to novel nucleic acids encoding novel human foetal

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            cells and methods for the recombinant production of such enzymes, which can be used in the treatment of cellulose-containing textiles, as feed additives, in the treatment of wood pulp, in the reduction of biomass to glucose, in the stone washing of indigo dyed denim, or as laundry detergent components (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present polypeptide represents a full-length sequence of a novel BGIII-like cellulase of Gliochadium roseum. It was deduced from a gene sequence isolated from genomic DNA using PCR primers (see AAX59180-91) based on conserved motifs (see AAY06325-29) of Trichodearma reseat BGIII-cliulase and related enzymes. PCR has been used to identify novel BGIII-like enzymes, including the present protein, from bacterial and fungal sources (see AAY06331-70)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cellulase; endoglucanase; EGIII; textile; feed additive; baking; food processing; grain wet milling; pulp; paper.
Also provided by the invention are vectors, host
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                                                                                                                                                      192.5%; Score 37; DB ilarity 83.3%; Pred. No. 63; Conservative 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity
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AAY06331-70).
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63 ADWSWS 68
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Search completed: February 18, 2004, 14:26:19 Job time: 22.7763 secs

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Gaps

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0; Indels

1; Mismatches

February 18, 2004, 14:16:39; Search time 7.06579 Seconds (without alignments) 35.929 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM protein - protein search, using sw model Run on:

US-09-643-260-5 40

1 LDWSWA 6 **BLOSUM62** Scoring table: Perfect score: Sequence:

328717 segs, 42310858 residues Searched:

Gapop 10.0 , Gapext 0.5

328717 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:* Issued Patents AA: Database

Pred. No. is the number of results predicted by chance to have a. score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	Sequence 3, Appli			Sequence 18367, A	28,	29,	28,	ď	2170	m	۳,	4,	ω,	4,	4	4	4	4,	~	2,	7,	4, 1	10,	3, 7	4	4	Sequence 2, Appli
SUMMAKIES	ΠD	US-09-345-236B-3	S.	US-09-252-991A-17312	G,	-08	US-08-241-853-29	-08-8	-08-	US-09-252-991A-21704	-08-88	US-09-023-321-3	US-08-890-853-4	US-09-032-475-3	US-09-099-125A-4	US-09-099-124A-4	US-09-032-476-4	US-08-890-854-4	9-023	-168	-80	۰	US-09-109-986-4	US-09-844-908-10	US-09-868-758-3	-08-88	US-09-023-321-4	US-08-890-853-2
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## ALIGNMENTS

Sequence 22368, Application US/09252991A

Sequence 22368, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICATION NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT PAPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22368 APPLICANT: Tukuo. Fukuda

APPLICANT: Tukuo. Fukuda

APPLICANT: Tukuo. Fukuda

APPLICANT: Moser, Betchina

APPLICANT: Moser, Betchina

APPLICANT: Medeen, Albert H.

APPLICANT: Undeen, Albert H.

TITLE OF INVENTION: Compositions, and Methods for Control of Invertebrates

TITLE OF INVENTION: Compositions, and Methods for Control of Invertebrates

TITLE OF INVENTION: Us/09/345,236B

CURRENT APPLICATION NUMBER: US/09/345,236B

CURRENT PILING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 148

SEQ ID NO 3

ENERGY PLENTIFF FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTE ö Gaps ö 100.0%; Score 40; DB 4; Length 242; 100.0%; Pred. No. 31; 0; Mismatches 0; Indels Sequence 3, Application US/09345236B; Patent No. 6521454; GENERAL INFORMATION: ORGANISM: mosquito baculovirus Query Match
Best Local Similarity 100. 79 LDWSWA 84 1 LDWSWA 6 RESULT 2 US-09-252-991A-22368 US-09-345-236B-3 US-09-345-236B-3 g ઠે

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                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Fang, Kathy S.
APPLICANT: Fang, Kathy S.
APPLICANT: ALIABMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 100;
50;
                                                                                                                                                                                                                                                                                                                                                                    COUNTIKI: USANGE COMPUTER FEADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,853
FILING DATE: 12-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Bsq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-078
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
ITELEFAX: 201 343-1684
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
TENTIFF: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Preq. ...
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                                                        RESULT 5
US-08-21-853-28
Sequence 28, Application US/08241853
Patent No. 569488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Klauber & Jackson STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-7
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18367, Application US/09252991A

Sequence 18367, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 18367
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                                                                                                  Score 38; DB 4; Length 445;
Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.1e+02;
                                                                                                                                          0; Indels
                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                      Sequence 17312, Application US/09252991A Patent No. 6551795
                  TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
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                                                                                                95.0%;
83.3%;
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Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                Query Match 95.0
Best Local Similarity 83.3
Matches 5; Conservative
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303 MDWSWA 308
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271 LDWAWA 276
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US-09-252-991A-17312
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US-09-252-991A-18367
                                                          US-09-252-991A-22368
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LENGTH: 445
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Patent No. 5854045

Patent No. 5854045

GERREAL INFORMATION:

APPLICANT: Hanafusa, Hidesaburo

TITLE OF INVENTION: A TRANSMENBRANE TYROSINE PHOSPHATASE

TITLE OF INVENTION: AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: All Hackensack Avenue

CITY: Hackensack Avenue

STATE: New Jersey

COUNTRY: USA

ZIPE: O'601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: DAY COMPATION

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/850,917

FILING DATE: 0.2-NAY-1997

PILING DATE: 12-NAY-1997

STILING DATE: 12-NAY-1994

ATTORNEY APPLICATION NUMBER: US 08/241,853

FILING DATE: TANA-1994

ATTORNEY APPLICATION NUMBER: US ORDANIA
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50;
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100.0%; Pred. No....
0; Mismatches
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tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                  INFORMATION FOR SEQ ID NO: 28.
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOCY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
  201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                      19 LDWSW 23
                                                                                                                                                                                                                                                                                                                                                                                         1 LDWSW 5
                                                                                                                                                                                                    HYPOTHETICAL: N
HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
US-08-850-917-28
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US-08-850-917-29
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TELEFAX:
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Patent No. 5854045
GENERAL INFORMATION:
APPLICANT: Fang, Kathy S.
APPLICANT: Hanafusa, Hidesaburo
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
       COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,853
FILING DATE: 12-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
REJERMA: 201 487-5800
TELEFRA: 201 487-5800
TELEFRA: 201 487-580
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,917
FILING DATE: 02-MAY-1997
CLASSIFICATION: 43-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/241,853
FILING DATE: 12-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: All Heckeneack Avenue CITY: Hackeneack STATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                           TELEX: 133521
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 90.0
Best Local Similarity 100.
Matches 5; Conservative
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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HYPOTHETICAL: NO
HATI-SENSE: NO
US-08-241-853-29
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APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 2; Length 745;
Pred. No. 3.7e+02;
                                                                                                  Length 745;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
                                                                                                Score 36; DB 2; Le
Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEPHONE: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-890-853-4
; Sequence 4, Application US/08890853
; Patent No. 5851812
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09023321; Patent No. 5844073
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Best Local Similarity 100.00
Conservative
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    single
                                    MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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Best Local Similarity
Matches 5; Conserv
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STRANDEDNESS:
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                                               ; MOLECULE T)
US-08-887-518-3
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US-09-023-321-3
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                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PLILING DATE: 1999-02-18
PRIOR PLILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21704
LENGTH: 462
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Patent No. 5843721
GENERAL INPORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Le...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 STATE: SAN FRANCISCO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.0%; Score 36; DB 100.0%; Pred. No. 2.3
                                                                                                                                                       Sequence 21704, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21704
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TELECOMMUNICATION INFORMATION
TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   745 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 DWSWA 173
                                                           19 LDWSW 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 DWSWA 6
                    LDWSW 5
                                                                                                                                       US-09-252-991A-21704
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Sequence 4. Application US/09099125A
Patent No. 5916760
GENERAL INFORMATION:
PAPPLICANT: Gooddel, David V.
APPLICANT: Gooddel, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 90.0%; Score 36; DB 2; Length 745; Best Local Similarity 100.0%; Pred. No. 3.7e+02; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE STATEMENT Release #1.0, Version #1.30 CURRETT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,125A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.0%; Score 36; DB 2; L 100.0%; Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Prec. ... 0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                        REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMNUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEPHONE: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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US-09-099-125A-4
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...rulCANT: Woronicz, John
TITLE OF INVENTION: IKK-Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP.
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Sequence 10. 5854003
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Roche, Mike
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: SAN FRANCISCO
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.0%; Score 36; DB 2; Length 745; 100.0%; Pred. No. 3.7e+02;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/032,475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
PLILCATION NUMBER: US/08/890,853
FILING DATE:
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ATTORNEY/AGENT INPORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,518
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 100.1
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         738 LDWSW 742
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Gaps

||||| 738 LDWSW 742

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US-00-09-124A-4

1 GENERAL INCORMATION:

SEQUENCE 4, Application US/09099124A

PEREIN NO. 2999902

SEQUENCE 4, Application US/09099124A

PEREIN COMMENT:

MAPLICANT: GOACHEL David V.

APPLICANT: GOACHEL David V.

APPLICANT: GOACHEL David V.

APPLICANT: GOACHER S.

CORRESPONDENCE ADDRESS:

ADDRESSEB: CLEMENT E TECHNOLOGY LAW GROUP

STREET: 26 BUSH STREET; SUITE 3200

STREET: 26 BUSH STREET; SUITE 3200

STREET: 26 BUSH STREET; SUITE 3200

STREET: 26 BUSH STREET; SUITE 3200

STREET: 26 BUSH STREET; SUITE 3200

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STREET: 26 BUSH STREET; SUITE 3200

STREET: 26 BUSH STREET; SUITE 3200

STREET: 26 BUSH STREET; SUITE 3200

STREET: 26 BUSH STREET; SUITE 3200

STREET: 1000 MUSH STREET; SUITE 3200

CURRENT APPLICATION DATE: US/09/099, 124A

FILING DATE: US/09/099, 124A

FILING DATE: US/09/099, 124A

PRICE APPLICATION DATE: US/09/099, 853

FILING DATE: US/09/0990, 853

FILING DATE: US/09/0990, 853

FILING DATE: US/09/0990, 853

FILING DATE: US/09/0990, 853

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FILING DATE: US/09/0990, 853

FILING DATE: US/09/0990, 853

FILING DATE: US/09/0990, 853

FILING DATE: US
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Query Match 90.0%; Score 36; DB 2; Length 745; Best Local Similarity 100.0%; Pred. No. 3.7e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gap

Oy 1 LDWSW 5

||||| 738 LDWSW 742 Search completed: February 18, 2004, 14:41:46 Job time : 7.06579 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

February 18, 2004, 13:37:19; Search time 22.7763 Seconds (without alignments) 41.814 Million cell updates/sec Run on:

US-09-643-260-5 40 1 LDWSWA 6 Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1107863 segs, 158726573 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A Geneseq 19Jun03:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA1981.DAT:*
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| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseqf/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	 Mutated IKKbeta NE	NBD mutant peptide	Anti-inflammatory	Anti-inflammatory	Human NEMO binding	Anti-inflammatory	Anti-inflammatory	Anti-inflammatory	Anti-inflammatory
		ID	ABB08728	AAM48510	AAM48537	AAM48559	ABU08421	AAM48563	AAM48556	AAM48564	AAM48555
			23	23	23	23	24	23	23	23	23
		Match Length DB	 ø	9	9	9	9	7	œ	80	6
de	Query	-	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
		Score	40	40	40	40	40	40	40	40	40
	Result	No.	-	7	m		S	9	7	Φ	6

		Anti-inflammatory	Anti-inflammatory	Anti-inflammatory	Anti-inflammatory	Human IKKalpha mut	Human IKKbeta muta	IKKbeta NEMO bindi	Anti-inflammatory	Anti-inflammatory	Anti-inflammatory		NEMO	Anti-inflammatory	Anti-inflammatory	Anti-inflammatory	Anti-inflammatory	Anti-inflammatory	Anti-inflammatory	IKK-alpha polypept	Anti-inflammatory	Anti-inflammatory				Anti-inflammatory	Anti-inflammatory	Anti-inflammatory	IKKbeta NEMO bindi	Anti-inflammatory	Anti-inflammatory	-inf		ద	Human IKKbeta pept
AAM48558		AAM48562	AAM48554	AAM48557	AAM48560	ABB77292	ABB77309	ABB08725	AAM48530	AAM48538	AAM48570	AAM48655	ABU08418	AAM48534	AAM48574	AAM48527	AAM48535	AAM48567	AAM48575	AAW96182	AAM48526	352	AAM48532	AAM48533	356	AAM48569	AAM48572	AAM48573	ABB77313	AAM48528	AAM48531	AAM48568	AAM48571	33	AAM48506
23	23	23	23	23	23	23	23	23	23	23	23	23	24	23	23	23	23	23	23	20	23	23	23	23	23	23	23	53	23	23	23	23	23	23	23
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0.0	100.0	0.0	100.0	0.0	9	0.0	0.00	0.0	0.0	90.06	0.0	0.0	90.0	90.0											0.06				•						
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40			40																						36										
10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

ABB08728 standard; peptide; 6 AA. ABB08728; RESULT 1 ABB08728 

(first entry) 14-JUN-2002

Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 5.

kinase activation; leukocyte; inflammation; E-selectin; offeoclast; autoimmune disease; transplant rejection; osteoporosis; cancer; Alzheimer; disease; transplant rejection; osteoporosis; cancer; rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV, corticosteroid; immunosuppression; antiinflammatory; immunosuppressive; osteopathic; cytostatic; nootropic, neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antiasthmatic; antiallergic; dermacological; antibacterial; antibacterial; antibacterial; antibacterial; mutein. IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;

Homo sapiens.

Synthetic.

/note= "Wildtype Leu substituted by Ala" Location/Qualifiers Misc-difference

WO200183547-A2

08-NOV-2001

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antirheumatic; antiarthritis; osteopathic; antibacterial; virucide; immunosuppressive; dermarclogical; neuroprotective; antiarherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteopprossis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Page 47; 88pp; English.
                                                                                                                                                                                                                                                                                                                     02-MAY-2001; 2001WO-US14346.
                                                                                                                                                                                                                                                                                                                                                        02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.
                                                                                                                                                                                                                                                                                                                                                                                                              (PRAE-) PRAECIS PHARM INC. (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-121889/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ghosh S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDWSWA
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                                                                                                                                                                                                                                             WO200183554-A2
                                                                                                                                                                                                                                                                                  08-NOV-2001.
                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arthritis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         May MJ,
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AAM48537
ID AAM4
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                                                                                                                                                                                                                                                                                                                           The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB08725-ABB08725) and some comprises contacting a cell with an anti-inflammatory compound (ABB08725-ABB08725) comprising at least one NRMO binding domain (ABB77313). The compound has acts through selective inhibition of cytokine-mediated NF-kB activation by blocking the interaction of NEMO with IXXDeta at the NRMO binding domain. Blockage of IXXDeta-NEMO interaction results in inhibition of IXADPAB. The compound may also act (directly) or indirectly) by blocking the recruitment of leukocytes into sites of acute and chronic inflammation. The compound may also act (directly or indirectly) by blocking the recruitment of leukocytes into sites of acute and chronic inflammation, by down-regulating the expression of E-selectin on neukocytes or by blocking osteoclast (differentiation. The compound is useful in treating osteoclast conditions, where the condition is an inflammatory disorder, an autoimmune disease, transplant rejection, osteoporosis, cancer, Alzheimer's disease, atherosclerosis, a viral infection or ataxia telangiectasia. The inflammatory disorder is asthma, allergies, creaming anaphylaxis, cutaneous inflammation, seppsis, psoriasis, osteoarthritis, psoriatic arthritis, lugus and bursitis. The inflammatory disorder may also be dermatitis, eczema, psoniasis, osteoarthritis, psoriatic arthritis, lugus and cursed by Epstein-barr, cytomegalovirus or herpes simplex, other viral infections crawsed by Epstein-barr, cytomegalovirus or herpes simplex, other viral constending anaphylaxis, drug and food sensitivity, contact dermatitis, and any application in which cormound may be used to replace corticosteroids in any application in which corticosteroids are used, including marrial and incompound may be used to replace corticosteroids in minimatory discreaming anaphylaxis and some and conservations of immunosuppression in university and decompound may as a second of immunosuppres
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                                                                                                                                                                                                                           ď
                                                                                                                                                                                                      Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting cell with an anti-inflammatory compound comprising at least one NEMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                   Claim 23; Page 44; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM48510 standard; Peptide; 6 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NBD mutant peptide SEQ ID NO 5.
02-MAY-2001; 2001WO-US40654.
                                    02-MAY-2000; 2000US-201261P
                                                      22-AUG-2000; 2000US-0643260
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                                                                                                                                                                   WPI; 2002-179350/23
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Best Local Similarity
Matches 6; Conserv
                                                                                           (UYYA ) UNIV YALE.
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                                                                                                                              May MJ, Ghosh S;
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                                                                                                                                                                                                                                                              binding domain
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 XXXXXX
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Phillips K;

Findeis MA,

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The invention relates to an antiinflammatory compound (especially AAM48645), comprising a membrane translocation domain (AAM48620-AAM48645), comprising a membrane translocation domain (AAM48620-or AAM48645) which comprises from 6-15 amino acid residues, fused to a NEWO binding sequence (AAM48619). The antiinflammatory compounds have antiasthmatic, artipacterial, immunosuppressive, dermatological, neuroprotective, antibacterial, immunosuppressive, dermatological, neuroprotective, antiatherosolerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKDeta) at the NEWO binding domain that results in inhibition of IKADpaB. The activation and subsequent decreased phosphorylation of IKADpaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoporosis, multiple solerosis, transplant rejection, osteoporosis, plubing and president rejection, and stavia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alzheimer's disease, atherosclerosis, viral infections, and ataxia telangiectasia. The compounds are also useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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100.0%; Pred. No. 9.3e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM48537 standard; Peptide; 6 AA.
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Best Local Similarity
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Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclarotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.

Anti-inflammatory peptide SEQ ID NO 62.

(first entry)

20-MAR-2002

AAM48559;

AAM48559 standard; Peptide; 6 AA

RESULT 4

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Sequence 6 AA;
                          WO200183554-A2.
    20-MAR-2002
                             08-NOV-2001
                       Synthetic.
                                                                                        arthritis.
                                                     psoriasis
 AAM48537;
                                           May MJ,
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The invention relates to an antiinflammatory compound (especially AAM48645), comprising a membrane translocation domain (AAM48620-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48645), shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall shall
                                                                                                                                                                                                                                                                  Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dertantological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEWO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; heumatold arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phillips K;
                                                                                                                                            Anti-inflammatory peptide SEQ ID NO 40.
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(first entry)
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Findeis MA, Phillips K;

May MJ, Ghosh S, (UYYA ) UNIV YALE.

(PRAE-) PRAECIS PHARM INC.

02-MAY-2001; 2001WO-US14346. 02-MAY-2000; 2000US-201261P.

WO200183554-A2. 08-NOV-2001.

Synthetic.

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AMM48620-AMM48645), comprising a membrane translocation domain (AAM48620-AMM48645), comprising a membrane translocation domain (AAM48620-AMM48645), comprising a membrane translocation domain acid residues, fused to a NEWO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, ortostatic, antiathrematic, antiathremator, compounds have antiasthmatic, antiathremscleroric, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NEKappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreaced phosphorylation of IKAppaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzehimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating end cancer, provinflammatory responses such as allergies, urticaria, anaphylaxis, carbeits, arthritis, infections; and ataxia telangiectasia. The compounds are also useful for treating and criminatory responses such as allergies, urticaria, anaphylaxis, arthritis, infection, dermatitis, sumburn, aging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an antiinflammatory compound (especially
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-121889/16.
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Gaps ö

100.0%; Score 40; DB 23; Length 6; 100.0%; Pred. No. 9.3e+05; Live 0; Mismatches 0; Indels

Conservative

Query Match Best Local Similarity Matches 6; Conserv

LDWSWA 6

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                                                                                                                                                                                                                                                                                                                                                          Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta; IkappaB kinaee-abeta; IkappaB kinaee-alpha; IKKalpha; NF-kappaB; nuclear factor-kappaB induction; inflammatory disorder; autoimmune disease; osteoporosis; cancer; Alzheimer's disease; atheroselerosis; viral infection; Ataxia telangiscteasis; transplantation detection; immunosuppressie; osteopathic; cytostatic; nootropic; neuroprotective; antiatheroselerotic; virucide;
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammatory disorders, autoimmune diseases, osteoporosis, cancer, Alzheimer's disease, atherosclerosis, viral infections, Ataxia telangiectasia, and for transplantation detection. The compounds of the invention block NF-kappaB induction by IKK but do not inhibit the basal activity of NF-kappaB. ABU08418-ABU08432 represent human NBD mutant peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel antiinflammatory peptide compounds comprising NEMO binding domain, useful for modulating NF-kappaB induction in a cell and for treating NF-kappaB-mediated inflammation disorders e.g., asthma, psoriasis, vasculitis -
                                        ö
 Length 6;
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vasotropic; antirheumatic; antiarthritic; mutant; mutein
                                        0
100.0%; Score 40; DB 23;
Similarity 100.0%; Pred. No. 9.3e+05;
6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                         Human NEMO binding site (NBD) mutant peptide #4.
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                                                                                                                                                                                                          ABU08421 standard; peptide; 6 AA.
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22-AUG-2000; 2000US-0643260.
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 Query Match
Best Local Similarity
Matches 6; Conserv
                                                                           1 LDWSWA 6
                                                                                                            LDWSWA 6
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100.0%; Score 40; DB 24; Length 6;

6 AA;

Query Match

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The invention relates to an antiinflammatory compound (especially AMM48628-AMM48645), comprising a membrane translocation domain (AMM48628-AMM48645), comprising a membrane translocation domain (AMM48628-AMM48619). The antiinflammatory compounds have antisthmatic, cytostatic, antipostriatic, antiheratic, dermatological, neuroprotective, cytostatic, antipostriatic, antiheratic, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking intracaction of IkappaB kinase beta (IKkbeta) at the NEWO binding domain that results in inhibition of IKkbeta kinase activation and subsequent decreased phosphorylation of IKkbeta kinase activation and subsequent decreased phosphorylation of IkkpeB The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoparthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, presimitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, prelimer's disease, atherosclerosis; transplant rejection; osteoporosis; Alzheimer's disease, atherosclerosis; varallifections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
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                                                                                                                                                                                                                                                                                                                                                                                            Antiinflammatory, antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEWO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKCbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
                                         Gaps
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                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ataxia telangiectasia, allergy, anaphylaxis, arthritis
                                       0
                 Pred. No. 9.3e+05;
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                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                           Anti-inflammatory peptide SEQ ID NO 66.
100.08; Pre-
                                                                                                                                                                                                                                 AAM48563 standard; Peptide; 7 AA.
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                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                        Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
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drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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                                                                                       Indels
                                                             100.0%; Score 40; DB 23;
100.0%; Pred. No. 9.3e+05;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                 Anti-inflammatory peptide SEQ ID NO 59.
                                                                                                                                                                                                      AAM48556 standard; Peptide; 8 AA.
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22-AUG-2000; 2000US-0643260.
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                                                                         Similarity
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                                    7 AA;
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                           bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosels; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis.
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sepsis, vasculitis,
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100.0%; Pred. No. 9.3e+05;
ive 0; Mismatches 0;
inflammatory bowel disease,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM48564 standard; Peptide; 8 AA.
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compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriacis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vascultis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis, transplant rejection; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
                                                                                                                                                                   Alzheimer's disease, atherosclerosis, viral infections, and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain

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'C' optostatic, antipsoriatic, antitathritic, osteopathic, antipsoriatic, antitathritic, osteopathic, antipsoriatic, antitathresolerotic, antitathresolerotic, variode and antiallerotic activity. The noctropic, antiatherosolerotic, variode and antiallerotic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NRMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IKKbeta kinase compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoparathritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, pursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, canulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's diseases, atherososlerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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(AAM48620-AMM48627 or AAM40010 AND binding sequence amino acid residues, fused to a NEWO binding sequence (AAM48525-AAM40619). The antiinflammatory compounds have antiasthmatic, (AAM48525-AAM40619) antiinflammatic, antiarthritic, osteopathic,
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WPI; 2002-121889/16.
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                                                                                                             psoriasis
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                                                                                                              anthon acid residues, fused to a NEMO binding sequence
(AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
cytostatic, antipsoritatic, antirheumatic, antiarthritic, osteopathic,
cytostatic, antipsoritatic, antirheumatic, antiarthritic, osteopathic,
antibacterial, immunosuppressive, dermatological, neuroprotective,
compounds act as selective inhibitors of cytokine-mediated NFkappaB
activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
the NEMO binding domain that results in inhibition of IKKpeta kinase
activation and subsequent decreased phosphorylation of IKKpeta B The
compounds are useful for treating inflammatory disorders, e.g. asthma,
lung inflammation or cancer, bowel disease, sepsis, vasculitis,
osteoparthritis, inflammacory bowel disease, sepsis, vasculitis,
bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
granulomatosis, multiple sclerosis; transplant rejection; osteoporosis,
colangicctasis, and tiple sclerosis; viral infections; and ataxia
telangicctasia. The compounds are also useful for treating
pro-inflammatory responses such as allergies, unburn, aging and
contractive; and contractive and anticomer contractive and anaphylaxis,
contractive and anticomer and an anaphylaxis,
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contractive and an anticomer and an anaphylaxis,
contractive and an anticomer and an anaphylaxis,
contractive and an anticomer and an anaphylaxis,
contractive and an anticomer and an anaphylaxis, and anaphylaxis,
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                                                                                     AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
                                                                      invention relates to an antiinflammatory compound (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 40; DB 23; Length 9; 100.0%; Pred. No. 9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ataxia telangiectasia; allergy; anaphylaxis; arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-inflammatory peptide SEQ ID NO 64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM48561 standard; Peptide; 9 AA.
                                   Claim 6; Page 62; 88pp; English.
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22-AUG-2000; 2000US-0643260.
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psoriasis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
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The invention relates to an antiinflammatory compound (especially AAM48629-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48620). CAM48665-AAM48651) which comprises from 6-15 (AAM48620-AAM48620). The AAM48651 which comprises from 6-15 (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, antibacterial, immunosuppressive, dermatological, neuroprotective, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappas compounds act as selective inhibitors of cytokine-mediated NFkappas activation by blocking interaction of Ikappas kinase beta (IKKObeta kinase activation and subsequent decreased phosphorylation of Ikappas. The compounds are useful for treating inflammatory disorders, e.g. asthma, ung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, bursitis; autoimmune diseases such as lupus, polymyalgia, and ataxia telangist and sisease; attaing inflammatory inflammatory inflammatory and ataxia and analysis, and ataxia telangist and alsease; attaingist are also useful for treating and ataxia
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Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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Similarity 100.0%; Score 40; DB 23;
Similarity 100.0%; Pred. No. 9.3e+05;
6; Conservative 0; Mismatchem n.
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                                                                                                                                                                                                                                                    Claim 6; Page 62; 88pp; English.
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Best Local Similarity
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Phillips K;

Findeis MA,

Ghosh S,

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02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260.
                                                                            02-MAY-2001; 2001WO-US14346.
                                                                                                                                                                                                        (PRAE-) PRAECIS PHARM INC.
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                          08-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                             AAM48628-AAM48645), comprising a membrane translocation domain

(AAM48620-AAM48645), comprising a membrane translocation domain

(AAM48620-AAM48619). The antiinflammatory comprises from 6-15

amino acid residues, fused to a NEWO binding sequence

(AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,

cytostatic, antipsoriatic, antirheumatic, antiarrbritic, osteopathic,

antibacterial, immunosuppressive, dermatological, neuroprotective,

nootropic, antiatherosclerotic, virucide and antiallergic activity. The

compounds act as selective inhibitors of cytokine-mediated NFkappaB

cotivation by blocking interaction of IkappaB kinase beta (IKKota Minase

ctivation and subsequent decreased phosphorylation of IkappaB. The

activation and subsequent decreased phosphorylation of IkappaB. The

compounds are useful for treating inflammatory disorders, e.g. asthma,

lung inflammation or cancer, psorlasis, rheumatoid arthritis,

osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,

chursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,

granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;

Alzheimer's disease; atherosclerosis; viral infections; and ataxia
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                                                                                                                                                                                                                                                       domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                             Novel antiinflammatory compound comprising membrane translocation
                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to an antiinflammatory compound (especially
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      telangiectasia. The compounds are also useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 40; DB 23; Length 9; 100.0%; Pred. No. 9.3e+05; ive 0; Mismatches 0; Indels
                                                                                                                           Ghosh S, Findeis MA, Phillips K;
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                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 62; 88pp; English.
22-AUG-2000; 2000US-0643260.
                                               (PRAE-) PRAECIS PHARM INC. (UYYA ) UNIV YALE.
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                           WPI; 2002-121889/16.
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The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48629-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48620-AAM48645), which comprises from 6-15 amino acid residues, fused to a NEWO binding sequence (AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarchritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antialherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of Cytokine-mediated NFKappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammation of IkappaB. The activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammation of IkappaB. The activation or cancer, psoriasis, rheumatoid arthritis, unginamatory bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, bursitisher, a disease, atheroselerosis, transplant rejection; osteoporosis; telangiectaia. The compounds are also useful for treating and ataxia and ataxia.
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Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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                                                                                                                                                                                             Claim 6; Page 62; 88pp; English.
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                                                                                                                                                                                                                                                                                                                                             Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
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osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
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                                                                                                                                                                                                                                                                               Ghosh S, Findeis MA,
                                                                                                                                                                             02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
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The invention relates to an antiinflammatory compound (especially AAM48629-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48645), comprising a membrane translocation domain and a selectives fused to a NEMO binding sequence (AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antiporiatic, antihemmatory compounds have antiasthmatic, antiboterial, antihemosuppressive, virucide and antiallergic activity. The contropic, antiatherosclerotic, virucide and antiallergic activity. The contropic, antiatherosclerotic, virucide and antiallergic activity. The contropic, antiatherosclerotic, virucide and antiallergic activity. The contropic, antiatherosclerotic, virucide and antiallergic activity. The contropic antiatherosclerotic, virucide and antiallergic activity. The compounds are useful for treating inflammation of IxkOpea kinase activation and subsequent decreased phosphorylation of IxkOpea kinase activation and subsequent decreased phosphorylation of Ixeopas. The compounds are useful for treating inflammation of arthritis, unginal antial activities, inflammatory bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, bursitis; autoimmune diseases such as lupus, polymyalgia, and ataxia transplaner's disease; atherosclerosis; viral infections; and ataxia telegation controller and also are also useful for treating controllers.
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antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallegic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autofimune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
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22-AUG-2000; 2000US-0643260.
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N	40	100.0	9	23	AAM48509	NBD mutant peptide
٣	40	100.0	9	23	AAM48536	Anti-inflammatory
4	40	100.0	9	23	AAM48548	Anti-inflammatory
S	40	100.0	φ	24	ABU08420	Human NEMO binding
9	40	100.0	7	23	AAM48552	Anti-inflammatory
7	40	100.0	8	23	AAM48545	Anti-inflammatory
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antirheumatic; antiarthritis; osteopathic; antibacterial; virucide; immunosuppressive; dermarological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telanglectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
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                                                                                                                                                                                                                                                                                                              Synthetic.
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  The invention relates to modulating NF-kappaB (NF-kB) induction in a cell comprises contacting a cell with an anti-inflammatory compound (ABB077313). The comprising at least one NEWO binding domain (ABB077313). The compound has acts through selective inhibition of KAB077313). The compound has acts through selective inhibition of Cytokine-mediated NF-kB activation by blocking the interaction of NEWO control of IkappaB. The compound may also interaction results in inhibition of IkappaB. The compound may also control of acts of acute and chronic inflammation, by down-regulating the expression of B-selectin on leukocytes or by blocking osteoclast differentiation. The compound is useful in treating NF-kB mediated conditions, where the condition is an inflammatory disorder, an autoimmune disease, transplant rejection, osteoporosis, cancer, alternated arthritis, osteoarthritis, osteoporosis, psoriasis, cutaincaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis, cuticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis, crematicis, rhe inflammatory disease, vasculitis, inflammatory disease, vasculitis, cecema, psoriasis, osteoarthritis, osteoarthritis, psoriatic arthritis, ingus and chursitis, net inflammatory disease, ulcerative colitis, copolymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis, polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis, cryoglobulinaemia or multiple sclerosis. Por chronic viral infections cryoglobulinaemia or multiple sclerosis. Por chronic viral infections cryoglobulinaemia or multiple sclerosis. Por chronic viral infections cryoglobulinaemia or multiple sclerosis. Rocker or colitis, cutact dermatis, multiple sclerosis. Rocker or criticosteroids in diseases include HIV and influenza. The compound may also be useful for treating anaphylaxis, drug and food sensitivity, contact dermatisis, multiple collections created by particular or miliah contact dermaticies in multiple collections researched and sense or criticosteroids in minich contact de
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                                                                                                                                                                                                                                                                                                     Modulating NF-kappaB induction in a cell, useful for treating e.g. inflammatory disorders, osteoporosis and cancer, comprises contacting a cell with an anti-inflammatory compound comprising at least one NEMO
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02-MAY-2001; 2001WO-US40654.
                                                    02-MAY-2000; 2000US-201261P.
22-AUG-2000; 2000US-0643260.
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Phillips K;

Findeis MA,

Ghosh S,

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The invention relates to an antiinflammatory compound (especially AAM48629-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEWO binding sequence (AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipporiatic, antiinflammatory compounds have antiasthmatic, antibacterial, immunosuppressive, dermatological, neuroprotective, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosolerotic, virucide and antiallargic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkAppaB kinase beta (IKKbeta kinase activation and subsequent decreased phosphorylation of IkKbeta kinase activation and subsequent decreased phosphorylation of IkAppaB. The compounds are useful for treating inflammatory disorders, e.g. asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatcry bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis, transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia relangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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AAM48509 standard; Peptide; 6 AA

RESULT 2 AAM48509

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NBD mutant peptide SEQ ID NO 4.

20-MAR-2002 (first entry)

AAM48509;

EXEXEX B

AAM48548 standard; Peptide; 6 AA.

RESULT 4 AAM48548

(first entry)

20-MAR-2002

AAM48548;

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The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48621) without comprises from 6-15 (AAM48620-AAM48621). The AAM48651 which comprises from 6-15 (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antisheuratic, antiasthatic, osteopathic, cytostatic, antipsoriatic, antisheuratic, antiasthatic, osteopathic, contoured, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB compounds are as ealective inhibitors of cytokine-mediated NFkappaB cetivation by blocking interaction of IkappaB kinase beta (IKKbeta kinase activation and subsequent decreased phosphorylation of IKKappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, poorlasis, rheumatoid arthritis, osteoporosis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis, transplant rejection; osteoporosis, labeniar's diseases atherosclerosis, viral infections, osteoporosis, arthritis, conflammatory responses such as lupus, polymyalgia, scleroderma, clansfermer's diseases atherosclerosis, viral infections, osteoporosis, arthritis, anticlammatory responses such as allergies, urticaria, anaphylaxis, arthritis, arthritis, anticlammatory responses such as allergies, urticaria, anaphylaxis, arthritis, arthritis, anticlammatory responses such as allergies, urticaria, anaphylaxis, arthritis, arthritis, anticlammatory decrease, dermatitis, sunburn, aging and
                                                                                                                                                                                                                                                                                     Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; anticheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; destactological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEWO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKWbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
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                                                                                                                                                                                                     Anti-inflammatory peptide SEQ ID NO 39.
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AAM48536;
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The Translation Feater Comprising a membrane translocation domain (APM48628-AAM48645), comprising a membrane translocation domain (APM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48619). The antinflammatory compounds have antisethmatic, ortostatic, antishermatic, immunosuppressive, dermatological, neuroprotective, nootropic, antishersoslerotic, virucide and antishlargic activity. The compounds act as selective inhibitors of cytokine-mediated NFKappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEW binding domain that results in inhibition of IKAppaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoperosis, transplant rejection; osteoporosis; bursitis; autoimmune diseases such as lugue, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzahaner's disease; atheroscalerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, arbitic; arbitichy, eczema, dermatitis, sunburn, aging and
                                                                                                                                Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclarotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Findeis MA, Phillips K;
                                                                                      Anti-inflammatory peptide SEQ ID NO 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 62; 88pp; English.
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22-AUG-2000; 2000US-0643260.
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6 AA;

Sequence

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Gaps ö

100.0%; Score 40; DB 23; Length 6; illarity 100.0%; Pred. No. 9.3e+05; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 6; Conserv

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The present invention relates to antiinflammatory compounds comprising NEMO binding domain (NBD) peptides. The NEMO binding domains are found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha are useful for modulating nuclear factor-kappaB (NF-kappaB) induction in a cell, where the compounds are capable of blocking the interaction between one or more IKKs such as IKKabipha or IKKbeta, and NEMO. The antiinflammatory compound further comprises at least one membrane inflammatory compound further comprises at least one membrane inflammatory disorders, autoimmune diseases, osteoporosis, cancer, alzheimer's disorders, autoimmune diseases, osteoporosis, cancer, alzheimer's disorders, autoimmune diseases, osteoporosis, cancer, telangiecteasia, and for transplantation detection. The compounds of the invention block NF-kappaB induction by IKK but do not inhibit the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
                                                                                                                                                                                                                                                                                                                                                                                                 IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB; muclear factor-kappaB induction; inflammatory disorder; autoimmune disease; osteoporosis; cancer; Alzheimer's disease; atherosclerosis; viral infection; Ataxia telangiectasia; transplantation detection; immunosuppressive, osteopathic; cytostatic; nootropic; neuroprotective; antiatherosclerotic; virucide; vasotropic; antirheumatic; antiatherosclerotic; virucide;
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    Length 6;
                                         Indels
100.0%; Score 40; DB 23;
100.0%; Pred. No. 9.3e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                        Human NEMO binding site (NBD) mutant peptide #3.
                                                                                                                                                                                                                     ABU08420 standard; peptide; 6 AA.
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                    Similarity 100.0%;
6, Conservative 0
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22-AUG-2000; 2000US-0643260.
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Best Local Similarity
Matches 6; Conserv
                                                                                1 ADWSWL 6
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100.0%; Score 40; DB 24; Length 6;

6 AA;

Sequence Query Match

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The invention relates to an antiinflammatory compound (especially AM48628-AM48645), comprising a membrane translocation domain (AM48620-AM48645), comprising a membrane translocation domain acid residues, tused to a NEWO binding sequence (AAM48625-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipostatic, antirheumatic, antiarthritc, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, oncropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine mediated NFkappaB activation by blocking interaction of IxappaB kinase beta (IXAppaB activation and subsequent decreased phosphorylation of IXAppaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, ung inflammation or cancer, psoriasis, rheumatoid arthritis, actorderma, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atheroscolerosis; viral infections; and ataxia telangiactasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
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                                    Gaps
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                                    Indels
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                No. 9.3e+05;
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                                Mismatches
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                  Pred.
100.08;
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                                    Conservative
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                       Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic; antirhumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antialergic; membrane translocation domain; NEWO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoprosis; Alzheimer's disease, atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
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drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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                                                               Length 7;
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                                                             100.0%; Score 40; DB 23;
100.0%; Pred. No. 9.3e+05;
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                                                                                                                                                                                                      AAM48545 standard; Peptide; 8 AA.
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Best Local Similarity
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                                                                                                               1 ADWSWL 6
                                     7 AA;
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             arthritis.
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osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, burstiis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis.
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factor kappaB activation, and for treating asthma, lung inflammation,
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100.0%; Pred. No. 9.3e+05;
ive 0; Mismatches 0;
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which comprises from 6-15

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compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEWO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatorid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, pranulomatosis, multiple sclerosis; transplant rejection; osteoporosis, Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, utricaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 40; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-inflammatory peptide SEQ ID NO 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM48544 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-2001; 2001WO-US14346.
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                                                                                                                                                                                                                                                                                     8 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ADWSWL
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Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,

Phillips K;

Findeis MA,

May MJ, Ghosh S,

WPI; 2002-121889/16.

The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain

Claim 6; Page 62; 88pp; English.

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Amino acid residues, fused to a NEMO binding sequence
(AAM486125-AAM48619). The antiinflammatory compounds have antiasthmatic,
cytostatic, antipsoriatic, antirheumatory compounds have antiasthmatic,
antibacterial, immunosuppressive, dermatological, neuroprotective,
compounds act as selective inhibitors of cytokine-mediated NFkappaB
compounds act as selective inhibitors of cytokine-mediated NFkappaB
compounds act as selective inhibitors of stokine-mediated NFkappaB
cotivation by blocking interaction of IkappaB kinase beta (IKKbeta kinase
compounds are useful for treating inflammatory disorders, e.g. asthma,
lung inflammation or cancer, psoriasis, rheumatoid arthritis,
compounds are useful for treating inflammatory disorders, e.g. asthma,
lung inflammation or cancer, psoriasis, rheumatoid arthritis,
costeoarthritis, inflammatory bowel disease, sepsis, vasculitis,
burstiis, autoimmune diseases such as lupus, polymyalgia, scleroderma,
granulomatosis, multiple sclerosis, transplant rejection; osteoporosis,
Alzheimer's disease; atherosclerosis, viral infections; and ataxia
telangiectasia. The compounds are also useful for treating
pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
archivettics, and the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of the secondary of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 40; DB 23; 100.0%; Pred. No. 9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-inflammatory peptide SEQ ID NO 50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ADWSWL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AA;
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02-MAY-2000; 2000US-201261P
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                                                                           The Invention relates to an autulation comprises to membrane translocation domain.

AMM48628-AAM48645), comprising a membrane translocation domain.

CAMM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
amino acid residues, fused to a NEMO binding sequence

(AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,

cytostatic, antiathematic, antiathematic, antiathritic, osteopathic,

antibacterial, immunosuppressive, dermatological, neuroprotective,

compounds act as selective inhibitors of cytokine-mediated NFkappaB

compounds act as selective inhibitors of cytokine-mediated NFkappaB

compounds are useful for treating inflammatory disorders, e.g. asthma,

compounds are useful for treating inflammatory disorders, e.g. asthma,

compounds are useful for treating inflammatory disorders, e.g. asthma,

compounds are useful for treating inflammatory disorders, e.g. asthma,

compounds are useful for treating inflammatory disorders, e.g. asthma,

compounds are useful for treating inflammatory disorders, e.g. asthma,

compounds are useful for treating inflammatory disorders, e.g. asthma,

compounds are useful for treating inflammatory disorders, e.g. asthma,

compounds are useful for treating inflammatory disorders, e.g. asthma,

contracting, inflammatory bowel disease, sepsis, vasculitis,

correcting multiple sclerosis, transplant rejection; osteoporosis;

conditionators, multiple sclerosis, irransplant rejection; osteoporosis;

conditionators and subsonses such as allergies, urticaria, anaphylaxis,

conditionators, and and a subsonses and a subsonse and a subsonses, and areasis,

conditionations, and a subsonses and a subsonses, and areasis,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                     The invention relates to an antiinflammatory compound (especially
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 40; DB 23; Length 9; 100.0%; Pred. No. 9.3e+05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-inflammatory peptide SEQ ID NO 53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM48550 standard; Peptide; 9 AA.
                                 Claim 6; Page 62; 88pp; English.
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22-AUG-2000; 2000US-0643260.
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1 ADWSWL 6
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psoriasis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
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The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48620). The AAM48645-1 which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence anio acid residues, fused to a NEMO binding sequence antibaterial, immunosuppressive, dermatological, neuroprotective, corpounds act as selective inhibitors of cytokine-mediated NEKappaB activation by blocking interaction of ItappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbpta kinase activation and subsequent decreased phosphorylation of IKKbpta kinase compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psortasis, rheumatoid arthitis, compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psortasis, rheumatoid arthitis, costeoarthitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; viral infections; and ataxia allosisctasia. The compounds are also useful for treating pro-inflammatory responses such as allorgies, urticaria, anaphylaxis, arthitis, anaphylaxis, dermatitis, sunburn, aging and
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                                                                            Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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100.0%; Pred. No. 9.3e+05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                   Claim 6; Page 62; 88pp; English.
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Best Local Similarity 100.00
Best Local Similarity 6; Conservative
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WPI; 2002-121889/16.
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                                                                                                                                                                                                           psoriasis
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Phillips K;

Findeis MA,

Ghosh S,

May MJ,

WPI; 2002-121889/16.

02-MAY-2000; 2000US-201261P. 22-AUG-2000; 2000US-0643260. 02-MAY-2001; 2001WO-US14346.

08-NOV-2001.

(PRAE-) PRAECIS PHARM INC

(UYYA ) UNIV YALE.

Claim 6; Page 62; 88pp; English.

psoriasis

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Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
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                                                                                                                                                                                                                                                                                                              AMM48620-AMM48645), comprising a membrane translocation domain.

(AAM48620-AMM48645), comprising a membrane translocation domain.

(AAM48620-AMM48645), romprising a membrane translocation domain.

(AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antiabectaria, antiinflammatory compounds have antiasthmatic, antibacterial, immunosuppressive, dermatological, neuroprotective, ontopic, antiathersolatoric, virucide and antiallargic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta kinase activation and subsequent decreased phosphorylation of IKKpeta kinase activation and subsequent decreased phosphorylation of IKKpeta kinase compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, costeoarthritis, inflammatory bowel disease, sepsis, vasculitis, costeoarthritis, inflammatory bowel disease, sepsis, vasculitis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and
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                                                                                                                                                                    Novel antiinflammatory compound comprising membrane translocation
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100.0%; Score 40; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                             Phillips K;
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                                                                                                                                                                                                                                                               Claim 6; Page 62; 88pp; English.
                                                                                             May MJ, Ghosh S, Findeis MA,
22-AUG-2000; 2000US-0643260.
                                    (PRAE-) PRAECIS PHARM INC. (UYYA ) UNIV YALE.
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CAMM48525-AAM48619). The antinflammatory compounds have antiasthmatic, cytostatic, antiporalatic, antinheumatic, antiarheumatic, conformation antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB compounds act as selective inhibitors of cytokine-mediated NFkappaB cutivation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEWO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, cy granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating
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WO200183554-A2

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AMM48620-AMM48645), comprising a membrane translocation domain AMM48620-AMM48645), comprising a membrane translocation domain (AAM48620-AAM48645), comprising a membrane translocation domain ammediate a missing sequence from 6-15 amino acid residues, fuesd to a NEWO binding sequence (AAM4825-AAM48619). The antiinflammatory compounds have antisthmatic, osteopathic, antipaterial, immunosuppressive, dermatological, neuroprotective, nootropic, antistherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB contivation by blocking interaction of fkappaB kinase beta (IKKbeta) at the NEWO binding domain that results in inhibition of IKAppaB. The activation and subsequent decreased phosphorylation of IKAppaB. The compounds are useful for treating inflammatoin of IKAppaB. The compounds are useful for treating inflammatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, burstitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, continuations of disease, alberosclerosis, viral infections, and ataxia at the antipal are also useful for treating continuations of actoporosis; continuations of a sease, and ataxia and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and a sease and sease and sease and sease and sease and sease and sease and sease and sease and sease and sease and sease and s
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osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
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AMM 86620-AMM 8645), comprising a membrane translocation domain (AMM 8620-AMM 8645), comprising a membrane translocation domain (AMM 8620-AMM 8645), comprising a mino acid residues, fused to a NEWO binding sequence amino acid residues, fused to a NEWO binding sequence (AAMM 8620-AMM 8619). The antiinflammatory compounds have antiasthmatic, antipactatic, antipactatic, antipactatic, antipactatic, antiablersocleroric, virucide and antiallergic activity. The compounds act as selective inhibitors of Cycokine-mediated NEKappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta kinase compounds are useful for treating inflammatory disorders, e.g. asthma, lum inflammation of ikappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lum inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatomis, multiple sclerosis; transplant rejection; osteoporosis; clanagiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticating, and ataxia pro-inflammatory responses such as allergies, urticating and ataxia, and controlled activity, eczema, dermatitis, annburn, aging and
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              immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergelve; dembrane translocation domain; NEWO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autofmmune disorder; multiple sclerosis; transplant rejection; osteooporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 18, 2004, 13:39:39; Search time 16.5789 Seconds (without alignments) 79.423 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-643-260-19 148 1 DRQIKIWFQNRRMKWKKTALDASALQTE 28

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .; NAS.
                                                                                                                                                                         MEDLINE=85024858; PubMed=6091895;
Levine M., Rubin G.M., Tjian R.;
"Human DNA sequences homologous to a protein coding region conserved
between homocitic genes of Drosophila.";
Cell 38:667-673(1984).
-!- FUNCTION: SEQUENCE-SEPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
                                                                            Shen W.-F., Largman C., Lowney P., Corral J.C., Detmer K.,
Hauser C.A., Simonitch T.A., Hack F.M., Lawrence H.J.;
"Lineage-restricted expression of homeobox-containing genes in human
hematopoletic cell lines."
Proc. Natl. Acad. Sci. U.S.A. 86:8536-8540(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 142961; ---
GO; GO:0005634; C:nucleus; NAS.
GO; GO:0005634; C:nucleus; NAS.
GO; GO:0003700; F:transcription factor activity; NAS.
GO; GO:0006355; P:determination of anterior/posterior axis, e...
GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
InterPro; IPR001356; Homeobox.
PEAM; PR00045; Antennapedia.
PRINTS; PR00025; ANTENNAPEDIA.
PRINTS; PR00025; ANTENNAPEDIA.
PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox.
ProDom; PD000010; Homeobox.
ProDom; PN000399; HOX; 1.
 'Generation and initial analysis of more than 15,000 full-length
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PROSITE; PS00032; ANTENNAPEDIA; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
Homeobox; DNA-binding; Developmental protein; Nuclear protein; Transcription regulation; Alternative splicing.
Transcription regulation; Alternative RapePFIIDE.
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Name=2; Synonyms=HOmeobox-less;
IsoId=P17509-2; Sequence=VSP_002389; SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
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/FTId=VSP 002388.
Missing (In isoform 2).
/FTId=VSP_002389.
             human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                             PRELIMINARY SEQUENCE OF 136-240 FROM N.A.
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EMBL; K02571; -; NOT_ANNOTATED_CDS.
PIR; S26400; S26400.
HSSP; P02833; IHOM.
                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS:
                                                     SEQUENCE OF 135-224 FROM N.A.
MEDLINE-90046832; PubMed-2573064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJ270993; CAB65909.1; -. AF287967; AAG31552.1; -.
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TRANSFAC; T01732; -
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-!- SUBGELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX PAMILY.
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MEDLINE=88085193; PubMed=2891608;
Hart C.P., Fainsod A., Ruddle F.H.;
"Sequence analysis of the murine Hox-2.2, -2.3, and -2.4 homeo boxes:
evolutionary and structural comparisons.";
Genomics 1:182-195(1987).
                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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SEQUENCE OF 144-224 FROM N.A.
MEDLINE=88054465; PubMed=2290503;
Lonai P., Arman B., Czosnek H., Ruddle F.H., Blatt C.;
"New murine homeoboxes: structure, chromosomal assignment, and differential expression in adult erythropoiesis.";
DNA 6:409-418(1987).
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                                                                                                                                                                                               Score 103; DB 1; Length 224;
Pred. No. 1.2e-08;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91187672; PubMed=1672751;
Shen W.F., Detmer K., Simonitch-Eason T.A., Lawrence H.J.,
  HV -> QL (IN REF. 3 AND 4).
A -> R (IN REF. 1).
P -> R (IN REF. 1).
D -> A (IN REF. 1).
GR -> A (IN REF. 5).
W; D8F96AFAC893D878 CRC64;
     3 AND 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1989 (Rel. 10, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Homeobox protein Hox-B6 (Hox-2.2) (MH-22A). HOXB6 OR HOXE-6 OR HOX-2.2.
                                                                                                                                                                             224 AA
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25 HV
33 A
60 P
73 D
150 GR
25427 MW;
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Best Local Similarity 70.v.,
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21; Conservative
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MEDLINE=85188311; PubMed=2986010;
Colberg-Poley A.M., Voss S.D., Chowdhury K., Gruss P.;
Structural analysis of murine genes containing homoeo box sequences and their expression in embryonal carcinoma cells.";
Nature 314:713-718(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kessel M., Schulze F., Fibi M., Gruss P.; "Primary structure and nuclear localization of a murine homeodomain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 129-197 FROM N.A.
MEDLINE=87053860; PubMed=2877873;
Bareier G., Bucan M., Francke U., Colberg-Poley A.M., Gruss P.;
"Sequential expression of murine homeo box genes during F9 EC cell
differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO J. 5:2209-2215(1986).
-!- PUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parikh H., Shah S., Hilt D., Peterkofsky A., Independence and regulation of expression of the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                Probon, PROVOLIO, HOMEODOX; 1.
SMART; SMO0189; HOX; 1.
PROSITE; PS000127; HOMEOBOX 1; 1.
PROSITE; PS000127; HOMEOBOX 1; 1.
PROSITE; PS00017; HOMEOBOX 2; 1.
HOMEODOX; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                           67.6%; Score 100; DB 1; Length 105; 70.4%; Pred. No. 1.5e-08;
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91 105 GLU-RICH (ACIDIC).
105 AA; 12552 MW; 106ClDF938F2864B CRC64;
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-!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
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01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
HOXA7 OR HOXA-7 (Hox-1.1) (M6-12) (M6).
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1; Mismatches
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MEDLINE=87260976; PubMed=2885847;
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    InterPro; IPR001356; Homeobox.
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19; Conservative
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PRINTS; PR00024; HOMEOBOX
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Gene 154:237-242(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                    PERMY PRODUCE; ANTENNAPEDIA.
PRINTS; PRODUCS; ANTENNAPEDIA.
PRINTS; PRODUCS; ANTENNAPEDIA.
PRODUCT; PRODUCOUS, HOMEOBOX.
PROSITE; PSOU027; HOMEOBOX 1; 1.
PROSITE; PSOU032; ANTENNAPEDIA; 1.
PROSITE; PSOU032; ANTENNAPEDIA; 1.
PROSITE; PSOU032; ANTENNAPEDIA; 1.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.6%; Score 103; DB 1; Length 224; 70.0%; Pred. No. 1.2e-08; rive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 186 186 T -> P (IN REF. 3).
224 AA; 25310 MW; E8FCOBDEB57F5C3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1989 (Rel. 10, Created)
01-WAR-1989 (Rel. 10, Last sequence update)
08-FBB-2003 (Rel. 41, Last annotation update)
Homeobox protein Hox-A7 (Hox-1.1) (R5) (Fragment).
HOXA7 OR HOXA-7.
                                                                                                                                                                                                                                                                                                                                                                        ANTP-TYPE HEXAPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DRQIKIWFONRRMKWKKTA--LDASALQTE 28
                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLU.
T -> P (I
                                                                                                                                                                                                                                                                                                                                                                                               HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M16807; -; NOT_ANNOTATED_CDS.
PIR; A27471; A27471.
HSSP; P02833; 9ANT.
TRANSFAC; T01707; -.
InterPro; IPR001827; Antennapedia.
                EMBL; M18401; AAC27130.1; ALT SEQ.
EMBL; J03782; AAA37843.1; -.
                                                                          HSSP, PO2833, 1HOM.
TRANSFAC, T01733, -.
AGD, MGI:96187, Hoxb6.
InterPro; IPR001827, Antennapedia.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Sprague-Dawley;
MEDLINE=87277429; PubMed=2886401;
EMBL; X56459; CAA39834.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                          PIR; A31324; A31324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                             146
216
186
                                                                                                                                                                                                                                                                                                                                                                                             BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00032; ANTENNAPEDIA; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.6%; Score 100; DB 1; Length 229; 70.4%; Pred. No. 3.5e-08; ive 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-ARG.
ASP/GLU-RICH (HIGHLY ACIDIC)
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AG -> APA (IN REF. 1).
D36E6BD61D8D5C6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from Atlantic salmon.";
Gene 62:141-152(1988).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTP-TYPE HEXAPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Salmo by protein S12-A (Fragment)
Salmo salar (Atlantic salmon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DRQIKIWFQNRRMKWKKTALDASALQT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                      MGD; MGI:96179; Hoxa7.
InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAG
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                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00046; homeobox; 1.
PRINTS; PR00025; ANTENNAPEDIA.
PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25682 MW;
                                                                                                                                                       EMBL; M17192; AAA37833.1; -. EMBL; U15972; AAC52160.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                  PIR; A03314; A03314.
PIR; A28329; A28329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                           HSSP; P02833; 9ANT.
TRANSFAC; T01278; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8030;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA BIND
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P09636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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  SO THE THE THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB=Brythrocyte;
MEDLINE=90126373; PubMed=2575515;
Wedden S.E., Pang K., Eichele G.;
"Expression pattern of homeobox-containing genes during chick
                                                                                                                                                                                                                                                                                                         Score 99; DB 1; Length 75;
Pred. No. 1.5e-08;
                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                 FC02C3672F35475D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homeobox protein Hox-B6 (GHOX-2.2) (Fragment) HOXB6 OR GHOX-2.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 AA
                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH_lambrepressr.
                                                                                                                                                                                                                                                                                                                                                                                        1 DRQIKIWFQNRRMKWKKTALDASA 24
                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                       66.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X16847; CAA34744.1; -. HSSP; P02833; 1HOM.
                                                                                                                                                                                                                                                                 75 AA; 9330 MW;
EMBL; M18903; AAA49559.1;
PIR; IS1341; IS1341.
                                                                                                                                                                                                                                                                                                                                                    18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00046; homeobox;
                                          HSSP; P02833; 9ANT
                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHICK
                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P14839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
HXB6_CHICK
                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HXB6
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HXC6_BRARE

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                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE=20144096; PubMed=10677514;

Kim C.B., Ameniya C., Balley W., Kawasaki K., Mezey J., Miller W.,

Minoshima S., Shimizu N., Wagner G., Ruddle F.;

"Hox cluster genomics in the horn shark, Heterodontus francisci.";

Proc. Natl. Acad. Sci. U.S.A. 97.1655-1660(2000).

-I- FUNCTION: SEQUENCE-SPECIPIC TRANSCRIPTION PACTOR WHICH IS PART OF

A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH

SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS (BY
                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
Elasmobranchii, Galeomorphii, Heterodontoidea, Heterodontiformes,
Heterodontidae, Heterodontus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 96; DB 1; Lengun acc
Pred. No. 1.38-07;
....rehaa 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71B661AB78E064D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Nuclear (By similarity).
SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTP-TYPE HEXAPEPTIDE
                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 AA
                                                                                                                                                                  208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                         28
                                                1 DRQIKIWFQNRRMKWKKTALDASALQT 27
                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                            Heterodontus francisci (Horn shark)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE, PS00032; ANTENNAPEDIA; 1. PROSITE; PS00027; HOMEOBOX 1; 1. PROSITE; PS50071; HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSFAC; T04478; -.
InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF224262; AAF44645.1; -. HSSP; P02833; 9ANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PROGOS5; ANTENNAPEDIA.
PRINTS; PROGOS4; HOMEGBGX.
Probom; PDG00010; HOMEGBGX; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23786 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.9%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                    Homeobox protein Hox-A7.
                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00046; homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 AA;
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7792;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HXC6_XENLA
ID HXC6_XENLA
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SEQUENCE
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01-APR-1990 (Rel. 14, Last sequence update)
28-FBS-2003 (Rel. 41, Last annotation update)
HOMEOBOX Protein HOX-C6 (ZF-61) (Fragment).
HOXCG OR HOXCGA OR HOX-C6 OR ZF-61.
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI TAXID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Njoletad P.R., Molven A., Apold J., Fjose A.;
"The zebrafish homeobox gene hox-2.2: transcription unit, potential regulatory regions and in situ localization of transcripts.";
EMBO J. 9:515-524 (1990).
-!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OR DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
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PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; DNA-binding; Developmental protein; Nuclear protein; Transcription regulation.
Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 96.5; DB 1; Length 96;
Pred. No. 4.7e-08;
3; Mismatches 5; Indels
                                                                                                         , DB 1; Leas.
, 2.4e-08;
6; Indels
                                                             HOMEOBOX.
BC06B10165B19E71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMEOBOX.
FIED7AFAA3B640C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: Nuclear.
-1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                        Score 98; DB 1; Pred. No. 2.4e-2; Mismatches
                                                                                                                                                                                                        28
                                                                                                                                                                                                                                1 DRQIKIWFQNRRMKWKK--TALDASALQTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X17266; CAA35170.1; -. PIR; S06639; S08639. HSSP; PO2833; 9ANT. 2DB-GENE-990415-113; hoxc6a. InterPro; IPR001827; Antennapedia. InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Embryo;
MEDLINE=90151628; PubMed=1968004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
SWART; SM00389; HOX; 1.
                                                                                84 AA; 10279 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 AA; 11638 MW;
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69.0%;
                                                                                                                        66.2%;
                                                                                                                  Query Match
Best Local Similarity 66.7
Matches 20; Conservative
                   ranscription regulation.
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                                      NON TER
DNA BIND
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DNA BIND
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DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
                                                                                                                                                                                                                                                                                             SEQUENCE OF 121-234 FROM N.A.
MEDLINE=88157707; PubMed=2894634;
Fritz A., de Robertis E.M.;
"Xenopus homeobox-containing cDNAs expressed in early development.";
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=84205675; PubMed=6327066; Carrageo A.E., McGinnis W., Gehring W.J., de Robertis E.M.; Carrageo A.E., McGinnis W., Gehring W.J., de expressed during early embryogenesis "Cloning of an X. laevis gene expressed during early embryogenesis coding for a peptide region homologous to Drosophila homeotic
                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                        "Differential utilization of the same reading frame in a Xenopus homeobox gene encodes two related proteins sharing the same DNA-binding specificity."; EMBO J. 7:2135-2149(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE: EXPRESSED EXCLUSIVELY IN EARLY XENOPUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0025; ANTENNALEDIA.
PRINTS; PRO0024; HOMEOBOX.
Prodom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00032; ANTENNAREDIA; 1.
PROSITE; PS050071; HOMEOBOX 2; 1.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                   SEQUENCE FROM N.A. MEDING=2901347; MEDINE=88329002; PubMed=2901347; Cho K.W.Y. Goetz J., Wright C.V.E., Fritz A., Hardwicke J., de Robertis E.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMEOBOX PROTEIN HOX-C6 HOMEOBOX PROTEIN HOX-C6 ANTP-TYPE HEXAPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
           21-JUL-1986 (Rel. 01, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
HOMEODOX protein Hox-C6 (XIHbox-1) (ACl).
HOXC6 OR XLHBOX1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X12499; CAA31020.1; ALT_INIT.
EMBL; X12500; CAA31021.1; -.
EMBL; X01943; AAA49743.1; -.
EMBL; X07101; CAA30122.1; -.
PIR; S00992; S00992.
HSSP; P02833; 9AMT.
TRANSFAC; T01745; -.
TRANSFAC; T01745; -.
                                                                                 Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 16:1453-1469(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 134-200 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell 37:409-414(1984)
                                                                                                                                         NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

COSDY N.C., Hernandez-Ledezma J., Mathialagan N., Roberts R.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                    Gaps
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Ovis aries (Sheep).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                           Length 234;
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                                                                                                                                                                 4; Indels
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141 200 HOMEOBOX.
139 139 T -> S.
234 AA; 26689 MW; 4C371CC5252D2C58 CRC64;
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POLY-GLY.
GLU/LYS-RICH.
291E24399159621E CRC64;
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                                                                                                           Score 96; DB 1; I
Pred. No. 1.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                               153 AA
                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                   100 ERQIKIWFONRRMKWKKESNLTSTL 124
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InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
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86 89 POI
126 130 POI
139 153 GLI
153 AA; 17804 MW; 2
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PRINTS; PR00025; ANTENNAPEDIA.
PRINTS; PR00024; HOMEOBOX.
                                                                                                           64.9%;
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                                                                                                   Query Match
Best Local Similarity 72.0°
Matches 18, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription regulation.
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EMBL; X84804; CAA59270.1; JOINED
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Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,
Gaudino G., Stornaiuolo A., Cafiero M., Faiella A., Simeone A.;
"Organization of human class I homeobox genes.";
Genome 31:745-756(1989).
-!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION PACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSITERIOR AXIS.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A. MEDMEd=9804983; MEDIARE=99033755; Pubmed=9804983; MCINBACTON M.A., Bremmer P.S., McMullin M.F., Maxwell A.P., Winter P.C., Lappin T.R.; Sequence characterisation and expression of homeobox HOX A7 in the multi-potential erythroleukaemic cell line TF-1."; Biophys. Acta 1442:329-333(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20369265; PubMed=10911612; Kim W.H., Jih H., Seol B.Y., Yoo M., Park H.W.; Seol B.Y., Tso B., You M., Park H.W.; Sequence analysis and tissue specific expression of human HOXA7."; Mol. Biotechnol. 14:19-24(2000).
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bradshaw H., Hinds K., Keppler D.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                        Polakowska R., LaCelle P.T.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Placenta;
Albrechtsen R., Wewer U.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-91 FROM N.A.
Cho M., Kim M.H., Hwang C.Y., Min W.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                P31268; 043368; 043486; 095655; 09NSC8; 09UDM1; 01.-UUL-1993 (Rel. 26, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 28-FBB-2003 (Rel. 41, Last annotation update) HOMEODOX protein HOX-A7 (HOX-1A) (HOX 1.1).
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                                                                                                                                                                   Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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U92543; AAD00727.1; -. X84803; CAA59270.1; -.

EMBL; EMBL; EMBL;

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(Xhox) gene producte.";
EMBO J. 5:1237-1244 (1986).
-!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Fritz A., de Robertia E.M.;
"Xenopus homeobox-containing CDNAs expressed in early development.";
Nucleic Acids Res. 16:1453-1469(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 155-214 FROM N.A.
BEDLINESER74626, PubMed=3015593;
Harvey R.P., Tabin C.J., Melton D.A.;
"Embryonic expression and nuclear localization of Xenopus homeobox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                           PERINTS; PR00046; homeobox; 1.

PRINTS; PR00025; ANTENNAPEDIA.

PRINTS; PR00024; HOMEOBOX.

PRODOM; PD000010; Homeobox; 1.

SWART; SM00389; HOX; 1.

PROSITE; PS00032; ANTENNAPEDIA; 1.

PROSITE; PS00032; HOMEOBOX 1; 1.

PROSITE; PS50071; HOMEOBOX 2; 1.

HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein; Transcription regulation.

ANNER MANNER PROSECTION ANNER PROPERTINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                   ASP/GLU-RICH (HIGHLY ACIDIC).
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 64.2%; Score 95; DB 1; Length 23C
Local Similarity 81.0%; Pred. No. 2.1e-07;
1es 17; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I -> V (IN REF. 4).
PT -> RL (IN REF. 5).
T -> I (IN REF. 5).
D -> Y (IN REF. 5).
W; 6E2F1991F1BBED21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
28-FBB-2003 (Rel. 41, Last annocation update)
HOMEODOX protein HOX-B5 (XlHbox-4) (Xhox-1B) (Fragment).
HOXBS OR XLHBOX4.
PIR; $15536; $15536.
HSSP; P02833; 9ANT.
TRANSPAC; T1075; -..
MIM; 142950; -.
GO; GO: 0001700; F: transcription factor activity; TAS.
InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                      ANTP-TYPE HEXAPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                           T -> A (IN REF. 3).
DA -> RR (IN REF. 6).
MISSING (IN REF. 5).
I -> V (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 AA.
                                                                                                                                                                                                                                                                                                                                                                          POLY-ARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                         HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                           POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DRQIKIWFQNRRMKWKKTALD 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25385 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195
222
230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HXB5 XENLA
P09019;
                                                                                                                                                                                                                                                                                                                                                     DNA BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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-i- SUBCELLULAR LOCATION: Nuclear.
-i- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                             Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 72.0°
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                       TRANSFAC; T01747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOXCE OR HOX3C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HXC6_HUMAN
                                                                                                                                                                                                                                                                                                                                                                    BIND
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
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                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
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"Isolation of potential vertebrate limb-identity genes.";
Development 105:813-820(1989).
-!- FUNCTION: SEQUENCE.SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea; Salamandridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89210814; PubMed=2907476;
Savard P., Gates P.B., Brockes J.P.;
"Position dependent expression of a homeobox gene transcript in
relation to amphibian limb regeneration.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
8
                                                                                                                                                                                                                                                                                                                            PROSITE; PSS0071; HOMEOBOX 2; 1.
Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                            HOMEOBOX.
AD040C030F85532B CRC64;

    -!- DEVELOPMENTAL STAGE: EMBRYO.
    -!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.

                                                                                                                                                                                                                                                                                                                                                                               ANTP-TYPE HEXAPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                              64.2%; Score 95; DB 1; Le 58.8%; Pred. No. 2.1e-07; live 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 ERQIKIWFONRRMKWKKDNKLKSMSLATGSSAFQ 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DRQIKIWFQNRRMKWKK-----TALDASALQ 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FBS-2003 (Rel. 41, Last sequence update)
48-FBS-2003 (Rel. 41, Last annotation update)
HOXCG OR NVHOXI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
  SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                         IKANSFAC; T03764; -.
InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 131-234 FROM N.A. MEDLINE=90091821; Pubmed=2574663;
                                                                                                                                                                                                                                                                                                    PROSITE; PS00027; HOMEOBOX 1; 1. PROSITE; PS00032; ANTENNAPEDIA;
                                                                                                                                                                                                                                       Pfam, PF00046; homeobox; 1.
PRINTS; PR00025; ANTENNAPEDIA.
PRINTS; PR00024; HOMEOBOX.
PRODOM; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      25276 MW;
                                                                                                                                                                EMBL, M26883; AAA49755.1; -.
PIR, S00592; 800592.
HSSP; P02833; 1SAN.
TRANSFAC; T03764; -.
                                                                                                                                                    EMBL; X07104; CAA30125.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBO J. 7:4275-4282(1988).
                                                                                                                                                                                                                                                                                                                                                       Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 58.8'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                          155 2
230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HXC6 NOTVI
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  NON TER
SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINES-7260899; PubMed-2885844.
Simeone A., Mavilio F., Acampora D., Giampaolo A., Faiella A.,
Zappavigna V., D'Esposito M., Pannese M., Russo G., Boncinelli E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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PROSITE; PS00032; ANTENNAPEDIA; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peschle C.;
"Two human homeobox genes, cl and c8: structure analysis and expression in embryonic development.";
Proc. Natl. Acad. Sci. U.S.A. 84:4914-4918(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 95; DB 1; Length 234;
Pred. No. 2.1e-07;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 AA; 26901 MW; EA15EED91ED294B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTP-TYPE HEXAPEPTIDE. HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1989 (Rel. 10, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Homeobox protein Hox-C6 (Hox-3C) (HHO.C8) (CP25).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.2%; Scor. 72.0%; Pred. No. 2... 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 ERQIKIWFQNRRMKWKKESNLTSTL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transcription unit.";
Nucleic Acids Res. 16:5379-5390(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DRQIKIWFQNRRMKWKKTALDASAL 25
                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-88262550; PubMed=2898768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97024425; PubMed=8870653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0025; ANTENNAPEDIA.
PRINTS; PRO0024; HOMEOBOX.
Probom; PD000010; HOMEOBOX; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [3]
SEQUENCE FROM N.A. (ISOFORM 2)
                                                                                                                                                                                                                                                                      EMBL, X13957; CAA32139.1; -. ERBL, X16848; CAA34745.1; -. PIR; SO2014; SO2014. HSSP; PO2833; 9ANT.
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MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0003714; F:transcription co-repressor activity; TAS.
GO; GO:0007275; P:development; TAS.
GO; GO:0006357; P:regulation of transcription from Pol II pro. . .; TAS.
InterPro; IPR001827; Autennapedia.
InterPro; IPR001356; Homeobox.
                                                             Gaps
 Gielen J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWART; SM00389; HUA; 1.

PROSITE; PS00027; HOMEDBOX 1; 1.

PROSITE; PS00032; ANTENNAPEDIA; 1.

PROSITE; PS50071; HOMEDBOX 2; 1.

Homeobox; DNA-binding; Developmental protein; Nuclear protein;

Transcription regulation; Alternative splicing.

ANTE-TYPE HEXAPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
Chariot A., Castronovo V., Le P., Gillet C., Sobel M.E., Giel
"Cloning and expression of a new HOXC6 transcript encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Missing (in isoform 2).
/FTId=VSP 002392.
M -> L (IN REF. 3).
BD68870347CB71C0 CRC64;
                                                                                                                                                                                                                                                                ISOId=P09630-2; Sequence=VSP 002392;
-!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95; DB 1; No. 2.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 95; DB 1; Pred. No. 2.1e-2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-ARG.
POLY-GLY.
GLU/LYS-RICH.
                                                                                                                                                                                                                                        IsoId=P09630-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRQIKIWFQNRRMKWKKTALDASAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00046; homeobox; 1.
PRINTS; PR00025; ANTENNAPEDIA.
PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, S82986; AAB46892.1; -.
EMBL, M16938; AAA3607.1; -.
PIR; B28030; WJHU3C.
HSSP; P02833; 9ANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 AA; 26933 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.2%;
                                      319:91-97 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 72.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFAC; T01742; -. Genew; HGNC:5128; HOXC6.
                           repressing protein."
Biochem. J. 319:91-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 142972; -.
                                                                                                                                                                                                                          Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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182

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RESULT 15

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Kidney;
MEDLINE=88328811; PubMed=2458223;
MEDLINE=88328811; PubMed=2458223;
MEDLINE=88328811; PubMed=2458223;
MEDLINE=88328911; PubMed=2458223;
"Isolation and expression of a new mouse homeobox gene.";
Development 102:397-407(1988).
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=92102952; PubMed=1684715;
Coletta P.L., Shimeld S.M., Chaudhuri C., Mueller U., Clarke J.P.,
                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                              SEQUENCE FROM N.A.

BEDLINES-84131843; PubMed=7905473;
Shimeld S.M., Gaunt S.J., Coletta P.L., Geada A.M., Sharpe P.T.;
"Spatial localisation of transcripts of the Hox-C6 gene.";
                                                                                                                                                                                                                                                                                                                                                              "Characterisation of the murine Hox-3.3 gene and its promoter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 133-235 FROM N.A.
MEDLINE=89357988; PubMed=2570032;
Schughart K., Pravtcheva D., Newman M.S., Hunihan L.W., Jiang Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kongsuwan K., Webb E., Housiaux P., Adams J.M.;
"Expression of multiple homeobox genes within diverse mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P10629-2; Sequence=VSP 002393;
-!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
          01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
HOXCG OR HOXC-6 OR HOX-3.3) (HOX-6.1).
235 AA
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-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Bone marrow, and Spleen;
MEDLINE=88329001; PubMed=2901346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 131-235 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 Mech. Dev. 35:129-142(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J03074; AAA37832.1; -.
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EMBL; X16511; CAA34518.1; -.
EMBL; X16510; CAA34517.1; -.
EMBL; S74185; AAB20717.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 15-235 FROM N.A.
                                                                                                                                                                                                                                                                   Anat. 183:515-523(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   haemopoietic lineages.";
EMBO J. 7:2131-2138(1988).
STANDARD;
                                                                                                                Mus musculus (Mouse)
                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=PRII;
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                                                                                                                                                                                                                                                                                                                                                Sharpe P.T.
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DR EMBL; X12504; CAA31022.1; -
DR EMBL; X12504; CAA31023.1; -
DR FIR, A23167; A33167.1; -
DR FIR, A32167; A33167.1; -
DR PIR, A32167; A33167
DR PIR, S00987; WJMSX6.
DR PIR, S00987; WJMSX6.
DR PIR, S00987; WJMSX6.
DR TRANSFAC; T01744; -
DR TRANSFAC; T01744; -
DR TRANSFAC; T01744; -
DR TRANSFAC; T01744; -
DR TRANSFAC; T01744; -
DR TRANSFAC; T01744; -
DR TRANSFAC; T01744; -
DR PRINTS; PR0001356; Monecobox; 1
DR PRINTS; PR0001356; Monecobox; 1
DR PRINTS; PR0001356; Monecobox; 1
DR PRINTS; PR00017; HOMECOBOX.
DR PRINTS; PR00017; HOMECOBOX.
DR PROSITE; PS00017; HOMECOBOX.
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Search completed: February 18, 2004, 14:28:15 Job time : 17.5789 secs

1 DRQIKIWFQNRRMKWKKTALDASAL 25 :|||||||||||||||||| 182 ERQIKIWFQNRRMKWKKESNLTSTL 206

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Q9xyt7 cassiopea x Q95yh8 daphnia mag Q85xw2 mus musculu Q80925 lingula ung Q26375 styela clav Q817C9 ciona intes Q26418 styela clav Q817C8 ciona intes Q26418 styela clav Q817C8 ciona intes Q9pwm4 brachydanio Q9pws0 oryzias lat Q9pws0 oryzias lat Q90vs2 gallus gall Q5759 brachydanio Q57359 brachydanio Q57359 brachydanio Q65008 artemia san Q9czv0 mus musculu
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                                                                                       February 18, 2004, 14:09:39; Search time 81.0526 Seconds (without alignments) 89.145 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                               830525 seqs, 258052604 residues
                                                                                                                                                    US-09-643-260-19
148
1 DRQIKIWFQNRRMKWKKTALDASALQTE
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Maximum Match 100%
Listing first 45 summaries
                                                          OM protein - protein search, using sw model
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Q8JZW2
Q9U9Z5
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Q2FWN4
Q9PXD5
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sp_plant: *
sp_lant: *
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sp_rodent: *
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sp_virus: *
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sp_unclassified: *
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Q8awy7 brachydanio Q8jh53 brachydanio Q9pwm0 brachydanio Q8wwr96 artemia san O57368 brachydanio Q9pvr9 oryzias lat Q27413 ctenodrilus Q23743 ctenodrilus Q287407 ctenodrilus Q29v188 priapulus Q29v188 priapulus c Q55268 junonia coe G57362 brachydanio Q8pvr9 oryzias lat Q97183 brachydanio Q8pvr9 oryzias lat Q77143 archegozete Q77143 archegozete Q7713 archegozete Q7713 petromyzon Q8q915 petromyzon Q8q918 petromyzon Q8q918 petromyzon Q8q919 petromyzon Q8q917 petromyzon		ï
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wy7 bra wm0 bra wm0 bra wm0 bra 368 bra 368 bra 368 bra 43 cten 07 cte	Cassiopeidae; xamachana:	3;
08awy7 08jh52 08gh75 08wrg6 057366 057313 0237413 0237413 025208 025208 025208 025208 025208 025208 027133 077133 08qg11 08qg11 08qq11 08qq11 08qq11 08qq11		Length 2 Indele
	AA. update) on update) an Cassiopeia (ox genes."; ILARITY).	
	NTS 74 AA. nce update) ation update a; Rhizostom a; Rhizostom i; Hox genes. SIMILARITY).	
·	TTS 17.4 TTS 17.6 SIN TO SIN T	re 110.5; DB 5 d. No. 1.7e-08; Mismatches 2
QBAWY7 QBJH53 QB9PW0 QBWRGG OS 7368 Q9PVR9 Q9PVR8 Q97188 Q97188 Q97184 Q971139 Q90GL5 Q8QGL5	VLT 1 YT7 Q9XYT7 Q9XYT7 O1-NOV-1999 (TERMELrel. 12, Created) O1-NOV-1999 (TERMELrel. 12, Last sequence updat O1-NOV-1999 (TERMELrel. 12, Last sequence updat O1-NOV-1999 (TERMELrel. 12, Last sequence updat O1-NOV-1999 (TERMELrel. 12, Last sequence updat O1-NOV-1999 (TERMELrel. 12, Last sequence updat O1-NOV-1999 (TERMELrel. 12, Last sequence updat O1-NOV-1999 (TERMELrel. 12, Last sequence updat O1-NOV-1999 (TERMELYOCA) (NOT CASSIOPEA. NCMI TAXID=12993; (1) SEQUENCE FROM N.A. KUHN K., Streit B., Schierwater B.; NCMI TAXID=12993; (1) SEQUENCE FROM N.A. KUHN K., Streit B., Schierwater B.; NCMI TAXID=12993; (1) SEQUENCE FROM N.A. KUHN K., Streit B., Schierwater B.; Implications for the early evolution of Hox gen J. Exp. Zool. 0:0-0(1999).	
0847 0947 0957 0957 0957 0957 0957 0957 0957 095		Score Pred 5, M
	ARY; el. 12, C el. 13, L el. 13, L crotein (F conidaria; Cnidaria;	74.7%; 67.7%; ive
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SEQUENCE FROM N.A.
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                                                                                                                                               Daphnia magna.
Bukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Diplostraca;
Cladocera; Anomopoda; Daphniidae; Daphnia.
NCBI_TaxID=35525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                               Shiga Y., Yasumoto R., Hayashi S., Yamagata H.;
"Functional diversification of homeotic protein Antennapedia in
arthropod evolution.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AB069680; BAB64346.1;
-InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
InterPro; IPR00146; homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 68.6%; Score 101.5; DB 5; Length 627; Best Local Similarity 69.0%; Pred. No. 9.2e-07; Matches 20; Conservative 2; Mismatches 4; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Strausberg R.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC036986; AAH36986.1; -.
InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH_lambrepressr.
                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0025; ANTENNAPEDIA,
PRINTS; PRO0024; HOMEOBOX.
PRON010; HOMEOBOX.
PROSITE; PRO0032; ANTENNAPEDIA; 1.
PROSITE; PS00032; ANTENNAPEDIA; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00071; HOMEOBOX 2; 1.
DNA-binding; HOMEOBOX; Nuclear protein.
SEQUENCE 627 AA; 69425 MW; A5A7962761CB5D10 CRC64;
                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
        627 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     587 ERQIKIWFQNRRMKWKKENKAKLDAGCLE 615
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PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
                                                                            PRELIMINARY;
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                                                                                                                                  Homeotic protein.
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Linguloidea; Lingulidae; Lingula.
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                                                                   Length 108;
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                                                                                                        Indels
PROSITE; PS50071; HOMEOBOX_2; 1.
Hypothetical protein.
SEQUENCE 108 AA; 13070 MW; 123A78FCDD0E7D90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Styela clava (Sea squirt).
Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Styelidae; Styela.
NCBI_TaxID=7725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 93 AA; 11224 MW; 5DC0379A30DF0137 CRC64;
                                                                                                                                                                                                                                                                                                      01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DNA binding protein AHOX2 (Fragment).
                                                                   Query Match 67.6%; Score 100; DB 11;
Best Local Similarity 70.4%; Pred. No. 2.5e-07;
Matches 19; Conservative 1; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                              Sex combs reduced homeodomain protein (Fragment)
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                                                                                                                                                                PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
                                                                                                                                             1 DRQIKIWFQNRRMKWKKTALDASALQT 27
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Ge T., Lee H., Tomlinson C.R.;
"Identification of an Antennapedia-like Homeobox Gene in the Ascidians Styela clava and plicata.";
Styela clava and plicata.";
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; U05571; AAA16226.1;
--- HSSP; P02833; 9ANT.
                                                                                                                                                                               Gerr, Lee H., Tomlinson C.R.;
"Identification of an Antennapedia-like Homeobox Gene in the Ascidians
Styela clave and plicata.";
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 97; DB 5; Length 181;
Pred. No. 1.2e-06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.5%; Score 97; DB 5; Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Urochordata, Ascidiacea,
Stolidobranchia, Styelidae, Styela.
  Styela plicata (Sea squirt).
Eukaryota, Metazoa, Chordata, Urochordata, Ascidiacea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AA; 20873 MW; AF39911408F06672 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 AA.
                                                                                                                                                                                                                                                                                                           HSSP; PO2833; 9ANT.
HSSP; PO2833; 9ANT.
INTERPRO; IPRO01356; HOMEOBOX.
INTERPRO; IPRO01356; HOMEOBOX.
INTERPRO; IPRO00047; HTH lambrepressr.
PRINTS; PRO0011; HTHREPRESSR.
PRODON; PRO0011; HTHREPRESSR.
PRODON; PRO0010; HOMEOBOX.
PROSITE; PS00027; HOMEOBOX.
PROSITE; PS00027; HOMEOBOX.
PROSITE; PS50071; HOMEOBOX.
DNA-binding; Homeobox; Nuclear protein.
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PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH lambrepressr.
Pfam; PF00046; homeobox; 1.
                                              Stolidobranchia, Styelidae, Styela.
NCBI_TaxID=7726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 DRQVKIWFQNRRMKWKK 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DRQIKIWFQNRRMKWKK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 65.5%;
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homeobox protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Styela clava (Sea squirt)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Ascidian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7725;
                                                                                                                                                               STRAIN=Ascidian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              026478
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                              Ge T., Lee H., Tomlinson C.R.; "1dentification of an antennapedia-like homeobox gene in the ascidians
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Spagnuolo A., Ristoratore F., Di Gregorio A., Aniello F., Branno M.,
Di Lauro R.,
"Unusual number and genomic organization of Hox genes in the tunicate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ciona intestinalis.
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
VCBI_TaxID=7719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ciona intestinalis.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ535674; CAD59670.1; -.
Homeobx; DNA-binding; Nuclear protein.
NON TER 1 1
SEQÜENCE 90 AA; 11352 MW; CAAAD6B261FE908E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 AA; 7630 MW; F506301E9679BA25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Homeobox protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.5%; Score 97; DB 5; I 64.3%; Pred. No. 5.9e-07; tive 2; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 AA
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                                                                                                                                                                                                        InterPro; IPR001356; Homeobox.
InterPro; IPR00047; HTH lambrepressr.
Pram; PR00046; homeobox.
PRINTS; PR00024; HOWEOBOX.
PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
SWART; SW00389; HOX; 1.
PROSITE; PS00027; HOWEOBOX 1; 1.
PROSITE; PS00027; HOWEOBOX 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DRQIKIWFQNRRMKWKKTALDASALQTE 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
MEDLINE=95011617; PubMed=7926803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DRQIKIWFONRRMKWKK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DROVKIWFONRRMKWKK 58
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Best Local Similarity 64.3<sup>†</sup>
Matches 18, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 94.1
nes 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Q26611;
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RESULT 6 Q817C9

RESULT 7 Q26611

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Gaps

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RESULT 9

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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryzias latipes (Medaka fish) (Japanese ricefish).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaunt S.J.;
"Conservation in the Hox code during morphological evolution.";
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                                                                    PROSITE; PS00032; ANTENNAPEDIA; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 231 AA; 26733 MW; 65164A13541D7E8A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
HOXC-6 product (HOXC-6 protein).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                1 DRQIKIWFQNRRMKWKK-TALDASALQTE 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DRQIKIWFQNRRMKWKKTALDASAL 25
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ERQIKIWFQNRRMKWKKESNLSSTL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Pfam; PF00046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Embryo;
MEDLINE=95151548; PubMed=7848839;
                       ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                               Query Match
Best Local Similarity 69.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                  SMART; SM00389; HOX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09PVS0;
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Q9PSD5
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Q9PVS0
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                                                  Gaps
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MEDLINE=99051425; PubMed=9831563;

A MEDLINE=99051425; PubMed=9831563;

A MEDLINE=99051425; PubMed=9831563;

A MEDLINE=99051425; PubMed=9831563;

A MEDLINE=9005145; PubMed=9831563;

A MEDLINE
A Medlin A., Fritz A., Frince V.,
A Postlethwait J.;
B Callethwait J.;
B 
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxIb=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Spagnuolo A., Ristoratore F., Di Gregorio A., Aniello F., Branno M.
Di Lauro R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ciona intestinalis.
Eukaryota, Metazoa, Chordata, Urochordata, Ascidiacea, Enterogona,
Phlebobranchia, Cionidae, Ciona.
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                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ciona intestinalis.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ535675; CAD59671.1; -.
Homeobox; DNA-binding; Nuclear protein.
SEQUENCE 435 AA; 48739 MW; D8D0F579C02BC9E2 CRC64;
                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative homeobox protein Hox10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
. No. 1.3e-06;
                                                                                                                                                                                                                                                                                 435 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish) (Danio rerio)
                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                 PRT;
                            94.1%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 DRQVKIWFQNRRMKWKK 311
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PRINTS; PR00025; ANTENNAPEDIA.
PRINTS; PR00024; HOMEOBOX.
                                                                                                    1 DRQIKIWFONRRMKWKK 17
                                                                                                                           1 DRQIKIWFQNRRMKWKK 17
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
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Best Local Similarity 94.1
Matches 16; Conservative
                                                  16; Conservative
                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                          Similarity
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                       Best Local
Matches 1
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Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=North arm of Great Salt Lake;
STRAIN=North arm of Great Salt Lake;
Averof M., Akam M.;
"HOM/HOX genes in a crustacean: inplication for the origin of insect
and crustacean body plans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Artemia sanfranciscana (Brine shrimp) (Artemia franciscana).
Bukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
Artemiidae; Artemia.
NCBI_TaxID=6661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prince V.E., Joly L., Ekker M., Ho R.K.;
Prince V.E., Joly L., Ekker M., Ho R.K.;
"Zebrafish hox genes: genomic organization and modified colinear expression patterns in the trunk ".
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 94.5; DB 13; Length 43;
Pred. No. 6.5e-07;
                                                             Length 219;
           DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 219 AA; 24952 MW; 4BAE9046D52C0705 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 AA; 5050 MW; 53034C37F3DFA596 CRC64;
                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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Last annotation update)
                                                           Score 95; DB 13;
Pred. No. 2.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 AA
                                                                              Pred. No. 2.96
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DRQIKIWFQNRRMKWKK-TALDASALQT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
DNA-binding; Homeobox; Nuclear protein.
                                                                                                                                             1 DRQIKIWFQNRRMKWKKTALDASA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                             64.2%;
70.8%;
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Local Similarity 67.9%;
Les 19; Conservative
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                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-OCT-2002 (TrEMBLrel. 22,
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                                                         Query Match
Best Local Similarity 70.8
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                             Hoxa5 protein (Fragment).
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ANTP.
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"Hox gene expression and regulation in the presumptive wing region of the chick lateral plate mesoderm (Abstract # 286).";
Dev. Biol. 210:228-228(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Gradients, and forward spreading of vertebrate Hox gene expression detected using a Hox/lacZ transgene.";
Dev. Dyn. 221:26-36(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                        Score 95.5; DB 13; Length 82; Pred. No. 9e-07; 1; Mismatches 4; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hoxa-7 protein (Homeodomain transcription factor HoxA-7).
                                                                  SEQUENCE 82 AA; 9939 MW; 6B6828D280511888 CRC64;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                        1 DRQIKIWFQNRRMKWKK-----TALDASALQ 26
                                                                                                                                                                                                                                                                                                                                                                                                                       219 AA
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PROSITE; PS50071; HOMBOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
NON-TER
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MEDLINE-21255551; PubMed=11357191;
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SMART; SW00189; HOX; 1.
PROSITE; PS000027; ANTENNAPDIA; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00071; HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00025; ANTENNAPEDIA.
                                                                                                                                                                                                                                                                                                                                        64.5%;
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60.0°
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00024; HOMEOBOX
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                                                      SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                           NCBI_TaxID=8090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaunt S.J.;
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| RL | Curr. Biol. 3:73-78(1993). | CC | -1 - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY). | CA49682.1; | -2 - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY). | CA49682.1; | -2 - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY). | CR | EMBLY X70077; | CA49682.1; | -2 - CA49682.1; | -2 - CA49682.1; | -2 - CA49682.1; | -2 - CA49682.1; | -2 - CA49682.1; | -2 - CA49682.1; | -2 - CA49682.1; | -2 - CA49682.1; | -2 - CA49682.1; | -2 - CA49682.1; | -2 - CA49682.1; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA49682.2; | -2 - CA4962.2; | -2
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Search completed: February 18, 2004, 14:36:01 Job time : 81.0526 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 18, 2004, 14:12:09; Search time 30.7632 Seconds (without alignments) 87.531 Million cell updates/sec Run on:

148 1 DRQIKIWFQNRRMKWKKTALDASALQTE US-09-643-260-19 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	homeotic protein H	homeotic protein H	homeotic protein H	protein				homeotic protein H	homeo box protein	homeotic protein H	antennapedia-like	antennapedia-like	homeotic protein z	homeotic protein H		homeotic protein H	protein				protein		homeotic protein H		homeotic protein H		c prot	c prot	homeotic protein H
SUMMARIES	ΩI	B29585	A05266	C27176	S26400	A31324	A27471	A03314	A28329	151341	S08303	PC2399	PC2400	808639	S00992	S15536	A32167	WJHU3C	WJMSX6	S00592	802014	A56568	S72429	A39164	A24777	JT0273	B24777	A43551	A45578	WJZFX2
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S57235	165241	PC1216	I51439	S15538	JC1161	A60084	D34510	S58852	C43559	I51342	S47605	808302	S47603	S50066	A34510
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63.5	63.5	63.	63	63	63	6	ف	Ψ	_		_		_	~	Ψ
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ALIGNMENTS

Cypace: 15-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 17-Oct-1997
Cypace: 15-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 17-Oct-1997
CyAccession: B29585
R;Lonai, P.; Arman, E.; Czosnek, H.; Ruddle, F.H.; Blatt, C.
DNA 6, 409-418, 1987
A;Title: New murine homeoboxes: structure, chromosomal assignment, and differential exp. A;Reference number: A29585; MUID:88054465; PMID:2890503
A;Accession: B29585
A;Accession: B29585
A;Accession: B29585
A;Accession: B29585
A;Accession: B29585
C;Seperferences: GB:M18167
C;Superferences: GB:M18167
C;Superferences: Change Apmeobox proteins; homeobox homology
C;Superfamily: unassigned homeobox inucleus; transcription regulation
F;4-60/Domain: homeobox homology <HOX>

.. 7 69.6%; Score 103; DB 2; Length 81; 70.0%; Pred. No. 4.5e-08; ive 2; Mismatches 5; Indels Query Match
Best Local Similarity 70.0°
Matches 21; Conservative

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1 DRQIKIWFONRRMKWKKTA--LDASALQTE 28 ò g

homeotic protein Hox B6 - human (fragment)

NyAlternate names: homeotic protein Hox 2B; homeotic protein Hu2

(Species: Homo sapiens (man)

C; Species: Homo sapiens

R; Levine, M.; Rubin, G.M.; Tjian, R.

C; Accession: A6526; S1537

R; Levine, M.; Rubin, G.M.; Tjian, R.

R; Levine, M.; Rubin, G.M.; Tjian, R.

R; Levine, M.; Rubin, G.M.; Tjian, R.

R; Levine, M.; Rubin, G.M.; Tjian, R.

R; Levine, M.; Rubin, G.M.; Tjian, R.

A; Reference number: A6526; MUID:85024858; PMID:6091895

A; Residues: 1-96 < LEV

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A,Molecule type: DNA A,Residues: 18-19,'R',21-83 <BON> C,Genetics:

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homoeo box sequences and their
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C;Species: Mus musculus (house mouse)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 24-Sep-1999
C;Accession: A31324
R;Schughart, K.; Utset, M.F.; Awgulewitsch, A.; Ruddle, F.H.
R;Schughart, K.; Utses, M.F.; Awgulewitsch, A.; Ruddle, F.H.
A;Title: Structure and expression of Hox-2.2, a murine homeobox-containing gene.
A;Reference number: A31324; MUID:88289762; PMID:2899893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homeotic protein R5 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cispecies Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Musculus (house mouse)
Cispecies: Musculus (house)
Ricolberg-Poley, A.M.; Voss, S.D.; Chowdhury, K.; Gruss, P.
Nature 314, 713-718, 1985
A;Title: Structural analysis of murine genes containing homoeo box sequences A;Reference number: A03314; MUID:85188311; PMID:2986010
                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB:J03782; NID:g193929; PIDN: AAA37843.1; PID:g387203
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                  DB 2; Length 224;
1.3e-07;
thes 5; Indels
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Pred. No. 1.3e-07;
Mismatches 5; Indels
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Pred. No. 1.6e-07;
1; Mismatches 7; Indels
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Gene 54, 23-32, 1987
A;Title: Cloning and expression of rat homeo-box-contain
A;Reference number: A91576; MUID:87277429; PMID:2886401
A;Accession: A27471
69.6%; Scor. 70.0%; Pred. No. ...
                                                                                                                                                                              Ouery Match 69.6%; Score 103; DB Best Local Similarity 70.0%; Pred. No. 1.3e Matches 21; Conservative 2; Mismatches
                                                                                                                                            1 DROIKIWFONRRMKWKKTA--LDASALOTE
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                                                                                 21; Conservative
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Best Local Similarity
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A; Residues: 1-105 <FAL>
                                                     Best Local Similarity
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A; Residues: 1-224 <SCH>
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                        Query Match
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Genomics 1, 182-195, 1987
A;Title: Sequence analysis of the murine Hox-2.2, -2.3, and -2.4 homeo boxes: evolutions A;Reference analysis of the murine Hox-2.2, -2.3, and -2.4 homeo boxes: evolutions A;Reference number: A27176; MUID:88085193; PMID:2891608
A;Residue: C27176
A;Residues: 1-97 <HAR>
A;Residues: 1-97 <HAR>
A;Residues: 1-97 <HAR>
A;Gross-references: GB:M18401; NID:g193936; PIDN:AAC27130.1; PID:g3335322
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati
F;147-203/Domain: homeobox homology <HOX>
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A;Note: the authors translated the codon ACT for residue 55 as Tyr, CGC for residue
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A,Experimental source: tissue-type placenta
A,Note: the authors translated the codon ACT for residue 55 as Tyr, CGC for residue
A,Note: the authors did not translate the codons for residues 139, and 140
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C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Sep-1999
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                                                 A,Map position: 17q21.3-17q21.3
C,Superfamily: unassigned homeobox proteins; homeobox homology
C,Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;19-75/Domain: homeobox homology <HOX>
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Pred. No. 5.3e-08;
2; Mismatches 5;
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Pred. No. 5.4e-08;
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                                                                                                                                                                                                                                                                                                                           1 DRQIKIWFQNRRMKWKKTA--LDASALQTE 28
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                        A;Cross-references: GDB:120659; OMIM:142961
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Best Local Similarity 70.0%;
Matches 21; Conservative
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Matches 21; Conservative
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A;Molecule type: DNA
A;Residues: 1-139,'E' <SH2>
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R; Hart, C.P.; Fainso
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A;Title: Molecular cloning and characterization of homeobox-containing genes from Atlan A;Reference number: 151341; MUID:88226009; PMID:2897318
A;Accession: 151341
A;Accession: 151341
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-75 <FJO>
A;Crose-references: GB/M18903; NID:g213797; PIDN:AAA49559.1; PID:g213798
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox, nucleus; transcription regulation
F;2-58/Domain: homeobox homology <HOX>
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C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jul-2000
C;Accession: PC3399
R;Ge, T.; Lee, H.; Tomlinson, C.R.
Rsice, T.; Lee, H.; Tomlinson, C.R.
Rsicence 1. 219-222, 1994
A;Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela c
A;Reference number: PC2399; MUID:95011617; PMID:7926803
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 02-06-1993 #sequence_revision 03-Aug-1995 #text_change 17-Oct-1997
C;Accession: S08303
R;Wedden, S.E.; Pang, K.; Eichele, G.
Development 105, 639-650, 1989
A;Title: Expression pattern of homeobox-containing genes during chick embryogenesis. A;Accession: S08303
A;Accession: S08303
A;Accession: S08303
A;Accession: S08303
A;Accession: S08303
A;Residues: 1-86 <WED>
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A,Residues: 1-60 <GET>
A,Residues: 1-60 <GET>
A,Cross-references: GB:S73920; NID:g693714; PIDN:AAB33061.2; PID:g7387472
A,Note: The authors translated the codon ATT for residue 47 as Glu
C,Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox, nucleus; transcription regulation
F;2-58/Domain: homeobox homology <HOX>
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C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Superfamily: unassigned homeobox; nucleus; transcription regulation
C;Reywords: DNA binding; homeobox; nucleus; transcription regulation
F;10-66/Domain: homeobox homology <HOX>
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Pred. No. 2.6e-07;
2; Mismatches 6;
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66.7%;
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Matches 18, Conservative
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Best Local Similarity
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A;Accession: A03314
A;Molecule type: DNA
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A;Residues: 1-19 < COL>
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A;Residues: 1-19 < COL>
A;Residues: 1-19 < COL>
A;Title: Sequential expression of murine homeo box genes during F9 EC cell differentiatiany accession: S14043
A;Rolecule type: DNA
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R;Kessel, M.; Schulze, F.; Fibi, M.; Gruss, P.
Proc. Natl. Acad. Sci. U.S.A. 84, 5306-5310, 1987
A;Title: Primary structure and nuclear localization of a murine homeodomain protein.
A;Reference number: A28329; MUID:87260976; PMID:2885847
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C;Species: Salmo salar (Atlantic salmon)
C;Species: Salmo salar (Atlantic salmon)
C;Date: 13-8ep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999
C;Accession: IS1341
R;Fjose, A.; Molven, A.; Eiken, H.G.
Gene 62, 141-152, 1988
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C;Species: Mus musculus (house mouse)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 20-Aug-1999
C;Accession: A28329; I49131
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Best Local Similarity
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A;Note: 216-Ser and 225-Gln were also found and are interpreted as minor allelic differe A;Accession: 800993
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A.Jitle: Organization of human class I homeobox genes.
A.Reference number: S15036; WUID:90215256; PMID:2576652
                                                                                              A,Molecule type: DNA
A,Residues: 83-215,'S',217-224,'Q',226-234 <CHW>
A,Residues: 83-215,'S',217-224,'Q',226-234 <CHW>
A,Residues: 83-215,'S',217-224,'Q',226-234 <CHW>
A,Crose-references: EMBL:X12499; NID:g64740; PIDN:CAA31020.1; PID:g64742
B,Carrasco, A.E.; McGinnis, W.; Gehring, W.J.; De Robertis, E.M.
Cell 37, 409-414, 1984 an Xenopus laevis gene expressed during early embryogenesis coding a,Reference number: A03316; MUID:84205675; PMID:6327066
A,Accession: A03316
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C; Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;1-234/Product: homeotic protein Hbox1, allelic version PRII #status predicted <MAT1>
F;82-215/Product: homeotic protein Hbox1, allelic version PRI #status predicted <MAT>
F;142-198/Domain: homeobox homology <HOX>
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C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 29-Aug-1997
C;Accession: S15536
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Nucleic Acids Ree. 16, 1453-1469, 1988

A; Title: Xenopus homeobox-containing cDNAs expressed in early development.

A; Reference number: S00589; MUID:88157707; PMID:2894634

A; Accession: S00590

A; Molecule type: mRNA

A; Residues: 121-215, 'S', 217-224, 'Q', 226-234 < FRI>
A; Residues: 121-215, 'S', 217-224, 'Q', 226-234 < FRI>
A; Cross-references: EMBL:X07101; NID:g64738; PIDN:CAA30122.1; PID:g1334649
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A;Rebidues: 134-138,'8',140-200 <CAR>
A;Cross-references: GB:KO1943; NID:G214242; PIDN:AAA49743.1; PID:G214243
A;Note: the authors translated the codon AGC for residue 200 as Arg
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C,Superfamily: unassigned homeobox proteins; homeobox homology
C,Reywords: DNA binding; homeobox; nucleus; transcription regulation
F;2-58/Domain: homeobox homology <HOX>
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Pred. No. 1.4e-06;
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3; Mismatches 4;
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A; Status: not compared with conceptual translation
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A,Cross-references: GDB:120647; OMIM:142950
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Matches 18; Conservative 3
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81.0%;
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Best Local Similarity
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A; Residues: 1-66 <BON>
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Unn-1989 #sequence revision 30-Jun-1989 #text_change 11-Jan-2002
C;Accession: S00992; S00993; A0310;S00599; T01066
R;Cho, K.W.Y.; Goetz, J.; Wright, C.V.E.; Fritz, A.; Hardwicke, J.; de Robertis, E.M.
EMBO J. 7, 2139-2149, 1988
A;Title: Differential utilization of the same reading frame in a Xenopus homeobox gene e A;Reference number: S00991; WUID:88329002; PMID:2901347
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CiAccesion: S08639
RyNjolstad, P.R.; Molven, A.; Apold, J.; Fjose, A.
EMBO J. 9, 515-524, 1990
A.Title: The zebrafish homeobox gene hox-2.2: transcription unit, potential regulatory
A.Title: The zebrafish homeobox gene hox-2.2: transcription unit, potential regulatory
A.Title: The zebrafish homeobox gene hox-2.2: transcription unit, potential regulatory
A.Title: The zebrafish homeobox gene hox-2.2: transcription unit, potential regulatory
A.Title: The zebrafish homeobox gene hox-2.2: transcription unit, potential regulatory
A.Title: The zebrafish homeobox nucleus; problems and the zebrafish potential regulatory
A.Scatus: Preliminary
A.Scatus: Preliminary
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A.Scatus: Preliminary
A.Scatus: A.Scatus: DNA
A.Residues: 1-96 kNO>
A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatus: A.Scatu
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R:Ge, T.; Lee, H.; Tomlinson, C.R.
R:Ge, T.; Lee, H.; Tomlinson, C.R.
A:Gene 147, 219-222, 1994
A:Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela of A:Accession: PC2400
A;Recence number: PC2399; MUID:95011617; PMID:7926803
A;Accession: PC2400
A;Molecule type: DNA
A;Residues: LG oGET>
A;Note: The authors translated the codon ATA for residue 47 as Glu
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;2-58/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                sea squirt (Styela plicata) (fragment)
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A;Residues: 1-234 <CHO>
A;Cross-references: EMBL:X12500; NID:g64743; PIDN:CAA31021.1; PID:g64744
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Pred. No. 2.5e-07;
1; Mismatches 0;
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Pred. No. 4.8e-07;
3; Mismatches 5;
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C;Species: Brachydanio rerio (zebra fish)
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Best Local Similarity 94.1%;
Matches 16; Conservative
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Best Local Similarity 69.0%;
Matches 20; Conservative
                               DROVKIWFONRRMKWKK
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PEPTIDE ANTIESTROGEN COMPOSITIONS AND METHODS
FOR TREATING BREAST CANCER
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COMPUTER: IBM PC compatible
COMPUTER: Pacentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/419,826
FILING DATE: 14-0CT-1999
PRIOR APPLICATION NUMBER: PCT/US98/07711
FILING DATE: 14-APR-1998
APPLICATION NUMBER: DC 60/043,545
FILING DATE: 14-APR-1997
INFORMATION FOR SEQ ID No: 34:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.2%; Score 95; DB 4; Length 24; 85.0%; Pred. No. 1.1e-07;
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OTHER INFORMATION: /note= "X = Phosphotysine"
US-09-346-847-25
US-09-057-363C-47
US-09-346-847-17
US-09-346-847-20
US-09-346-847-20
US-09-346-847-20
US-09-346-847-27
US-09-346-847-27
US-09-658-517-27
US-09-658-517-23
US-09-66-772-3
US-09-46-847-16
US-09-346-847-16
US-09-346-847-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 34, Application US/09419826
| Patent No. 6306832
| GENERAL INFORMATION:
| TILLE OF INVENTION: PEPTIDE ANTIEST
| TITLE OF INVENTION: FOR TREATING BR
| NUMBER OF SEQUENCES: 39
| COMPUTER READABLE FORM:
| MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-040-725A-2; Sequence 2, Application US/09040725A; Patent No. 6399584; GENERAL INFORMATION: APPLICANT: Institut Curie; APPLICANT: CNRS
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Matches 17; Conserv
   RESULT 1
US-09-419-826-34
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                               148
1 DRQIKIWFQNRRMKWKKTALDASALQTE
                                                                                                                                                                                                                                                                                                                          328717 segs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued Patents AA: *
                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                  US-09-643-260-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length
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Gaps

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MOLECULE TYPE: peptide HYPOTHETICAL: NO
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                                us
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US-08-751-344B-3
                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
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APPLICANT: Crepaldi, Tiziana
APPLICANT: Crepaldi, Tiziana
APPLICANT: Gautreau, Alexis
APPLICANT: Gautreau, Alexis
TITLE OF INVENTION: Daniel
TITLE OF INVENTION: On tyrosine 353
FILE REFERENCE: 39108200100
CURRENT APPLICATION NUMBER: US/09/040,725A
CURRENT FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 27
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: variation

: LOCATION: (22)

: OTHER INFORMATION: Xaa = tyrosine or a phosphorylated tyrosine

US-09-040-725A-2
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APPLICANT: Howley
APPLICANT: Howley
APPLICANT: Howley
APPLICANT: Howley
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: PAPILLCMAVIRUS-INFECTED CELLS
TITLE OF INVENTION: PAPILLCMAVIRUS-INFECTED CELLS
TITLE OF INVENTION: PAPILLCMAVIRUS-INFECTED CELLS
CURRENT APPLICATION NUMBER: US/09/347,504
CURRENT FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.2%; Score 95; DB 4; Length 27; 66.7%; Pred. No. 1.2e-07; Live 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.5%; Score 94; DB 4; Length 34; 94.1%; Pred. No. 2.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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Patent No. 5858973
GENERAL INFORMATION:
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Best Local Similarity 66.74
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 94.1
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-347-504-79
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(617) 345-9100

TELEPHONE:

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RESULT 8
US-09-057-363C-50
US-09-057-363C-50
Sequence 50, Application US/09057363C
Sequence 50, Application US/09057363C
Sequence 50, Application US/09057363C
Sequence 50, Application Coret W.
GENERAL INFORMATION:
GOUR, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INHIBITING THE
                                                                                                                 Sequence 9, Application US/08751344B
; Sequence 9, Application US/08751344B
; Patent No. 6210960
; GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
CORRESPONDENCES: 29
CORRESPONDENCES: 29
CORRESPONDENCES: 29
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CONTY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.5%; Score 94; DB 3; Length 61; 94.1%; Pred. No. 4.3e-07;
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ADDRESSEE: Seed Intellectual Property Law Group STREET: 701 Fifth Avenue, Suite 6300 CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPARY: US

ZIP: 02111
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPANIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERfect 6.1
CURRENT APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-No. 6210960-1996
FILING DATE: 19-No. 6210960-1996
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REPERSURG/DOCKET NUMBER: 34,380
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFONE: (617) 345-9110
TELEFONE: (617) 345-9111
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DRQIKIWFQNRRMKWKK 17
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Best Local Similarity 94.1'
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
FRAGMENT TYPE:
                                                                                                               US-08-751-344B-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08751344B
; Patent No. 6210960
; GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
APPLICANT: Miller Ph.D., Christopher P.
TITLE OF INVENTION: NOVEL TRANSCRIPTION FACTOR AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Booston
STATE: MA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 63.5%; Score 94; DB 3; Length 61; Best Local Similarity 94.1%; Pred. No. 4.3e-07; Matches 16; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                       Score 94; DB 3; Length 61;
Pred. No. 4.3e-07;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
CORFWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,344B
FILING DATE: 19-No. 6210960-1996
PRIOR APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D. Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELEPHONE: (617) 345-9110
TELEPHONE: (617) 345-910
TELEPHONE: (617) 345-911
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 61 anino acids
TYPE: amino acids
TYPE: amino acids
TELEFAX: (617) 345-9110
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 61 amino acids TYPE: amino acid TYPE: amino acid TYPE: unknown
                                                                                                                                                                                                                                                                                                                                                                                        1 DRQIKIWFQNRRMKWKK 17
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                         internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                 ANTI-SENSE: NO FRAGMENT TYPE:
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US-08-751-344B-6
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Gaps

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1 DRQIKIWFQNRRMKWKK 17

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APPLICANT: Van der Geer
TITLE OF INVENTION: Peptide Inhibitors of a Phosphotyrosine-Binding Domain
TITLE OF INVENTION: Containing Protein
FILE NEFERENCE:
CURRENT FILING DATE: 1980-04-22
CURRENT FILING DATE: 1986-04-20
EARLIER FILING DATE: 1996-02-20
EARLIER FILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 60/010,384
EARLIER FILING DATE: 1996-01-22
EARLIER FILING DATE: 1996-01-22
EARLIER FILING DATE: 1996-01-27
NUMBER OF SEQ ID NOS: 60
SOFTWARE PILLNG DATE: 1995-10-27
NUMBER OF SEQ ID NOS: 60
SEQ ID NO 52
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7. Application US/08751344B
Fatent No. 6210960
GENERAL INFORMATION:
APPLICANT: Habener M.D., Joel F.
TITLE OF INVENTION: THEREFOR TITLE OF INVENTION: THEREFOR TITLE OF INVENTION: THEREFOR TITLE OF INVENTION: THEREFOR TITLE OF INVENTION: THEREFOR TITLE OF INVENTION: THEREFOR TITLE OF INVENTION: THEREFOR TITLE OF INVENTION: THEREFOR THEREFOR THE OF INVENTION: ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 62.8%; Score 93; DB 3; Length 27; Best Local Similarity 80.0%; Pred. No. 2.5e-07; Matches 16; Conservative 2; Mismatches 2; Indels
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FILING DATE: 19-No. 6210960-1996
PRIOR APPLICATION NUMBER: 08/202,044
FILING DATE: 23-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS Ph.D., Kathleen M.
REGISTERATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,137-A (11274/02148)
TELECOMMUNICATION INFORMATION:
MANE: WILLIAMS Ph.D., KATHLEEN M.
REGISTERATION NUMBER: 36,137-A (11274/02148)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: phosphotyrosine binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (24)
; OTHER INFORMATION: Phosphorylated at Tyr
US-09-051-934-52
     Application US/09051934C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 RQIKIWFQNRRMKWKKTALD 21
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TELEFAX: (617) 345-9111
INFORMATION FOR SEO ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                              Patent No. 6028053
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MOD RES
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US-08-751-344B-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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APPLICANT: Van der Geer
TITLE OF INVENTION: Peptide Inhibitors of a Phosphotyrosine-Binding Domain
TITLE OF INVENTION: Containing Protein
TITLE OF INVENTION: Containing Protein
TITLE OF ILING DATE: 1998-04-22
EARLIER APPLICATION NUMBER: 60/011,799
EARLIER PILING DATE: 1996-02-20
EARLIER PILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 60/010,384
EARLIER APPLICATION NUMBER: 60/010,384
EARLIER PILING DATE: 1996-01-22
EARLIER FILING DATE: 1996-01-22
EARLIER FILING DATE: 1995-10-27
NUMBER OF SEQ ID NOS: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
                                               ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/057,363C
FILING DATE: 08-Apr-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 62.8%; Score 93; DB 4; Length 22; Best Local Similarity 94.1%; Pred. No. 2e-07; Matches 16; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                       NAME: Christiansen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 100086.406
TELECONAUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-631
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-057-363C-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: phosphotyrosine binding domain US-09-051-934-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 51, Application US/09051934C Patent No. 6028053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 RQIKIWFQNRRMKWKKTALD 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 NROIKIWFONRRMKWKK 22
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-09-051-934-52
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Gaps

61 amino acids

LENGTH:

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Sequence 3, Application US/08810540

Patent No. 5929042
GENERAL INFORMATION:
APPLICANT TATOY, Carol M.
APPLICANT: Shelanski, Michael L.
TITLE OF INVENTION: DEATH AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08810540
Patent No. 5929042
CENERAL INFORMATION:
APPLICANT: Troy, Carol M.
APPLICANT: Shelanski, Michael L.
TITLE OF INVENTION: BATH AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSES: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: RIADABLE FORM:
MEDIUM TYPE: RIADABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,540
FILING DATE: 03-MAR-1997
CLASSIFICATION: S14
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28 678
REFERENCE/DOCKET NUMBER: 0575/51247
TELEPONMICATION INFORMATION:
TELEPHONE: 212-278
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RQIKIWFQNRRMKWKK 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 62.2
Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-810-540-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08928958
| Sequence 7, Application US/08928958
| Patent No. 2877282
| Patent No. 2877282
| APPLICANT: NADLER, STEVEN G.
| APPLICANT: CLEAPTELAND, JEFFREY S.
| APPLICANT: HAFFAR, OMAR K.
| TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN
| TITLE OF INVENTION: METHODS OF USE THEREOF
| TITLE OF INVENTION: METHODS OF USE THEREOF
| NUMBER OF SEQUENCES: 24
| CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: A
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Pred. No. 1.98-07;
                                                                                                                                                                                                                                                                                                    Length 61;
                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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ZIP: 94025

ZOUNTRY: USA

ZIP: 94025

COMPUTER READBLE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,958
FILING DATE: 12-SEP-1997
CLASSIPICATION NUMBER: US 60/026978
FILING DATE: 20-SEP-1996
ATTONEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0019
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 7:
SEQUENCE CHARACTERISTICS:
LUMB THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION OF THE COMMUNICATION 
                                                                                                                                                                                                                                                                                        Query Match 62.8%; Score 93; DB 3; Best Local Similarity 88.2%; Pred, No. 6e-07; Matches 15; Conservative 2; Mismatches
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100.0%; Pre
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Best Local Similarity 100.
                                                                                                                                                                           ; FRAGMENT TYPE: internal US-08-751-344B-7
                                                              MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                   unknown
amino acid
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STRANDEDNESS: si
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TYPE: ami
TOPOLOGY:
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STATE:
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Length 16;

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COMPOSITIONS COMPRISING A PEPTIDE
INHIBITOR OF NUCLEAR PROTEIN TRANSLOCATION AND AN
IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.2%; Score 92; DB 2; Length 16; 100.0%; Pred. No. 1.9e-07;
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SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,540
FILING DATE: US/08/810,540
CLASSIFICATION: 514
ATTONNEY/AGENT INPORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51247
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION 190206
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,429
FILING DATE: 04-MAY-1998
CLASSIFICATION: S14
ATTORNEY/AGENT INFORMATION:
NAME: Klein, Christopher A.
REGISTRATION NUMBER: 34,363
RECISTRATION NUMBER: 34,363
RECISTRATION INFORMATION:
TELLEPHONE: (609) 252-3714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Bristol-Myers Squibb Company
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09072429
Patent No. 5962415
SEMERAL INFORMATION:
APPLICANT: Nadler, Steven G.
TITLE OF INVENTION: COMPOSTIONS OF TITLE OF INVENTION: IMMUNOSUPPRESS
TITLE OF INVENTION: IMMUNOSUPPRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RQIKIWFQNRRMKWKK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 RQIKIWFQNRRMKWKK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (609) 252-4526
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                  TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 amino acids
                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
; TOPOLOGY: linear
WOLECULE TYPE: peptide
US-08-810-540-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: peptide US-09-072-429-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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US-09-072-429-7
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Query Match 62.2%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 RQIKIWFQNRRMKWKK 17
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Db 1 ROIKIWFQNRRMKWKK 16

Search completed: February 18, 2004, 14:41:52 Job time : 32.9737 secs

Q8wrm9 lithobius a Q9bvr5 coryzias lat O77143 archegozete O77143 archegozete Q8qg15 petromyzon Q8qg15 petromyzon Q8qg12 petromyzon Q8qg12 petromyzon Q8qg12 petromyzon Q8qg17 petromyzon Q8qg17 petromyzon Q8qg17 petromyzon Q8qg17 petromyzon Q8qg17 petromyzon Q8qg17 petromyzon Q8qg17 petromyzon Q9qg17 petromyzon Q9qu18 archegozete Q8mxb2 holopneuste O57356 brachydanio Q9u9t4 nereis vire Q9bmf7 haliotis as Q967w5 folsomia ca Q9pvs1 oryzias lat Q9yu8 oryzias lat

OM protein

Run on:

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Eukaryota; Metazoa; Cnidaria; Scyphozoa; Rhizostomeae; Cassiopeidae;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Kuhn K., Streit B., Schierwater B.;

Isolation of Hox genes from the scyphozoan Cassiopeia xamachana:

Implications for the early evolution of Hox genes.";

J. Exp. Zool. 0:0-0(1999).

J. Exp. Zool. 0:0-0(1999).

HSRD; AR114593; AAD32577.1;

HSSP; P02833; PANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58EE91F6E540C3A9 CRC64;
                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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S
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                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro, IPR001356; Homeobox.
InterPro, IPR000047; HTH lambrepressr.
                                                                                                                                                                                                                                                                                                                   Scox-3 homeodomain protein (Fragment) SCOX-3.
                             077143
077139
080GL5
080GL6
080GL6
080GL7
080GL7
080GL7
08733
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       Q8WRM9
Q9NB42
Q9PVR5
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Q9Y187
Q9U9Z4
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; HOMEOBOX; 1.
SWART; SWO0389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1.
PROSITE; PS00071; HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 AA; 31041 MW;
01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                              PRELIMINARY;
 8888899999999999
                                                                                                                                                                                                                                                                                                                                  Cassiopea xamachana.
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=12993;
Cassiopea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                              O9XYT7
QB5xx2 mus musculu
QB5x611 styela plic
Q26478 styela clav
QB47c8 ciona intes
QB47c9 ciona intes
O57368 brachydanio
O57359 brachydanio
O57359 brachydanio
QB0x79 oryzias lat
Q2743 ctenodrilus
Q2743 ctenodrilus
Q26407 ctenodrilus
Q26407 ctenodrilus
Q29x8 oryzias lat
Q29x8 oryzias lat
Q29x8 oryzias lat
Q29x8 oryzias lat
Q9y188 priapulus coe
                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9xyt7 cassiopea x
Q26375 styela clav
                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                  February 18, 2004, 14:09:39; Search time 81.0526 Seconds (without alignments) 89.145 Million cell updates/sec
       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                     830525 segs, 258052604 residues
                                                                               US-09-643-260-18
162
1 DRQIKIWFQNRRMKWKKTALDWSWLQTE
                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                    - protein search, using sw model
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Q6JZW2
Q6JZW2
Q26478
Q817C9
Q817C9
Q57368
Q57359
Q57359
Q57359
Q27413
Q27413
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Q26208
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Gapop 10.0 , Gapext 0.5
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_bacteria:*
sp_fungi:*
sp_human:*
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seq length: 200000000
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sp_plant: *
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Match Length DB
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Perfect score:
Sequence:
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97
                                                                                                               Scoring table:
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Minimum DB Maximum DB

Database

Result ě

Searched:

Gaps

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Length 274; Indels

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RESULT 2

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Ge T., Lee H., Tomlinson C.R.; "Identification of an Antennapedia-like Homeobox Gene in the Ascidians
                                                                                                                                               Score 97; DB 11; Length 108;
Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 181;
                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
                                                                                          Hypothetical protein.
SEQUENCE 108 AA; 13070 MW; 123A78FCDD0E7D90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 181
181 AA; 20873 MW; AF39911408F06672 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOX-1903 (TrEMBLrel. 23, Last annotation update)
Homeobox protein (Fragment).
Styela clava (Sea squirt).
Elwaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Styelidae; Styela.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stypla pilcata (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Styelidae; Styela.
                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reaton 59.9%; Score 97; DB 5; l
Local Similarity 94.1%; Pred. No. 1.9e-05;
es 16; Conservative 1; Mismarches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 AA
                                                                                                                                                                                                                                                                                                                                                         181 AA
                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEAM: PF00046; homeobox; 1.
PRINTS; PR00024; HOWEDBOX.
PRINTS; PR00031; HTHREPRESR.
PRODOM; PD000010; Homeobox; 1.
SWART; SW00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50011; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
                                                                                                                                                                                                                                                             49 ERQIKIWFONRRMKWKKEHKDESQAPT 75
                                                                                                                                                                                                                          1 DRQIKIWFQNRRMKWKKTALDWSWLQT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH lambrepressr.
                                                     PROSITE; PS00027; HOMEOBOX 1; 1. PROSITE; PS50071; HOMEOBOX 2; 1.
                 ProDom; PD000010; Homeobox; 1
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 DROVKIWFONRRMKWKK 96
                                                                                                                                                 59.9%;
PRINTS; PR00031; HTHREPRESSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U05600; AAA16288.1; -. HSSP; P02833; 9ANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homeobox protein (Fragment)
                                                                                                                                    Query Match
Best Local Similarity 70.4%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Styela clave and plicata."
                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Ascidian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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026478;
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                                                                                                                                                                                                                                                                                                                 RESULT 4
Q26611
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                                                                                                                                                                                                                                                                                                                                                                                        Ge T. Lee H., Tomlinson C.R.;
"Identification of an antennapedia-like homeobox gene in the ascidians
Styela clava and S. plicata.";
Gene 147:219-222(1994).
-! SMDELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; $73920; AAB33061.2;
HSSP; P02833; 9ANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 97; DB 5; Length 60;
Pred. No. 6.3e-06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.; Strausberg R.; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases. Submitted (AUG-2002) to the EMBL/BCDS6986; AAH36986.1; -. InterPro; IPR001356; Homeobox. InterPro; IPR00047; HTH lambrepressr. PF00046; homeobox; 1. PR001049; HOMEOBOX.
                                                                                                                                                                                                                                          Styela clava (Sea squirt).
Bukaryota, Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Styelidae; Styela.
NCBI_TaxID=7725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 AA; 7630 MW; F506301E9679BA25 CRC64;
                                                                                                                                                                                  (TrEMBLrel. 01, Last sequence update) (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
11-ORT-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
                       60 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 AA.
DRQIKIWFQNRRMKWKK---TALDWSWLQTE 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NA-binding; Homeobox; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH lambrepressr.
Dfam. DF000046; homeobox; 1.
                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                        DNA binding protein AHox2 (Fragment)
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=95011617; PubMed=7926803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
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94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 94.1%
...hen 16; Conservative
                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                    01-NOV-1996
01-MAR-2003
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SEQUENCE
                                                                                                                            Q26375
Q26375;
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Q8JZW2;
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Gaps

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RESULT 3 Q8JZW2

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Di Lauro R.;
"Unusual number and genomic organization of Hox genes in the tunicate ciona intestinalis.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ535674; CAD59670.1;
Homeobox; DNA-binding; Nuclear protein.
                                                                                                                                                                                     SEQUENCE FROM N.A. Spagnuolo A., Ristoratore F., Di Gregorio A., Aniello F., Branno M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                  Ciona intestinalis.
Eukaryota, Metazoa, Chordata, Urochordata, Ascidiacea, Enterogona,
Phlebobranchia, Cionidae, Ciona.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                90 AA; 11352 MW; CAAAD6B261FE908E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 AA; 4827 MW; 592A0FEC12E58860 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 59.0%; Score 95.5; DB 5; Local Similarity 57.6%; Pred. No. 1.5e-05; hes 19; Conservative 3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DRQIKIWFQNRRMKWKKTALDWS-----WLQTE 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 AA
Putative homeobox protein Hox6/7 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA-binding, Homeobox, Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, Y14539; CAA74874.1; -. ZFIN; ZDB-GENE-980526-533; hoxc5a. InterPro; IPR001356; Homeobox. InterPro; IPR00047; HTH_lambrepressr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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PRINTS; PRO0031; HTHREPRESSR.
Probom; PD000010; Homeobox; 1.
SMART; SMO0199; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hoxc5 protein (Fragment). HOXC5A OR HOXC5.
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nes 16; Conservative
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                                                                                                                                      NCBI_TaxID=7719;
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SEQUENCE
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                                                                                                 Ge T., Lee H., Tomlinson C.R.;
"Identification of an Antennapedia-like Homeobox Gene in the Ascidians
Stycla clava and plicata.";
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
-1 - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; U05571; AAA16226.1; -.
HSSP; P02833; 9ANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Spagnuolo A., Ristoratore F., Di Gregorio A., Aniello F., Branno M., Di Lauro R., "Unueual number and genomic organization of Hox genes in the tunicate Ciona intestinalis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Urochordata, Ascidiacea, Enterogona,
Phlebobranchia, Cionidae, Ciona.
NCBI_TaxID=7719;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, A5535675, CADS9671.1; -1
Homeobox; DNA-binding; Nuclear protein.
SEQUENCE 435 AA: 48739 MW; DBDDF579C02BC9E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON TER 1 1 1 SEQUENCE 194 AA; 21886 MW; 8ADIB15B3E4800BC CRC64;
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Last sequence update)
Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.9%; Score 97; DB 5; illarity 94.1%; Pred. No. 2e-05; Conservative 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
                                                                                                                                                                                                                                                                                       (nterPro, IPR001356; Homeobox.
InterPro, IPR000047; HTH_lambrepressr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                               Pfam; PF00046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DRQIKIWFQNRRMKWKK 17
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Matches 16; Conservative
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Ciona intestinalis.
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Matches 16; Conserv
                                               SEQUENCE FROM N.A.
NCBI_TaxID=7725;
                                                                           STRAIN-Ascidian;
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01-MAR-2003
01-MAR-2003
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Bukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
Terebellida; Ctenodrilidae; Ctenodrilus.
NCBI_TaxID=40316;
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Terebellida; Ctenodrilidae; Ctenodrilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=94356262; PubMed=7915607;
DICK M.H., Buss L.W.;
"A PCR-based survey of homeobox genes in Ctenodrilus serratus
  58.0%; Score 94; DB 13; Length 46; 94.1%; Pred. No. 1.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 51;
                                           0; Indels
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Dick M.H., Buss L.W.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 AA; 6278 MW; 88C8F65161E94A22 CRC64;
                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
U-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
LOXS ORTHOLOG homeobox (Fragment).
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Last annotation update)
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94.1%; Pred. No. 1.4e-05;
                                                                                                                                                                                                                                               51 AA
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                                             1; Mismatches
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InterPro; IPR001047; HTH lambrepressr.
Pfam; PF001046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
SWART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Annelida: Polychaeta).";
Mol. Phylogenet. Evol. 3:146-158(1994).
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PROSITE; PS50071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-NAX-2003 (TrEMBLrel. 23, Last anno
Deformed ortholog homeobox (Fragment)
                                                                                                                                                                                                                                               PRT;
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EMBL; S76226; AAB31777.1; -.
HSSP; P02833; 9ANT.
                                                                                        1 DRQIKIWFQNRRMKWKK
Query Match
Best Local Similarity 94.1<sup>1</sup>
Matches 16; Conservative
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                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                      Ctenodrilus serratus.
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Matches
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Q27413
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Q23743
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                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
NCBI_TaxID=7955,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Teleostei; Euteleostei; Neoreleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Prince V.E., Joly L., Ekker M., Ho R.K.;
Zebrafish hox genes: genomic organization and modified colinear expression patterns in the trunk.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.0%; Score 94; DB 13; Length 43 94.1%; Pred. No. 1.1e-05; wismatches 0; Indels
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Kondo S., Naruse K., Shima A.;
Kondo S., Naruse K., Shima A.;
"Hox genes of the medakafish Oryzias latipes.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-! SHDEELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
ESMB.; AB026860; BAA86243.1;
-- HSSP; P02833; 1HOM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 AA; 5050 MW; 53034C37F3DFA596 CRC64;
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                                                                  Last sequence update)
Last annotation update)
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Last annotation update)
  43 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 AA
                                                                                                                                                      Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000010; Homeobox; 1.
PROSTIE: PS00027; HOWEOBOX 1; 1.
PROSTIE: PS50071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWART; SM0389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00017; HOMEOBOX 2; 1.
DNA-binding; Homeobox; NucTear protein.
NON TER 1 1 1
SEQUENCE 46 AA; 5955 MW; 6039999ED4;
                                             Created)
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PRT;
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ZFIN, ZDB-GENE-000823-6; hoxb5b.
InterFor, 1FR001356; Homeobox.
Pfam; PF00046; homeobox.
PRINTS; PR00024; HOMEOBOX.
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Pfam; PF00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
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                                         01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-OCT-2002 (TrEMBLrel. 22, HOXAS protein (Fragment).
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2003 (TrEMBLrel. 23,
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  PRELIMINARY;
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Gaps

SO OR OR OR SET THE SET OF SET

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SEQUENCE FROM N.A.

MEDLINE-99318125; PubMed=10391241;

MEDLINE-99318125; PubMed=10391241;

de Rosa R., Grenier J.K., Andreeva T., Cook C.E., Adoutte A., Akam M.,

Carroll S.B., Balavoine G.,

"Hox genes in brachiopods and prispulids and protostome evolution.";

"Hox genes in brachiopods and prispulids and protostome evolution.";

"Hox genes in brachiopods and prispulids and protostome evolution.";

"Hox genes in brachiopods and prispulids and protostome evolution.";

"EMBL, API44888; AAD40644.1; -..

HSSP; P02833; 9ANT.
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                      Oryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota, Metazoa, Chordata; Craniata; Eutebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
NUBL TaxID=8090;
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Pred. No. 1.5e-05;
1; Mismatches 0; Indels
Query Match 58.0%; Score 94; DB 5; Length 51; Best Local Similarity 94.1%; Pred. No. 1.4e-05; Matches 16; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Kondo S., Naruse K., Shima A.;
Kondo S., Naruse K., Shima A.;
"Hox genes of the medakafish Oryzias latipes.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-1 - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; BAD05691; BAA86244.1;
-1 - SHOSP; PO2833; 1HOM.
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Eukaryota; Metazoa; Priapulida; Priapulidae; Priapulus.
NCBI_TaxID=37621;
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                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                         57 AA
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Pfam; PP00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
                                                                                                          22 ERQIKIWFQNRRMKWKK 38
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94.1%;
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01-MAR-2003
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NCBI_TaxID=40316,
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                                                                             Dick M.H., Buss L.W.;
"A PCR-based survey of homeobox genes in Ctenodrilus serratus
(Annelida: Polychaeta).";
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Dick M.H., Buss L.W.;
"A PCR-based survey of homeobox genes in Ctenodrilus serratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.0%; Score 94; DB 5; Length 51; 94.1%; Pred. No. 1.4e-05; ive 1; Mismatches 0; Indels
                                                                                                                                                                           SEQUENCE FROM N.A.
Dick M.H., Buss L.W.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-1 - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL, U26627; AAC46849.1; --
HSSP; P02833; 9ANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 AA; 6533 MW; 9EDB50C927FBCBD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Annelida: Polychaeta).;
Mol. Phylogenet. Evol. 3:146-158(1994).
--. SUBCELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; S76416; ANT.
HSSP; PO2833; 9ANT.
InterPro; IPR001356; Homeobox.
InterPro; IPR001356; Homeobox.
PRam; PF00046; homeobox; I.
PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00024; HTHEPRESSR.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
CTS-DED protein (Fragment).
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PROSITE; PS50071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
NON TER 1 1
SEQÜENCE 51 AA; 6533 MM; 9EDB50C9271
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InterPro; IPR000047; HTH lambrepressr.
Pfam; PF000046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
                                                          MEDLINE=94356262; PubMed=7915607;
                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000010; Homeobox; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
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SMART; SM00389; HOX; 1.
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NCBI_TaxID=40316;
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DR InterPro; IPR001356; Homeobox.

DR Figar, PF00046; homeobox.

DR PRINTS; PR00004; homeobox.

DR PRINTS; PR000014; HOMEOBOX.

DR PRINTS; PR00010; HTHREPRESSR.

DR PROSITE; PS00021; HOMEOBOX.

DR PROSITE; PS00027; HOMEOBOX.

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DR PROSITE; PS00027; HOMEOBOX.

TOWER PROSITE; PS00027; HOMEOBOX.

AND -binding; Homeobox; Nuclear protein.

FT NON TER

SR AA; 7323 MW; 572F30DA57C9A613 CRC64;

Autches 16; Conservative 1; Mismatches 0; Indels 0; Gaps

Overy Matches 16; Conservative 1; Mismatches 0; Indels 0; Caps

Overy Matches 16; Conservative 1; Mismatches 0; Indels 0; Caps

DD 23 ERQIKIWFQURRAKWKK 17
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Search completed: February 18, 2004, 14:36:01 Job time : 83.0526 secs

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P09629
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 DRQIKIWFQNRRMKWKKTALDWSWLQTE
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HUMAN
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Maximum DB seq length: 200000000
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Match
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                                                                                                                                      Perfect score:
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6
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No.
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                                                   brachydanio
heterodontu
                                                                                                                                                                                  brachydanio
                                                                                                      xenopus lae
                                                                                                                                    mus musculu
                                                                                                                                                          xenopus lae
                                                                                                                                                                                                             rattus norv
                                                                                                                                                                                                                                      homo sapien
                                                                                                                                                                                                                                                                 notophthalm
                                                                                                                                                                                                                                                                                       xenopus lae
                                morone saxa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R PRINTS; PRO0024; HOMEOBOX:

R PARINTS; PRO0024; HOMEOBOX: 1.

R SMART; PRO01010; Homeobox: 1.

R PROSITE; PS00027; HOMEOBOX_1; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

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R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

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R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE; PS00027; HOMEOBOX_2; 1.

R PROSITE HOMEOBOX_2; 1.

R PROSITE HOMEOBOX_2; 1.

R PROSITE HOMEOBOX_2; 1.

                           Q9pwd4 m
P15861 b
Q91a29 b
P09019 b
P09002 m
P09070 x
P09074 b
P52949 r
P11267 f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HXA7_RAT STANDARD, PRT, 105 AA. P09634.
P09634.
01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
HOMEODOX PROTEIN HOX-A7 (HOX-1.1) (R5) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
HXC5_MOUSE
HXB6_BRARE
HXB6_BRARE
HXB6_HETFR
HXB6_MOUSE
HXB6_MOUSE
HXC6_MOUSE
HXC6_RARE
HXC6_RARE
HXC6_RARE
HXC6_RARE
                                                                                                                                                                                                                                HXA6 HUMAN
HXC6 NOTVI
HXC6 XENLA
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PIR; A27471; A27471.
HSSP; P02833; 9ANT.
TRANSFAC; T01707; -.
InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
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  Query Match
Best Local Similarity
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PR00025; ANTENNAPEDIA.
             PR00024; HOMEOBOX
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                                                                                                                     DNA BIND
DOMAIN
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DNA BIND
NON TER
SEQUENCE
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           PRINTS;
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HMSA_SALSA
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J. 5:2209-2215(1986).
-!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 126-229 FROM N.A. MEDLINE-65188311; PubMed-2986010; Colberg-Poley A.M., Voss S.D., Chowdhury K., Gruss P.; Structural analysis of murine genes containing homoeo box sequences and their expression in embryonal carcinoma cells.";
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=87286976; PubMed=2885847;
Kessel M., Schulze F., Fibi M., Gruss P.;
"Primary structure and nuclear localization of a murine homeodomain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 129-197 FROM N.A. MEDLINE=80653865; PubMed=2877873; MEDLINE=80653866; PubMed=2877873; Pareier G., Bucan M., Francke U., Colberg-Poley A.M., Gruss P.; "Sequential expression of murine homeo box genes during F9 EC cell differentiation.";
                                                                                                                                                                                                                                                                                                                                                                              Parikh H., Shah S., Hilt D., Peterkofsky A.; "Organization, sequence and regulation of expression of the murine
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
  ö
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARIȚY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 84:5306-5310(1987).
 7;
                                                                                                                               1-17U-1986 (Rel. 01, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
HOXA7 OR HOXA-7 (HOX-1.1) (M6-12) (M6)
                                                                                                           229 AA
 1; Mismatches
                       1 DRQIKIWFQNRRMKWKKTALDWSWLQT 27
                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, P02833, 9ANT.
TRANSFAC, T01278;
MGD, MGI:96179; Hoxa7.
InterPro; IPR001827; Antennapedia.
InterPro; IPR001365; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95197009; PubMed=7890170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M17192; AAA37833.1; -. EMBL; U15972; AAC52160.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00046; homeobox; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 314:713-718(1985).
 Conservative
                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                      Hoxa-7 gene.";
Gene 154:237-242(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A03314; A03314.
PIR; A28329; A28329.
                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=BALB/c;
                                                                                                                                                                                                                                 NCBI_TaxID=10090;
 19;
                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                        protein."
                                                                                                                     P02830;
                                                                                              HXA7 MOUSE
Matches
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"Molecular cloning and characterization of homeo-box-containing genes from Arlantic salmon.";
from Arlantic salmon.";
dene 62:141-152(1988).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
NCBI_TaxID=8030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
Probon; PD000010; Homeobox; 1.
SMART; SM0389; HOX; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS000027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homeobox; DNA-binding; Developmental protein; Nuclear protein.
                                                                                                                                                                                                                                           POLY-ARG.
ASP/GLU-RICH (HIGHLY ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                               Length 229;
                                                                                                                                                                                                                                                                                                                                                                            Score 97; DB 1; Lengtn 22., Pred. No. 2.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 75;
                                                                                                                                                                                                                                                                                                                    GAG -> APA (IN REF. 1).
D36E6BD61D8D5C6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FC02C3672F35475D CRC64;
                                                                                                                                                                                       ANTP-TYPE HEXAPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Homeobox protein S12-A (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 ERQIKIWFONRRMKWKKEHKDESQAPT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DRQIKIWFQNRRMKWKKTALDWSWLQT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 96;
                                                                                                                                                                                                                                                                                              POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88226009; PubMed=2897318;
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                                                                                                                                                                                                                                                                                                                         45 GF
25682 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmo salar (Atlantic salmon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M18903; AAA49559.1; -. PIR; I51341; I51341.
                                                                                                                                                                                                                                                                                                                                                                                                     59.98;
                                                                                                                                                                                                                                                                                                                                                                                                                          70.4%;
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                                                                                                                                                               Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 70.4
hes 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                 229 AA;
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                                                                                                                                                                                                                                           156
211
215
43
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nematopoietic cell lines.";
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Kausner R.D. (Collins F.S., Wagner L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Stapleton M., Soaree M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Robar S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

A Richarde S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

A Raha S.A., McMany D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Rahay J., Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

A Rahay J., Woung A.C., Shevchenko Y., Bouffard G.G.,

A Rahay J., Wollay K.C., Shevchenko Y., Bouffard G.G.,

A Rahay J., Wollay K.S., Schimuz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Salska W., Sanilus D.E.,

R. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. "Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 135-224 FROM N.A.
MEDLINE=90046821; PubMed=2573064;
Shen W.-F., Largman C., Lowney P., Corral J.C., Detmer K.,
Hauser C.A., Simonitch T.A., Hack F.M., Lawrence H.J.;
"Lineage-restricted expression of homeobox-containing genes in human
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Frezza D., D'Esposito M., Migliaccio E., Santini S.M., Fruscalzo A.; "Expression of HOX genes in T lymphocytes and hairy leukemia cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kidd K.K., Busygina V., DeMille M.M.C., Speed W.C., Ruggeri V., Kidd J.R., Pakeris A.J.;
"Overall linkage disequilibrium in 33 populations for highly informative multisite haplotypes spanning the HOXB gene cluster.";
Am. J. Hum. Genet. 67:235-235(2000).
                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                 .
                                                                                                                                                                                                                                                                                                                                                                                 "Alrenative splicing of the HOX 2.2 homeobox gene in human hematopoietic cells and murine embryonic and adult tissues."; Nucleic Acids Res. 19:539-545(1991).
                                                                                                                                                                                                                                                                                                                                                       Shen W.-F., Detmer K., Simonitch-Eason T.A., Lawrence H.J.,
              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lines."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                      HXB6_HUMAN STANDARD; PRT; 224 AA. P17509; P09068; Q9HB11; Q9UGH2; 01-NOV-1988 (Rel. 9); Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) HOMBO OR HOXEO HOXEO.
                 4
 78.3%; Pred. No. 1e-06;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
              Mismatches
                                                         1 DRQIKIWFQNRRMKWKKTALDWS 23
                                                                                                                                                                                                                                                                                                                           TISSUE=Placenta;
MEDLINE=91187672; PubMed=1672751;
              1;
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             18; Conservative
Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                   WCBI_TaxID=9606;
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                                                                                                                                                                             Q.
                                                            MEDLINE=85024888; PubMed=6091895;
Levine M., Rubin G.M., Tjian R.;
"Human DNA sequences homologous to a protein coding region conserved
"Human DNA sequences homologous to a protein coding region conserved
between homeoric genes of Drosophila.";
cell 38:667-673(1984).
-!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION PACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTIFIES ON THE ANTERIOR-POSTERIOR AXIS.
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 142961; -. GO; GO:0005634; C:nucleus; NAS. GO; GO:0005634; C:nucleus; NAS. GO; GO:0003700; F:transcription factor activity; NAS. GO; GO:0008595; P:determination of anterior/posterior axis, e. . .; GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 224;
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P -> R (IN REF. 1).
D -> A (IN REF. 1).
GR -> A (IN REF. 5).
W, D8P96AFAC893D878 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₹
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S -> E (in isoform 2).
/FITG=VSP 002389.
/FITG=VSP 002389.
/FITG=VSP 002389.
HV -> QL (IN REF. 3 AND 4)
                                                                                                                                                                                                                                                                                                                                 Isoid=P17509-1; Sequence=Displayed;
Name=2; Synonyms=Homeobox-less;
Isoid=P17509-2; Sequence=USP_002389;
-!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
Proc. Natl. Acad. Sci. U.S.A. 86:8536-8540(1989).
                                           PRELIMINARY SEQUENCE OF 136-240 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M30597; AAA36004.1; -.
EMBL; K02571; -; NOT_ANNOTATED_CDS.
PIR; S26400, S26400.
THSSP; P02833; 1HOM.
TRANSFAC; T01732; -.
Genew; HGNC:5117; HOXB6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR001827; Antennapedia.
InterPro, IPR001356; Homeobox.
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33 A 60
60 P
73 D
150 GR
25427 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X58431; CAA41335.1; -. EMBL; X58431; CAA41336.1; -.
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220
140
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58.6%; Score 95; DB 1; 1 66.7%; Pred. No. 4.5e-06;

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Hart C.P., Fainsod A., Ruddle F.H.;
"Sequence analysis of the murine Hox-2.2, -2.3, and -2.4 homeo boxes:
evolutionary and structural comparisons.";
Genomics 1:182-195(1987).
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    Gaps
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-i- SUBCELLULAR LOCATION: Nuclear.
-i- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schughart K., Utset M.F., Awgulewitsch A., Ruddle F.H.; "Structure and expression of Hox-2.2, a murine homeobox-containing
    5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-88054465; PubMed-2890503;
Lonal P., Arman E., Czoenek H., Ruddle F.H., Blatt C.;
"New murine homeoboxes: structure, chromosomal assignment, and
differential expression in adult erythropoiesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Alternative splicing of the HOX 2.2 homeobox gene in human hematopoietic cells and murine embryonic and adult tissues."; Nucleic Acids Res. 19:539-545(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91187672; PubMed=1672751;
Shen W.F., Detmer K., Simonitch-Eason T.A., Lawrence H.J.,
    Indels
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                                                                                                                                                                                                                                                01-NOV-1988 (Rel. 09, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
408-FEB-2003 (Rel. 41, Last annotation update)
HOMEDDOX protein HOX-B6 (HOX-2.2) (MH-22A).
HOXB6 OR HOXB-6 OR HOX-2.2.
                                                                                                                                                                                                        224 AA
                                                                         Mismatches
                                            1 DROIKIWFONRRMKWKKTA--LDWSWLQTE 28
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EMBL; J03782; AAA37843.1; -.
PIR; A31324; A31324.
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InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=88289762; PubMed=2899893;
2;
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  Conservative
                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA 6:409-418(1987).
                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
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FRANSFAC; T01733; -
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20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Winter P.C., Lappin T.R.; "Sequence characterisation and expression of homeobox HOX A7 in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE OF 130-195 FROM N.A.
MEDLINE=90215256; PubMed=2576652;
Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
;
                                                                                                                             PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00032; ANTENNAPEDIA; 1.
PROSITE; PS00071; HOMEOBOX 2; 1.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-99023755; PubMed-9804983;
McIlhatton M.A., Bremner P.S., McMullin M.F., Maxwell A.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                         58.6%; Score 95; DB 1; Length 224; 66.7%; Pred. No. 4.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Polakowska R., LaCelle P.T.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Bradshaw H., Hinds K., Keppler D.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE OF 1-91 FROM N.A.
Cho M., Kim M.H., Hwang C.Y., Min W.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Albrechtsen R., Wewer U.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                 220 POLY-GLU.
186 T -> P (IN REF. 3).
25310 MW; E8FCOBDEB57F5C3D CRC64;
                                                                                                                                                                                                                                                                   ANTP-TYPE HEXAPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          multi-potential erythroleukaemic cell line TF-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HXA7_HUMAN STANDARD; PRT; 230 AA.
P31268; 093168; 043148; 034148; 091001.
01_U11_1993 (Rel. 26, Created)
15_DEC_1998 (Rel. 37, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Last annotation update) Homeobox protein Hox-A7 (Hox-1A) (Hox 1.1). HOXA7 OR HOXIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
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Pfam; PF00046; homeobox; 1.
PRINTS; PR00025; ANTENNAPEDIA.
PRINTS; PR00024; HOMEOBOX.
PRODOM; PD00010; HOMEOBOX; 1.
SMART; SM00389; HOX; 1.
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205
220
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HXA7 HUMAN
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Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
                                                                                                                                                                                             Ovis aries (Sheep).
Wakaryota Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Caprinae; Ovis.
                                                   Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
SWART; SW00389; HOX; 1.
SWART; SW00389; HOX; 1.
PROSITE; PS000027; HOMEOBOX 1; 1.
PROSITE; PS500012; ANTENNAPEDIA; PARTIAL.
PROSITE; PS50071; HOMEOBOX 2; 1.
Homeobox; DNA-binding; Developmental protein; Nuclear protein;
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Pred. No. 1.2e-06;
Homeobox protein Hox-B6 (XlHox-2.2) (Fragment).
HOXB6 OR XLHOX-2.2.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence
28-FEB-2003 (Rel. 41, Last annotatic
Homeobox protein Hox-A5 (Fragment).
HOXAS OR HOXA-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro, IPR001827; Antennapedia.
InterPro, IPR001356; Homeobox.
Pfam; PP00046; homeobox; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 ERQIKIWFONRRMKWKK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M91587; AAA49750.1; -. PIR; IS1439; IS1439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.0%;
94.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 94.1
tes 16; Conservative
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                                                                                                                                Xenopodinae; Xenopus
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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ID HXAS_SHEEP
AC Q28599;
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DNA BIND
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          8
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PRINTS; PRO0025; ANTENNAREDIA.
PRINTS; PRO0024; HOMEOBOX.
Prodom: PD000010, Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00032; ANTENNAPEDIA; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00027; HOMEOBOX_2; 1.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein;
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POLY-GLU.
T -> A (IN REF. 3).
DA -> RR (IN REF. 5).
MISSING (IN REF. 5).
T -> V (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.6%; Score 95; DB 1; Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 95; LL ...
Pred. No. 4.6e-06;
Pred. no. 4.6e-18
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T -> I (IN REF. 7).
D -> Y (IN REF. 5).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AC004080; -: NOT ANNOTATED_CDS.
EMBL; AF032095; AAD01939.2; -.
EMBL; V32543; CAA59270.1; -.
EMBL; X84803; CAA59270.1; -.
EMBL; X84804; CAA59270.1; -.
EMBL; X8536; S15536.
HSSP; P02833; 9ANT.
TRANSFAC, T01105; -.
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POLY-ALA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR001827; Antennapedia.
InterPro, IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DRQIKIWFQNRRMKWKKTALD 21
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF026397; AAB94604.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25385 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ005814; CAA06713.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF00046; homeobox; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:5108; HOXA7.
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195
222
230 AA;
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01-JUL-1993
01-JUL-1993
28-FEB-2003
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DOMAIN DOMAIN DOMAIN

RESULT 7 HXB6_XENLA HXB6

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Gaps

Gaps

. 0

Score 94; DB 1; Length 71; Pred. No. 1.8e-06; L; Mismatches 0; Indels

1; Mismatches

71 AA; 8888 MW; 931049FAC1BAACB7 CRC64;

58.0%; 94.18;

HOMEOBOX.

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SMART: SM00389; HOX; 1.
PROSITE; PS00027; HOMEDBOX 1; 1.
PROSITE; PS500071; HOMEDBOX 2; 1.
HOMEDBOX; DNA-binding; Developmental protein; Nuclear protein;
Transcription regulation.
   InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH_lambrepressr.
                                                    PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                1 DROIKIWFONRRMKWKK 17
                                                                                                                                                                                                                                                                                            Best Local Similarity 94.1
Matches 16; Conservative
                                       Pfam; PF00046; homeobox;
                                                                                                                                                                                NON TER
DNA_BIND
NON_TER
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                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roche P.J.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSIERIOR AXIS.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS. ALSO BINDS TO ITS OWN PROMOTER. BINDS SPECIFICALLY TO THE MOTIF: 5'-CYNATTA[TG]Y-3'. SUBCELLULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
HOMEODEX protein HOX-A7 (Fragment).
HOXA7 OR HOXA-7.
Ovis arises (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                      Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.0%; Score 94; DB 1; Length 49; 94.1%; Pred. No. 1.2e-06; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 AA; 6331 MW; 1EE702315E7C099B CRC64;
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                                                                                                                                                                                                                                                                                                           InterPro; IPR001356; Homeobox.
Pfam; PF000046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
SWART; SM00389; HOX; 1.
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nes 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovidae, Caprinae, Ovis
                                                                                                                                                                                                                                                                                             P02833; 1HOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Q28600;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTIFIES ON THE ANTERIOR-POSITERIOR AXIS.
-1- SUBGELLULAR LOCATION: Nuclear.
-1- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                       01-JUL_1993 (Rel. 26, Created)
1-JUL_1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Homeobox protein Hox-C5 (NvHbox-3.4) (Fragment).
Homotophthalmus viridescens (Eastern newt) (Triturus viridescens).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92290273; PubMed=1351019; MEDLINE=92290273; PubMed=1351019; Belleville S., Beauchemin M., Tremblay M., Noiseux N., Savard P.; Homeobox.containing genes in the newt are organized in clusters similar to other vertebrates."; Gene 114:179-186 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00032; ANTENDAPEDIA; PRRTIAL.
PROSITE; PS50071; HOWEOBOX 2; 1.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                    71 AA
                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP, P02833, ISAN.
InterPro, IPR001827, Antennapedia.
InterPro, IPR001356, Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00046; homeobox; 1.
PRINTS; PR00024; HOWEDBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
    61
45 ERQIKIWFONRRMKWKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription regulation.
                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JC1161; JC1161.
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8316;
                                                                                                                                                                                                                                                                                 Notophthalmus.
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1 DRQIKIWFQNRRMKWKK 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M37567; AAA41343.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 94.1
les 16; Conservative
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                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HXAS SALSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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        SO THE STANK SERVICE COURSE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SE
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Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
                                                                                                                                                               ö
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PIR; D34510; D34510.
HSSP; P02833; JHOM.
InterPro; IPR001356; Homeobox.
Pfam; PP000046; Homeobox; 1.
ProDom; PD000010; Homeobox; 1.
PROSITE; SM00389; HOX; 1.
PROSITE; PSS00027; HOMEOBOX 1; 1.
PROSITE; PSS00071; HOMEOBOX 2; 1.
HOMEOBOX; DAA-binding; Developmental protein; Nuclear protein.
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MEDLINE=90099384; PubMed=2574865;
Walldorf U., Fleig R., Gehring W.J.;
Comparison of homeobox-containing genes of the honeybee and Drosophila.";
                                                                                                      Query Match
Best Local Similarity 94.1%; Pred. No. 1.8e-06;
Matches 16; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 74;
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                                                      07999FDE89995B42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 86:9971-9975(1989).
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 AA; 9263 MW; 5FC8FB4F723D3837 CRC64;
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94.1%; Pred. No. 1.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Apris mellifera (Honeybee).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 AA.
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     HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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P18865;
01-NOV-1990 (Rel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DROIKIWFONRRMKWKK 17
                                                                                                                                                                                                                                              SERQIKIWFQNRRMKWKK 61
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  4 63
71 71
71 AA; 8979 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 94.1 tes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apidae; Apis
                                                                                                                                                                                                                                                                                                                                                                                        HM90 APIME
P15860;
                             NON TER
SEQUENCE
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DNA_BIND
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SEQUENCE
DNA_BIND
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                                                                                                                                                                                                                                                                                                                                          RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSITERIOR AXIS.
                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butaleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapa
                                                                                                                                                                                                                                                                                                      STRAIN=Sprague-Dawley;
MEDLINE=89231502; PubMed=2907739;
Ralzon M., Chung S.Y.;
"The expression of rat homeobox-containing genes is developmentally regulated and tissue specific.";
Development 103:601-610(1988).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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SMART; SM0039; HOMEOBOX; 1.
SMART; SM00399; HOX; 1.
PROSITE; PS00003; HOWEOBOX 1; 1.
PROSITE; PS00071; HOMEOBOX 1; 1.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: PREDOMINANTLY SPINAL CORD AND KIDNEY.
SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
"DEFORMED" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.0%; Score 94; DB 1; Length 76; 94.1%; Pred. No. 1.9e-06; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 AA; 9293 MW; 5235F665C0672385 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1989 (Rel. 10, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
HOXAS.
28-FEB-2003 (Rel. 41, Last annotation update)
Homeobox protein Hox-C4 (R3) (Fragment)
HOXC4 OR HOXC-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 AA
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HSSP; P02833; 9ANT.
InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTM lambrepressr.
Pfam; PF00046; homeobox; 1.
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-!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                       "DEFORMED" SUBFAMILY.
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NON_TER
SEQUENCE
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                                                           MEDLINE=88226009; PubMed=2897318;
Fjose A., Molven A., Eiken H.G.;
"Molecular cloning and characterization of homeo-box-containing genes
                                                                                                                                                   Gene 62:141-152(1988).
-!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 95:3030-3035(1998).
-!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINES-2916.9491; PubMed=9501210;

Kmita-Cunisse M., Loosli F., Bierne J., Gehring W.J.;

"Homeobox genes in the ribbonworm Lineus sanguineus: evolutionary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lineus sanguineus (Ribbon worm).
Eukaryota; Metazoa; Nemertea; Anopla; Heteronemertea; Lineidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00032; ANTENNAREDIA; PARTIAL.
PROSITE; PS50071; HOMEOBOX 2; 1.
Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            828DEBDDF78AC820 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 94; DB 1;
Pred. No. 2e-06;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HATALINSA STANDARD; PRT; 80 AA. P81192; 81 5-JUL-1998 (Rel. 36, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homeobox protein Hox-A4 (LsHox 4) (Fragment).
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PIR; I51342; 151342.
HSSP; PO2833; 9ANT.
InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
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SMART; SM00389; HOX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :||||||||||||||||||||||||| ERQIKIWFQNRRMKWKK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 AA; 9489 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.0%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Franscription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                   from Atlantic salmon.";
                                         SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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28-FEB-2003 (Rel. 41, Last annotation update)
Homeobox protein Hox-B5 like (ZF-54) (Fragment).
HOXB5B OR ZF54 OR ZF-54.
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 94; DB 1; Length 80;
Pred. No. 2.1e-06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       80 AA; 9860 MW; F2CE1B01CB8042F1 CRC64;
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InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
InterPro; IPR001356; Homeobox.
InterPro; IPR00064; HTH_lambrepressr.
Pfam; PP001046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
PRODOM; P0000010; Homeobox; 1.
SWART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00027; HOMEOBOX 2; 1.
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InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
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ProDom; PD000010; Homeobox; 1.
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94.1%;
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Best Local Similarity 94...
Loca 16; Conservative
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Q8cbt3 mus musculu
Q95kv0 bos taurus
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Q8zra5 salmonella
Q8z8t6 salmonella
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Maeda S., Badger M.R., Price G.D.;
Maeda S., Badger M.R., Price G.D.;
Tidentification of ChpX and ChpY, catalyzing light-dependent CO2 bydration involved in CO2 uptake in Cyanobacteria.";
Submitted (APR-2001) to the BMBL/GenBank/DDBJ databases.
EMBL, AY029338; AAK37764.1; -..
InterPro; IPR0013918; NADHub_oxred4.
InterPro; IPR001750; Oxidored_q1.
PFINTS; PR01437; NUOXNRDTASE4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NGI_TaxID=1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB 2; Length 513;
Pred. No. 2.1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAD; Oxidoreductase; Plastoquinone.
SEQUENCE 513 AA; 54237 MW; 2732576E525224AB CRC64;
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Last sequence update)
Last annotation update)
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Q8IMX4
Q8IC35
Q26213
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Q8FU02
Q8YGX7
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Q8Q1B0
Q8Q1B0
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83.3%;
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 5; Conservative
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59 IDWEWL 64
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Q8vtt pseudomonas
Q8kzs2 acetobacter
Q94380 caenorhabdi
Q94380 caenorhabdi
Q8x058 yersinia pe
Q8x054 ralstonia s
Q9x147 pseudomonas
Q8g3a8 brucella su
Q8yeh7 brucella su
Q9yeh7 brucella su
Q8yeh7 brucella su
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OBG354 wiggleswort
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Q9fzx5 bacteriopha
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89.145 Million cell updates/sec
                                                                                                          February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Database

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Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori
Aksoy S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wigglesworthia brevipalpis.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Wigglesworthia.
NCBI_TaxID=164609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the endocellular obligate symbiont of tsetse
                                                                                                                                                                                 Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the thermophilic cyanobacterium Thermosphechococus elongatus BP-1.";

EMBL; AP005371; BAC08354.1; -.
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Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 AA; 30329 MW; 021D35F51D8AB77E CRC64;
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Cytochrome o ubiquinol oxidase A (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.2%; Score 37; DB 16; L
100.0%; Pred. No. 2.2e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       flies, Wiggleeworthia glossinidia.";
Nat. Genet. 32:402-407(2002).
EMBL; AB063521; BAC24293.1; -.
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                                                                                                                                                           MEDLINE=22225144; PubMed=12240834;
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MEDLINE=22297718; PubMed=12219091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Conservative
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SEQUENCE
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"Functional characterization of the genes coding for the terminal protein and DNA polymerase from bacteriophage GA-1. Evidence for a sliding-back mechanism during protein-primed GA-1 DNA replication.";
J. Mol. Biol. 264:453-464(1996).
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=97094855; PubMed=8940089;
Freire R., Serrano M., Salas M., Hermoso J.;
Activation of replication origins in phi29-related phages requires the recognition of initiation proteins to specific nucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Horcajadas J.A., Meijer W.J.J., Rojo F., Salas M.;
"Transcriptional map of the Bacillus bacteriophage GA-1. Analysis
the viral C2 promoter.";
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                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
phi-29-like viruses.
NCBL_TaxID=12345;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=20280072; PubMed=10773070;
Gascon I., Lacaro J.M., Salas M.;
"Differential functional behavior of viral phi29, Nf and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; X96987; CAC21518.1;
Hypothetical protein.
SEQUENCE 107 AA; 12636 MW; ABEF24E68A255E02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Meiler W.J.J., Horcajadas J.A., Salas M.;
"The phi29 family of phages.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 12.6 kDa protein.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 28:2034-2042(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complexes.";
J. Biol. Chem. 271:31000-31007(1996)
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MEDLINE=97123975; PubMed=8969297;
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Best Local Similarity 100.
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;
Rhabditidae; Peloderinae; Caenorhabditis.
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Characterization of the toluene-sensitive mutants of Pseudomonas putida KT2442TOL.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB066295; BAB83393.1; -.
InterPro; IPR001505; Copper CuA.
InterPro; IPR001505; Cyper CuA.
InterPro; IPR002429; Cyt_c_ox_2.
Pfam; PP00116; COX2; I.
ProDom; PD00111; Copper CuA; 1.
TIGRFAMA; TIGR01433; CyoA; 1.
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Bacteria; Proceeo, Pseudomonas.
Pseudomonadacee; Pseudomonas.
VCBI_TaxID=303;
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                                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                            McMurray A.A.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                   investigation blology."; Science 282:2012-2018(1998).
BMBL, 281141; CAB01488.2; -...
WRIPEPP; ZG47.13; CE25668.
InterPro; IPR0012900; DUF38.
InterPro; IPR001810; F-box.
Pfam; PF00646; F-box; 1.
Pfam; PF00847; FTH; 1.
SEQUENCE 311 AA; 36603 MW; 928464208868C48B CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                            MEDLINE=99069613; PubMed=9851916;
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 23,
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Matches 5; Conservative
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295 LEWEWL 300
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                                                                                                                                SEQUENCE FROM N.A.
                                                                       NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=PMI1;
Syn C.K.C., Liew C.F., Swarup S.;
Syn C.K.C., Liew C.F., Swarup S.;
"Pseudomonas putida cytochrome o ubiquinol oxidase A, B, C, and
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match 90.2%; Score 37; DB 2; Length 288; Best Local Similarity 83.3%; Pred. No. 2.3e+02; Matches 5; Conservative 1; Mismatches 0; Indels
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EMBL; AB086015; BAB9773.1; -.
InterPro; IPR001515; Copper_CuA.
InterPro; IPR005033; CyOA II.
InterPro; IPR002429; Cyt_Cox_2.
Pfam; PP00116; COX2; I.
PRINTS; PR00116; CXCOXIDASEII.
PRODOM; PM00131; Copper_CuA; I.
PIGRRAMS; TIGR01433; CyOA; 1.
                                                                                                                              genes.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
BMB. AF321090; AAL37192.1; -.
InterPro; IPR001505; Copper CuA.
InterPro; IPR00533; CyDA II.
Probom; P0000131; Copper Cub; 1.
IIGREAMS; TIGR01433; CyOA; 1.
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SEQUENCE 288 Aa; 31882 MW; 60E40B3A36516BFC CRC64;
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01-FEB-1997 (TrEMBLrel. 02, C)
01-MAY-2000 (TrEMBLrel. 13, Ls
01-MAY-2003 (TrEMBLrel. 23, Ls
2C47.13 protein.
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135 LDWKWL 140
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                        SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
STRAINEATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-10984043;
Stroat C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener D.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino B., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; "Genome sequence of the plant pathogen Ralstonia solanacearum."; Mature 415:497-602(2002).

EMBL; ALG46072; CAD16624.1; -
InterPro; IPR001505; COpper CuA.
InterPro; IPR001505; CyoA II.
InterPro; IPR001429; Cyt Cox. 2.
InterPro; IPR001092; HiH. basic.
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Pseudomonadaceae; Pseudomonas.
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TIGREAMS; TIGRO1433; CycA; 1.

PROSITE; PSO0038; HIM-1; 1.

Oxidoreductase; Complete protecome.

SEQUENCE 329 AA; 35781 MW; 08DA178C39A5964A CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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InterPro; IPR005333; CyoA.II.
InterPro; IPR002429; Cyt C ox 2.
InterPro; IPR001092; HLH-DasiG.
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TIGRFAMS; TIGR01433; CyoA; 1.
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Matches 5; Conserv
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SEQUENCE 331 AA;
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01-MAR-2001 (
01-MAR-2001 (
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Matches
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STRAIN=KIMS / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21470413; PubMed=11586360;
MEDLINE-21470413; PubMed=11586360;
MEDLINE-21470413; PubMed=11586360;
Parkhill J., Warn B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
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Simmonds M., Skelton J., Stevens K., Whitchead S., Barrell B.G.;
"Genome sequence of Yersinia pestis, the causative agent of plague.";
Nature 413:523-527(2001)
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Probable transmembrane cytochrome O ubiquinol oxidase (Subunit II)
oxidoreductase protein (EC 1.10.3.-).
CYOAI OR RSC2917 OR RS00308.
                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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MEDLINE=21681879; PubMed=11823852;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Cytcohrome O ubiquinol oxidase subunit II (EC 1.10.3.-).
CYOA OR YPO3164 OR Y1021.
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J. Bacteriol. 1844(601-4611(2002).
BMBL; AJ414155; CAC92399.1;
EMBL; AAJ41455; CAC92399.1;
EMBL; AE013705; AAM84602.1;
Enterpro; IPRR0101505; COPPER CUA.
InterPro; IPRR0101505; COPPER CUA.
InterPro; IPRR01031; COPPER CUA.
FODOM; PD000131; COPPER CUA; 1.
ProDom; PD000131; COPPER CUA; 1.
CACAGOREGUCASE; COMPLETE COPPER COMPLETE COPPER COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COMPLETE COM
                 318 AA.
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Best Local Similarity 83.3.
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             PRELIMINARY;
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|35 LDWKWL 140
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Q8XVB4 RESULT 10

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344 AA; 38948 MW; B643C91321B600EC CRC64;

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SEQUENCE
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STRAIN=1330 / Biovar 1;
STRAIN=1330 / Biovar 1;
REDINE=2224741; PubMed=12271122;
Raulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
Bugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
"The Brucella suis genome reveals framemental similarities between
animal and plant pathogens and symbionts.";
Proc. Natl. Acad. Sci., U.S.A. 99:13148-13153 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN=16M / ATCC 23456 / Biotype 1;

MEDLINEs20020109; PubMed=11756688;

MEDLINEs20020109.

DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharypa A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., "The genome sequence of the facultative intracellular pathogen Brucella melitensis.";
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                                                                                                                                             Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
VODI_TaxID=29461;
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83.3%; Pred. No. 2.8e+02;
ive 1; Mismatches 0; Indels
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Brucellaceae, Brucella.
NCBI_TaxID=29459;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annocation update)
Cytochrome O ubiquinol oxidase subunit II (EC 1.10.3.-).
                                                                                                                                                                                                                                                                                                                                                                              Complete protecome.
SEQUENCE 341 AA; 38563 MW; 38856F0751223F5D CRC64;
                                           Q8G3A8 PRELIMINARY, PRT; 341 AA. O8G3A8; 01-MAR-2003 (TrEMBLrel. 23, Created 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Ubiquinol oxidase, subunit II.
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EMBL; AE009623; AAL53082.1; -.
InterPro; IPR001505; Copper CuA.
InterPro; IPR006333; CyoA II.
ProDom; PD000131; Copper CuA;
TIGRFAMB; TIGR01433; CyoA; 1.
Oxidoreductase; Complete proteome.
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Matches 5, Conservative
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|38 LDWKWL 143
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                                                                                                                                      Brucella suis.
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X MEDLINE=21173698; PubMed=11259647;

MEDLINE=21173699; PubMed=11259647;

A Bisen J., Heidelberg J.F., Alley M.R.K., Ohte N., Maddock J.R.,

A Bisen J., Heidelberg J.F., Alley M.R.K., Ohte N., Maddock J.R.,

A Potcock I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

A Folonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

A Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

A Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

R. Complete genome sequence of callobacter creecentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

R. EMBL, AEOSSS1; AAK23749:1;

R. TIGR, CC1773;
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                                                                                                                     Gape
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Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteracee, Caulobacteraces, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caulobacterace, Caul
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Match 90.2%; Score 37; DB 16; Length 344; Local Similarity 83.3%; Pred. No. 2.8e+02; es 5; Conservative 1; Mismatches 0; Indels
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22, Last annotation update)
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MEDLINE-98344137; PubMed-9679194;
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InterPro; IPR006333; CyOA_II.
ProDom; PD000131; Copper_CuA; 1.
IIGRPAMs; TIGR01433; CyOĀ; 1.
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Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
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Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
D. Hanahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N.,
A Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
A Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
A Aoki K.-I., Yoshizawa T., Nakamura Y.,
D. Robb F.T., Horikoshi K.,
A Aoki K.-I., Shizuya H., Kikuchi H.,
D. Mak Res 5.55-76(1998)
L. Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.",
DNA Res 5.55-76(1998)
L. DIA Res 5.55-76(1998)
L. DIA Res 7.5-76(1998)
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90.2%; Score 37; DB 17; Length 377;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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Search completed: February 18, 2004, 14:35:59 Job time : 18.3684 secs

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Scoring table:

Searched:

Title: Perfect score:

Sequence:

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-!-SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL HYDROLASES).
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Aljinovic G., Pohl T.M.;
"Sequence and analygis of 24 kb on chromosome II of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaces; Saccharomyces.
NCBI_TaxID=4932;
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R PTR; S45914; S45914.

R SGD; S0000260; YBR056W.

DR InterPro; IRR001547; Glyco hydro 5.

R PROSITE; PS00659; GLyCOSYL_HYDROL_F5; FALSE_NEG.

DR Hypothetical protein; Hydrolase; Glycosidase.

FT ACT_SITE 236 236 NUCLEOPHILE (BY SIMILARITY).

ACT_SITE 333 333 NUCLEOPHILE (BY SIMILARITY).

ACT_SITE 334 57822 NW; 5133A161736ADDD3 GRC64;
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Q01582
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Q13415
Q13412
Q9413
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01-0CT-1994 (Rel. 30, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical 57.8 kba protein in PRF6-MUM2 intergenic region.
YBR056W OR YBR0510.
  905880
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llarity 83.3%; Pred. No. 28;
Conservative 1; Mismatches
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79.423 Million cell updates/sec
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Y373_MYCPN
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Query

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P57544;
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                                                                                                                                                                                                                                                                                                                                                          RECAINS # STAINS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                          MEDLINE=93003330; PubMed=1327149;
Abaigar L.T., Yeh Y.I., Jong A.Y.;
"Eunctional and structural conservation of Schizosaccharomyces pombe
dTMP kinase gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQHEKAE -> LNMKRLK (IN REF. 1)
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Pfam; PF02223; Thymidylate kin.
TIGRFAMS; TIGR00041; DTMP kinase; 1.
PROSITE; PS01331; THYMIDYLATE KIRASE; 1.
Transferase; Kinase; Nucleotide biosynthesis; ATP-binding.
NP BIND 37 SOHEKAE -> INMKPIK (IN DDF 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PATHWAY: BIOSYNTHESIS Of GTTP from GTMP.
                                                                                                                      Sukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                      Schizosaccharomycetales; Schizosaccharomycetaceae;
ul-JUN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Thymidylate kinase (EC 2.7.4.9) (dTMP kinase).
TMP OR SPCC70.07C.
                                                                                                  Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                               Biochim. Biophys. Acta 1132:222-224(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GeneDB SPombe; SPCC70.07c;
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HSSP; P00572; 1TMK.
                                                                                                                                                          Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5'-diphosphate.
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                           NCBI_TaxID=4896;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEM, custration the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-0cT-2001 (Rel. 40, Created)
16-0cT-2001 (Rel. 40, Last sequence update)
16-0cT-2001 (Rel. 40, Last sequence update)
16-0cT-2001 (Rel. 40, Last sequence update)
10-0cT-2001 (Rel. 40, Last sequence
K -> T (IN REF. 1)..
TIQYIYEQINKGVT -> PSIYYRANQQRCN (IN REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBL_TaxID=2104;
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 1; Length 210;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 1; Length 281;
Pred. No. 33;
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281 AA; 32569 MW; FC70957510D7BEF3 CRC64;
                                                                                                                                                                                                                                                                                                              4266144AEDAB68C0 CRC64;
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F -> I (IN REF. 1).

F -> L (IN REF. 1).

S -> YA (IN REF. 1).

H -> D (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. No. 25; ive 0; Mismatches
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STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
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Hypothetical protein
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 LDWEW 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 DWEWL 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LDWEW 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ø
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Fukaya M., Tayama K., Tamaki T., Ebisuya H., Okumura H.,
Rawamura Y., Horinouchi S., Bappu T.;
"Characterization of a cytochrome al that functions as a ubiquinol
oxidase in Acetobacter aceti.";
-1 Bacteriol. 175:4307-4314 (1993)
-1 PATHARY: TERMINAL OXIDASE FOR ETHANOL OXIDATION.
-1 SUBUNIT: HETEROTETRAMER OF THE SUBUNITS 1, 2, 3 AND 4.
-1 SUBLULAR LOCATION: Integral membrane protein.
-1 SIMILARITY: SOME. TO MITOCHONRIAL OR BACTERIAL COXZ SUBUNITS.
BUT LACK HEME-BINDING DOMAIN.
                                    STRAIN=1023;
MEDLINE=93322308; PubMed=8392509;
Toyama K.. Tamaki T., Ebisuya H., Okumura H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                         23
307
24
66
107
                                                                                                                                                                                                                                                                                   PIR; A36885; A36885.
HSSP; P18400; 1CYW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 LDWKWL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LDWEWL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=303;
 WCBI_TaxID=435;
                                                                                                                                                                                                                                                                                                                                                                                                                Lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYOA PSEPU
Q9WWR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                              HASP, APUULLS, CLAHESP, BURGO, LCYM.

INTERPRO; IPRO01505, COPPER CUA.

INTERPRO; IPRO01505, CYL C OX 2.

INTERPRO; IPRO01403, CYL C OX 2.

INTERPRO; IPRO0116, COX2, 1.

Prodom; PPO0116, COX2, 1.

TIGRAMS; TIGRO113; CYOA, 1.

PROSITE; PS00013; PROKAR LIPOPROTEIN; FALSE NEG.

Oxidoreductase; Respiratory chain; Blectron transport; Transmembrane;

'innrotein; Complete protecome.

'innrotein; Complete protecome.
                                                                          Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UUL-1999 (Rel. 34, Last senocation update)
16-UUL ovidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome Al subunit 2) (Oxidase BAI(3) subunit 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Acetobacteraceae; Acetobacter.
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UBIQUINOL OXIDASE POLYPEPTIDE
N-ACYL DIGLYCERIDE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.2%; Score 37; DB 1; Length 296; llarity 83.3%; Pred. No. 35; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
EXTRACELLULAR (POTENTIAL).
1AB2B4F0408FFBAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34180 MW;
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            symbiotic bacterium)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 .
296 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDWKWL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acetobacter aceti.
                                            NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LDWEWL 6
                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QOX2_ACEAC
P50653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIPID
DOMAIN
TRANSMEM
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Matches
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30-MAY-2000 (Rel. 39, Last sequence update)
310-MAY-2000 (Rel. 39, Last annotation update)
Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase subunit 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
UBIQUINOL OXIDASE POLYPEPTIDE II.
N-ACL DIGLYCERIDE (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.2%; Score 37; DB 1; Length 307; 83.3%; Pred. No. 36; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00013; PROKÂR LIPOPROTEIN; 1.
Oxidoreductase; Transmembrane; Respiratory chain; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E66734B84410996D CRC64;
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MEDLINE=99085656; PubMed=9868765;
Hirayama H., Takami H., Inoue A., Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01166; CYCOXIDASEII.
ProDom; PD000131; Copper Cua; 1.
TIGRFAMB; TIGR01433; CyoA; 1.
                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001505; Copper_CuA.
InterPro; IPR006133; CyOA II.
InterPro; IPR002429; Cyt. C_ox_2.
Pfam; PF00116; COX2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33921 MW;
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                                                                                                                                                                                                                                                                                   EMBL; D13185; BAA02480.1; -.
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Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WormPep; C07A9.1; CE00S02.
InterPro; IPR002619; CX.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_C; 1.
ProDom; PD006744; CX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q50864;
01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z29094; CAA82340.1; -. PIR; S40706; S40706.
HSSP; P23807; 11XX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                            Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 35, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997
01-NOV-1997
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                                                                                                                      elegans.
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    SOTT THE STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STA
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                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                   Pseudomonas putida IH-2000.";
FEMS Microbiol. Lett. 169:219-225(1998).
-!- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT
OF THE ALENE STRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE
GROWN AT HIGH AERATION (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: Ubiquinol-8 + 0(2) = Ubiquinone-8 + H(2)0.
                                                                                                                                                                -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
BUT LACK HEME-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lickrams; lickolis; Cyoa; l.
PROSITE; PSO0013; PROVAR_LIPORROTEIN; l.
Oxidoreductase; Respiratory chain; Electron transport; Transmembrane; Inner membrane; Signal; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfald J., Burton J., Conlean A., Copsey T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Merazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
'Isolation and characterization of toluene-sensitive mutants from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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UBIQUINOL OXIDASE POLYPEPTIDE II.
N-ACYL DIGLYCERIDE (POTENTIAL).
PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical protein C07A9.1 in chromosome III precursor.
C07A9.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001505; Copper_CuA.
InterPro; IPR006333; CyoA II.
InterPro; IPR002429; Cyt. C_ox_2.
Pfam; PP00116; COX2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000131; Copper CuA; 1.
TIGRFAMS; TIGR01433; CyoA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB016787; BAA76356.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34702 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P18400; 1CYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5,
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SEQUENCE
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YKT1_CAEEL
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Guo D., Bowden M.G., Pershad R., Kaplan H.B.;

Guo D., Bowden M.G., Pershad R., Kaplan H.B.;

"The Myxococcus xanthus ribaBC operon encodes an ATP-binding cassette transporter homolog required for 0-antigen biosynthesis and multicellular development.";

J. Bacteriol. 178:1631-1639(1996).

-!- FUNCTION: INVOLVED IN 0-ANTIGEN BIOSYNTHESIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
"2.2 Mb of contiguous nucleotide sequence from chromosome III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
HYPOTHETICAL PROTEIN C07A9.1 IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Deltaproteobacteria, Myxococcales,
Cystobacterineae, Myxococcaceae, Myxococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 1; Length 488;
Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels

    -!- SIMILARITY: Contains 1 C-type lectin family domain.

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187 N-LINKED (GLCNAC. .) (PC
237 N-LINKED (GLCNAC. .) (PC
4109 N-LINKED (GLCNAC. .) (PC
54717 MW; 9022691E47078814 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; FULLOS, STATE TO TAKE THE STATE OF THE PROSITE; PSS00615; C TYPE LECTIN 1; FALSE NEG. PROSITE; PSS0041; C TYPE LECTIN 2; 1.
PROSITE; PSS0041; C TYPE LECTIN 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHROMOSOME III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 56; ive 0; Mismatches
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SEQUENCE
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TRANSMEM
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                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94161495; PubMed=8117072; Patck M., Krumbach K., Eggeling L., Sahm H.; Eucline synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis.";
                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                 Bacceria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                 Length 1275;
                                                                  EMBL, U36795; AAB05019.1; -.
PIR, T18556; T18556.
InterPro; IPR001296; Glyco_trans_1.
InterPro; IPR001139; Glyco_trans_2.
Pfam; PF00534; Glycos_transf_1; 1.
Pfam; PF00535; Glycos_transf_1; 1.
Lipopolysaccharide biosynthesis.
SEQUENCE 1275 AA; 139596 WW; 3AF9662A10A140F1 CRC64;
                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum (Brevibacterium flavum).
                                                                                                                                                                90.2%; Score 37; DB 1; Le
100.0%; Pred. No. 1.4e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein Cg10250 (ORFX).
GGL0250.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Appl. Environ. Microbiol. 60:133-140(1994).
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POTENTIAL.
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                                                                                                                                                    Query Match
Best Local Similarity 100.00
There 5; Conservative
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                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                             349 DWEWL 353
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                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1718;
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P42459;
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TRANSMEM
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                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ubiquinol oxidase polypeptida II precursor (EC 1.10.3.-) (Cytochrome O subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase Subunit 2).
CYOA OR BUSG456.
Buchnera aphidicola (subsp. Schizaphis graminum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PROII66; CYCOXIDASEII.
Prodom; PD000131; Copper CuA; 1.
TIGRAMA; TIGRO1433; CyoA; 1.
PROSITE; PS00013; PROKAR LIPOPROTEIN; FALSE NEG.
Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
                                                                                                                                  Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UBIQUINOL OXIDASE POLYPEPTIDE II
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                                                                                            DB 1; Length 289; 48;
                                                                                                                                  0; Indels
                                    POTENTIAL.
5C7A38DC8BFF078A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3D80A02A84732963 CRC64;
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POTENTIAL.
                                                                                                                                                                                                                                                                                                          290 AA.
                                                                                            Score 36; DB 1
Pred. No. 48;
2; Mismatches
                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome
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  POTENTIAL
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InterPro; IPR001505; Copper CuA.
InterPro; IPR006333; CyoA II.
InterPro; IPR006429; Cyt c ox 2.
InterPro; IPR006437; Prok Ilpoprot.
Pfam; PF00116; COX2; 1.
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                                                        31381 MW;
                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
                                                                                          87.8%;
66.7%;
                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal; Lipoprotein;
SIGNAL 1
196 2
230 2
258 2
289 AA;
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255
255
43
64
88
109
290 AA;
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256 VDWEWI 261
                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                        1 LDWEWL 6
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                                                                                                                                                                                                                                                                                                        CYOA BUCAP
Q8K993;
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MEDLINE=97354468; Pulwhed=9252186;
DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
"A cytokine-responsive IkappaB kinase that activates the transcription
                                                                                                                                                                                                                                                                                                                                                                                             015111; 014666; Q13132; Q92467; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 15-SEP-2003 (Rel. 42, Last annotation update) 1nhibitor of nuclear factor kappa-B kinase alpha (IKK-alpha) (IKK-alpha) (IKK-alpha) (IKK-alpha) (IKK-alpha) (IKK-alpha) (IKK-alpha) (IKK-alpha) (IKK-alpha) (IKK-alpha) (IKK-alpha) kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKBIKA).
                                                                    Gaps
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TISSUB=Cervical carcinoma;
MEDLINE=96258427, bubMed=8777433;
Connelly M.A., Marcu K.B.
"CHUK, a new member of the helix-loop-helix and leucine zipper families of interacting proteins, contains a serine-threonine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND SER-180.
MEDINE=98188283; PubMed=9520446;
Ling L., Cao Z., Goeddel D.V.;
"NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98008813; PubMed=9346484; Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L., Meruni D.B., Barbosa M., Mann M., Manning A., Rao A.; I. J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.; I. I. J.W., and IKK-2: cytokine-activated IkappaB kinases essential for NF-kappaB activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hu M.C.-T., Wang Y.-P.;
TikappaB kinase-alpha and -beta genes are coexpressed in adult and
embryonic tissues but localized to different human chromosomes.";
Gene 222:31-40(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB=T-cell;

MEDLINE=97386461, PubMed=9244310;

Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;

"Identification and characterization of an IkappaB kinase.";
                                                                    ٠<u>;</u>
Length 290;
                                                                    1; Indels
   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
                                                                                                                                                                                                                                                                                                                                                                     745 A.A.
                                                                 0; Mismatches
   Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell. Mol. Biol. Res. 41:537-549(1995)
                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99032998; PubMed=9813230;
   87.8%;
                                     83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Cervical carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 278:860-866(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 388:548-554(1997).
                                                                 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell 90:373-383(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHUK OR IKKA.
Homo sapiens (Human)
                                                                                                                                                                                                134 LDWRWL 139
                                     Best Local Similarity
                                                                                                                                  1 LDWEWL 6
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                                                                                                                                                                                                                                                                                                                                                                     IKKA_HUMAN
   Query Match
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IKKA HUMAN
                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IKK PHOSPHORYLATION.
MEDLINE=99038238; PubMed=9819420;
Nemoto S., Dibonato J.A., Lin A.;
"Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase land NF-kappaB-inducing kinase.";
MOI. Cell. Biol. 18:7336-7343(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21968797; PubMed=11971985; MCDA2; NCOA3; IKKB AND IKBKG. MEDLINE=21968797; PubMed=11971985; Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J., O'Malley B.W.; Tsai M.J., Malley B.W.; Tsai M.J., Molley B.W.; Tsai M.J., Molley B.W.; Tsai M.J., Molley B.W.; Tsai M.J., D. I kappa B. Kinase."; Molley B.W.; Tsai M.J., Call. Biol. 22:3549-3561(2002).

-:-FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates
                                                                                                                                                                                                          Delhase M., Hayakawa M., Chen Y., Karin M.;
"Positive and negative regulation of IkappaB kinase activity through
IKKDeta subunit phosphorylation.";
Science 284:309-313(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENZYME REGULATION: Activated when phosphorylated and inactivated
                                                                                                            'NF-kappaB activation by tumour necrosis factor requires the Akt
                                                              MEDLINE=99413720; PubMed=10485710;
Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M.,
Donner D.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.", Am. J. Physiol. 278:C451-C462(2000).
                                              AND MUTAGENESIS OF THR-23
Ser-176.";
Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998)
                                                                                                                                                                                           MEDLINE=99212141; PubMed=10195894;
                                                                                                                                                                                                                                                                                                                                                                                                    REVIEW.
MEDLINE=20178139; PubMed=10712233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF009225; AAC51671.1; -. EMBL; AF080157; AAD08996.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U22512; AAC50713.1; -. HSSP; Q63450; 1A06.
Genew; HGNC:1974; CHUK.
MIM; 600664; -.
                                                                                                                            serine-threonine kinase.";
Nature 401:82-85(1999),
                                              PHOSPHORYLATION BY AKT,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Jobin C., Sartor R.B.;
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Genomics 27:348-351(1995).
                                     STRAIN-BALB/C;
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                          SECUENCE
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[KKA MOUSE STANDARD; PRT; 745 AA.

[G606B0; Q9D2X3;

[G-07-2001 [Rel. 40, Last sequence update)

[G-07-2001 [Rel. 42, Last annotation update)

[Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)

[Inhibitor of nuclear factor kappa-B kinase alpha subunit (KC 2.7.1.-)

[I kappa-B kinase alpha) (IRRA) (IKK-alpha) (IKK-Alpha)

[I kappa-B kinase 1] (IKK,1) (Conserved helix-loop-helix ubiquitous kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKBIKA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIJUE=9604444; PubMed=7558004; Mock B.A., Connelly M.A., McBride O.W., Kozak C.A., Marcu K.B.; Mock B.A., Connelly M.A., McBride O.W., Kozak C.A., Marcu K.B.; "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome 10 and mouse chromosome 19.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleogtomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                 LOSS OF AUTOPHOSPHORYLATION.
LOSS OF PHOSPHORYLATION AND OF
                                                                                                                                                                                                                                                                                                                                        T-A: NO CHANGE IN PHOSPHORYLATION.
S-A: NO CHANGE IN PHOSPHORYLATION.
E -> G (IN REF. 2).
TS -> AY (IN REF. 5).
TS -> AY (IN REF. 5).
P -> A (IN REF. 3).
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                                                                                                                                                                                                                                                                  T->A: LOSS OF PHOSPHORYLATION AND DECREASE OF KINASE ACTIVITY.
K->A: LOSS OF KINASE ACTIVITY.
GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:000384; F:IkappaB kinase activity; TAS.
GO; GO:000384; F:IkappaB kinase activity; TAS.
GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.
GO; GO:000525; P:immune response; TAS.
InterPro; IRR0019; Prot kinase.
InterPro; IRR001245; Tyr pkinase.
InterPro; IRR001245; Tyr pkinase.
Pfam; PR00109; TyrKINASE.
PRINTS; PR00109; TyrKINASE.
PROSTITE; PS00107; PROTEIN KINASE ATP; 1.
PROSTITE; PS00107; PROTEIN KINASE ST; 1.
PROSTITE; PS00108; PROTEIN KINASE ST; 1.
PROSTITE; PS00101; PROTEIN KINASE DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                             PHOSPHORYLATION (BY PKB/AKT1). PHOSPHORYLATION (BY MAP3K14).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                            LEUCINE-ZIPPER (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                   7A90B59BC98A56C2 CRC64;
                                                                                                                                                                                                                                                                                                                    ACTIVITY.
S->E: FULL ACTIVATION.
T->A: NO CHANGE IN PHC
                                                                                                                                                                                                                (BY SIMILARITY). (BY SIMILARITY).
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Pred. No. 1.2e+02;
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TS -> DL (IN RE
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Matches 5, Conservative
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144
23
176
23
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686
745 AA;
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                                                                                                                                                                       Phosphorylation Phosphorylation |
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Caralbues Royans, 1. (1507 pt.)

Station Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shibataa K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibataa K., Yoshino M., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalo V., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Rachim D., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Anone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerte P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Saya T., Shibata Y., Storch K.-F., Wumnihaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Nachahana Y., Wannihaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Nemoto S., DiDonato J.A., Lin A.;
"Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase kinase kinase kinase kinase (1840) MP-kappaB-inducing kinase.";
Mol. Cell. Biol. 18:7336-7343 (1998).
                                                                                                                                     Connelly M.A., Marcu K.B.; "CHUK, a new member of the helix-loop-helix and leucine zipper families of interacting proteins, contains a serine-threonine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking leucine zipper and helix-loop-helix domains reveal that IKKalpha and IKKbeta have different activation requirements.";
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"Positive and negative regulation of IkappaB kinase activity through IKKbeta subunit phosphorylation.";
Science 284:309-313(1999).
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Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
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"The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";
Am. J. Physiol. 278:c451-c462[2000].
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McKenzie F.R., Connelly M.A., Balzarano D., Mueller J.R.,
Geleziunas R., Marcu K.B.;
                                                                                                                                                                                                                                                                           catalytic domain.";
Cell. Mol. Biol. Res. 41:537-549(1996).
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                                                                                          MEDLINE=96258427; PubMed=8777433;
FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 3)
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                                                                                                                                                                                                                                                                                          Name=1: Squence=Displayed;
Name=2: Synonyms=Delta LH;
IsoId=060680-1; Sequence=VSP_004866, VSP_004867;
Name=3: Synonyms=Delta LH;
Name=3: Synonyms=Delta H;
IsoId=060680-3: Sequence=VSP_004868, VSP_004869;
-!- TISSUE SPECIPICITY: Ubiquitous only for isoform 1, isoforms 2 and 3 are expressed predominantly in brain and T-lymphocytes.
-!- DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by E11, E15 and E17 days. In the limb development, its expression predominates in the limb buds at E12.5 day.
-!- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by MERN: and dephosphorylated by PP2A. Autophosphorylated.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                  -!- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but also as an homodimer. Directly interacts with IKK-gamma/NEMO. Heterodimers form the active complex. The tripartite complex can also bind to MAP3K14/NIK, MEKK1, IKAP and IKB-alpha-P65-P50 complex. A weak interaction with TRAR2 cannot be excluded. Part of a complex composed of NCOA2, NCOA3, IKKB, IKBKG and CREBBP (By
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**SLERVANDATURMORTIS -> IFRKAVKSMERNGRKGH
SLF (in isoform 2)
/FIId=VSP_004866.
              the dissociation of the inhibitor/NP-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates
                                                                   ENZYME REGULATION: Activated when phosphorylated and inactivated
FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Missing (In isoform 2).
/FIId=VSP 004867.
/PIId=VSP_004867.
/FIId=VSP_004868
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PROMINS; PRO0109; TYKKINASE.
PRODOM; PTOCK KINASE; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00119; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEMO-BINDING.
ATP (BY SIMILARITY)
ATP (BY SIMILARITY).
BHY SIMILARITY.
PHOSPHORYLATION (BY PKB/AKTI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY).
PHOSPHORYLATION (BY MAP3K14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN KINASE.
LEUCINE-ZIPPER (POTENTIAL)
                                                                                                                                                                                                                         SUBSCELLULAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphorylation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:99484; Chuk.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR001245; Tyr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AK018671; BAB31335.1; -.
                                                                                       when dephosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U12473; AAC52589.1;
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29
44
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23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; 149101; 149101.
HSSP; Q63450; 1A06.
                                                                                                                                                                                                              similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144
23
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                                                    NCOA3
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MOD_RES
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BINDING
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MEDLINE=98008814; PubMed=9346485; Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.; Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.; "IkappaB kinase-bea: NP-kappaB activation and complex formation with IkappaB kinase-alpha and NIK."; Science 278:866-869(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Lung;
MEDLINE=22389857; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                             IKKB HUMAN STANDARD; PRT; 756 AA.
014920; 075327;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2:7.1.-)
(I-kappa-B-kinase beta) (IKBKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
2) (IKKZ) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIKB)
IKBKB OR IKKB.
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mihara M., Okumura K.;
to human chromosome band
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Cervical carcinoma; MEDLINE=98008813; PubMed=9346484; MEDLINE=98008813; PubMed=9346484; Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.; Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.; In W.K.-1 and IKK-2: cytokine-activated IkappaB kinases essential for NF-kappaB activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99032998; PubMed=9813230;
Hu M.C.-T., Wang Y.-P.;
"IkappaB kinase-alpha and -beta genes are coexpressed in adult and
embryonic tissues but localized to different human chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                     ö
                                                                                                             Length 745;
                                                                                           Score 36; DB 1; Length /*2.
Pred. No. 1.2e+02;
1; Indels
             /FTId=VSP 004869.

K -> E (IN REF. 3).

S -> Y (IN REF. 3).

3FEF5582AFF92233 CRC64;
3
Missing (in isoform
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [4]
SEQUENCE FROM N.A., AND GENE MAPPING.
MEDLINE-98438415; PubMed=9763654;
Shindo M., Nakano H., Sakon S., Yagita H.,
Assignment of Ikappas kinase beta (IKBKB)
8D12-->pll by in situ hybridization.";
                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytogenet. Cell Genet. 82:32-33(1998).
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د
                                                       400 S
84728 MW;
                                                                                                                 87.8%;
                                                                                                                                 83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 278:860-866(1997).
                                                                                                                                                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 222:31-40(1998).
                                 236 2
400 4
745 AA;
                                                                                                                                                                                                                               738 LDWSWL 743
                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                           1 LDWEWL 6
                                                     CONFLICT
VARSPLIC
                                   CONFLICT
                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                             IKKB HUMAN
                                                                                                                                                     Matches
FTFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99038218; PubMed=9819420; ...
Nemoto S., DiDonato J.A., Lin A.;
"Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase Land NF-kappaB-inducing kinase.";
Mol. Cell. Biol. 18:7336-7343(1998).

    LYBEDF.
    SUBCELULIAL LOCATION: Cytoplasmic.
    TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal muscle, kidney, pancreas, spleen, thymus, prostate, testis and peripheral blood.
    PTM: Phosphorylated by MEKK1 and probably also by MAPSK14/NIK.

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Luu X., Glibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeelley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S., Schmutz J., Myers R.M., Schein J.E., Jones S.J.M., Marra M.A.; Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weakly autophosphorylated.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. IKAPPAB KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         603258; -. GO: Cortoplasm; NAS. GO: 0005737; C: cytoplasm; NAS. GO: 0005524; F: ATP binding activity; NAS. GO: 0004674; F: protein serine/threonine kinase activity; NAS. GO: 0016563; F: transcriptional activator activity; NAS.
                                                                                                                                                                                                                                                                                                                                                                Jobin C., Sartor R.B.;
"The I kappa BNP-kappa B system: a key determinant of mucosal inflammation and protection.";
Am. J. Physiol. 278:C451-C462(2000).
                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20178139; PubMed=10712233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF029684; AAC51860.1; -. EMBL; AF080158; AAD08997.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF031416; AAC64675.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BC006231; AAH06231.1; -.
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                                                                                                                                                                                                                   PHOS PHORY LATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; Q63450;
                                                                                                                                                                                                                                                                                                                                   REVIEW
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PHOSPHORYLATION.

K->A: LOSS OF KINASE ACTIVITY AND NO EFFECT ON BINDING TO NIK.

S->A: DECREASE OF ACTIVITY.

S->E: FULL ACTIVATION.

S->E: FULL ACTIVATION.

S->E: FULL ACTIVATION.

S->E: FULL ACTIVATION.

WHSKVRQKSEVDIVVSEDIMGTVKF -> CVRMWPGTVAHS

CNPSTLGGGRGRMI (IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.,;
"Murine IKB kinase-B, a developmentally regulated protein kinase that
constitutively phosphorylates serine residues of IkB.",
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TKKB MOUSE STANDARD; PRT; 757 AA.
088351; OSR1JG;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Inhibitor of nuclear factor kappa B kinase bets aubunit (EC 2.7.1.-)
Inhibitor of Inclear factor NF-kappa B (IKK-beta) (IKK-beta) (IKK-beta) (IKK-beta) (IKK-beta) (IKK-beta) (IKK-Beta) (IKK-Beta) (IKK-Beta) (IKK-BETA) (IKK-BETA) (IKK-BETA) (IKK-BETA) (IKK-BETA) (IKK-BETA) (IKK-BETA) (IKK-BETA) (IKK-BETA) (IKK-BETA) (IKK-BETA) (IKK-BETA) (IKK-BETA) (IKK-BETA) (IKK-BETA) (IKK-BETA) (IKK-BETA) (IKK-BETA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98188238; PubMed-9520401;
Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Differential regulation of IkappaB kinase alpha and beta by two upstream kinases, NF-kappaB-inducing kinase and mitogen-activated protein kinase/ERK kinase kinase-1."; Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                    BY SIMILARITY.
PHOSPHORYLATION (BY SIMILARITY)
PHOSPHORYLATION.
            Interpro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser thr_pkinase.
InterPro; IPR002290; Ser thr_pkinase.
Pfam; PP000069; pkinase; 1.
ProDom; PP000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; PALSE_NEG.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
Transferase; Serine/threomine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 756;
P:protein amino acid phosphorylation; NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                PROTEIN KINASE.
LEUCINE-ZIPPER (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                       -> H (IN REF. 1).
F9CADF671AE9E14E CRC64;
                                                                                                                                                                                          NEMO-BINDING.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEKKI STRAIN=C57BL/6; TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 1; I
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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86563 I
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479
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1177
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177
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255
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                                                                                                                                                                                                                                                                                                                                                                                                                                     756 AA;
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 30; GO:0006468;
                                                                                                                                                                   15
458
737
21
21
44
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145
177
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181
231
                                                                                                                                                  Phosphorylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okumura K.;
                                                                                                                                                                                                                                                                                                                                              MUTAGEN
MUTAGEN
MUTAGEN
CONFLICT
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MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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DOMAIN
DOMAIN
NP BIND
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MOD_RES
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DEVELOPMENTAL STAGE

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MOD_RES
MOD_RES
CONFLICT
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CONFLICT
CONFLICT
                                         CONFLICT
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                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                            RESULT 15
IKKB_RAT
                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                              MEDLINE=99038238; PubMed=9819420; Nemoto S., DiDonato J.A., Lin A.; Nemoto S., DiDonato J.A., Lin A.; Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase 1 and MP-kappaB-inducing kinase."; Mol. Cell. Biol. 18:7336-7343(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Cytoplasmic.
TISSUB SPECIFICITY: Expressed in liver, kidney and spleen.
DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout the mouse embryo, at B9.5 day its expression begins to be localized to the brain, neural ganglia, neural tube, and in liver at E12.5 day. At E15.5 day, the expression is further restricted to specific tissues of the embryo.

PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
                                                                                                                                                                                                                                   Jobin C., Sartor R.B.,
"The I kappa B/NF-kappa B system: a key determinant of mucosal
inflammation and protection.";
Am. J. Physiol. 278-c451-c462(2000).
-!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
the dissociation of the inhibitor/NF-kappa-B complex and
ultimately the degradation of the inhibitor. Also phosphorylates
                                                                                                                                                                                                                                                                                                                                                                    also as a homodimer. Directly interacts with IKK-gamma/NEMO. Heterodimers form the active complex. The tripartite complex can also bind to MEKKI, MAP3K14/NIK, IKAP and IKB-ALPHA-P65-P50 complex. Phosphorylated IKB-alpha is further released from the complex. Found in a complex composed of NCOA2, NCOA3, IKRA, IKBKG and CREBBP (By similarity).
            Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.; "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling pathway activates ItappaB kinases (IKK-alpha/beta) and IKK-beta is a developmentally regulated protein kinase."; Oncogene 18:5514-5524(1999).
                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK Weakly autophosphorylated.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
IKAPPAB KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEUCINE-ZIPPER (POTENTIAL)
NEMO-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1338071; IXbkb.
InterPro; IPR000719; Prot kinase.
InterPro; IPR00290; Ser Thr pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                      MEDLINE=20178139; PubMed=10712233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF026524; AAC23557.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF088910; AAD52095.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphorylation
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BINDING
ACT_SITE
MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nemoto S., Dibonato J.A., Lin A.; "Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase kinase."; Mol. Cell. Biol. 18:7336-743(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammation and protection.";
Am. J. Physiol. 278:C451-C462(2000)
-!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complex. Phosphorylated IKB-alpha is further released from the complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKBKG and CREBBP (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
Inhibitor of nuclear factor Kappa B (Kinase beta subunit (EC 2.7.1.-)
I. KRDpa-B-kinase beta) (IKBKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIKB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          also as a homodimer. Directly interacts with IKK-gamma/NEMO. Heterodimers form the active complex. The tripartite complex can also bind to MEKKI, MAP3K14/NIK, IKAP and IKB-alpha-P65-P50
                                                             N -> D (IN REF. 2).
N -> D (IN REF. 2).
K -> E (IN REF. 2).
L -> F (IN REF. 2).
F -> Q (IN REF. 2).
K -> R (IN REF. 2).
TLDWSWLQMEDBERCSLEQACD -> VTA (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weakly autophosphorylated.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
IKAPPAB KINASE SUBFAMILY.
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SIMILARITY)
SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 1; Length 757; Pred. No. 1.2e+02;
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"IKK beta in megakaryocyte differentiation.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                 86690 MW; FED962F095449C5E CRC64;
      (BY
(BY
                                   PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKK PHOSPHORYLATION.
MEDLINE=99038238; Pubmed=9819420;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEKB OR IKKB
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds (without alignments)

B7.531 Million cell updates/sec

Title: US-09-643-260-17

Perfect score: 41

Sequence: 1 LDWEWL 6
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Fotal number of hits satisfying chosen parameters: 28330

283308 seqs, 96168682 residues

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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cbbBc protein (U60 integral membrane	cytochrome ba(3) (hypothetical prote	conserved hypothet cytochrome ba(3) c sensor histidine k	hypothetical prote probable membrane hypothetical prote	hypothetical prote chitinase - Strept protein R09E10.3 [hypothetical prote hypothetical prote
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ALIGNMENTS

RESULT 1 S45914 probable glucan 1,3-beta-glucosidase (BC 3.2.1.8 N;Alternate names: hypothetical protein YBR0510	RESULT 1 845914 probable glucan 1,3-beta-glucosidase (EC 3.2.1.58) YBR056w - yeast (Saccharomyces cerev N.Alternate names hypothetical protein YBR0510
C; Species: Saccintomyces Carevisace C; Date: 26-Aug-1994 #sequence revision O C; Accession: 845914; 849511; \$58855 R:Alinovic G: Pohl F.M.; Pohl T.M.	C.)Decres: Saccinatumyces Cerevisiae C.)Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 19-Apr-2002 C.)Accession: S45914; S49511; S55855 R.Alijnovic, G.: Pahl, F.M.: Pohl, T.M.
submitted to the Protein Sequence Databa A. Reference number: \$45906	juence Database, August 1994
A;ACCEBBION: S45914 A;MOLECULE LYDE: DNA A:Desiding: 1-501 /ALT	
A;Cross-references: EMBL:235925; NID:953 A;Experimental source: strain S288C	A:Cross-references: EMB:Z35925; NID:g536292; PID:g536293; MIPS:YBR056w A:Experimental source: strain S288C
R,Aljinovic, G. submitted to the EMBL Data Library, October 1994 A:Description: Secuence and analysis of 24 kb on chromosome	Jibrary, October 1994 analysis of Saccharomyces cerevis
A;Reference number: S49503 A;Accession: S49511	
A;Molecule type: DNA A;Residues: 1-501 <al2></al2>	
A;Cross-references: EMBL:246260; NID:g559942; PID:g559952 A:Experimental source: strain S288C	2260; NID:9559942; PID:9559952 n S288C
R;Aljinovic, G.; Pohl, T.M.	
Teast 11, 4,3-4/7, 1373 A;Title: Sequence and analysis of 24 kb on chromosome II A:Reference number: S55846; MUID:95321020; PMID:7597852	sis of 24 kb on chromosome II of Saccharomyces cerevisiae. MUID:95321020: PMID:7597852
A; Accession: S55855	and the translation not obtain
A;Molecule type: DNA	suce not snown; transtation not snown
A,Crosiques: 1-301 All A.S. A,Crosic Teferences: A.Notes - references: A.Notes - the nucleotide sequence was submitted	A; Acsiduces: 1.501. Ann A; Cross-references: EMBL:246260; NID:9559942; PIDN:CAA86399.1; PID:9559952 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994
C;Genetics:	
A, Map position: 2R C; Keywords: glycosidase; hydrolase	irolase
Query Match 95.1%; Score Best Local Similarity 83.3%; Pred. Matches 5; Conservative 1; Mis	3#; 3#;
Qy 1 LDWEWL 6	
Db 109 IDWEWL 114	
RESULT 2 T41553 thymidylate kinase - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe	n yeast (Schizosaccharomyces pombe) ses pombe

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A;Gene: coxW
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; resp
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C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Peb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
C;Accession: 873617
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A;Reference number: 87327; MUID:97105885; PMID:8948633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AE000027; GB:U00089; NID:g1673941; PIDN:AAB95939.1; PID:g167396
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                          C;Accession: JC5900
R;Surpin, M.A.; Luebben, M.; Maier, R.J.
Gene 183, 201-206, 1996
A;Title: The Bradyrhizobium japonicum coxWXYZ gene cluster encodes a bb3-type ubiquinol A;Reference number: JC5900; MUID:97149299; PMID:8996107
A;Accession: JC5900
A;Accession: JC5900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-281 <HIM>
                                                                                                                                                                                                                                                                                    bo-type ubiquinol oxidase (EC 1.10.3.-) chain II - Bradyrhizobium japonicum
C;Species: Bradyrhizobium japonicum
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                        Gaps
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Score 37; DB 2;
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1; Mismatches
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70;
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Query Match
Best Local Similarity 83.3
Matches 5, Conservative
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226 LEWEWL 231
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A; Residues: 1-277 <SUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: S28955
R;Abaigar, L.T.; Yeh, Y.I.S.; Jong, A.Y.
R;Abaigar, L.T.; Yeh, Y.I.S.; Jong, A.Y.
R;Abaigar, L.T.; Yeh, X.I.S.; Jong, A.Y.
R;Accession: S28955
R;Rolcoule rype: mRNA
R;Residues: 1-210 cABA>
A;Residues: 1-210 cABA>
A;Cross-references: EMBL:X65868; NID:g4973; PIDN:CAA46698.1; PID:g4974
C;Superfemily: afTPP kinnase
C;Superfemily: afTPP kinnase
C;Keywords: ATP; nucleotide binding; nucleotide biosynthesis; P-loop; phosphotransferase
F;14-21/Region: nucleotide-binding motif A (P-loop)
  C;Accession: T4153.

C;Accession: T4153.

R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D.

submitted to the EMBL Data Library, June 1998

A;Reference number: Z22001

A;Accession: T4153.

A;Accession: T4153.

A;Actatus: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-210 <WOO>

A;Catus: Experimental source: EMBL:AL023794; PIDN:CAA19357.1; GSPDB:GN00068; SPDB:SPCC70.07c

A;Experimental source: strain 972h-; cosmid c70

C;Genetics:
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C;Species: Schizosaccharomyces pombe
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein ZC47.13 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Accession: T27590
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C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20
C; Accession: T27590
R; McMurray, A.
submitted to the EMBL Data Library, October 1996
A; Reference number: Z20391
A; Reference number: Z20391
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-242 <WIL>A; Residues: 1-242 <WIL>A; Cross-references: EMBL; Z81141; PIDN: CAB03488.1; CESP: ZC47.13
A; Experimental source: clone ZC47
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 172/3
C;Superfamily: Caenorhabditis elegans hypothetical protein 2C47.9
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 210;
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52;
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Best Local Similarity 100.v
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                                                                                                                                                                                                                                                                                                         A,Gene: SPDB:SPCC70.07c
A,Map position: 3
A;Introns: 45/1; 110/3
C;Superfamily: dTMP kinase
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Best Loc Matches

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Gaps

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Indels

Length 318;

Score 37; DB 2; Pred. No. 80; 1; Mismatches

90.2%; 83.3%;

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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule: 1-318 «KUR»
A;Cross.references: GB:ALS90842; PIDN:CAC92399.1; PID:g1S981102; GSPDB:GN00175
G;Genetics:
A;Gene: cyos
C;Genetics: Cyos
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; res
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Best Local Similarity 83.3%
Then 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 LDWKWL 140
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J. Bacteriol. 175, 4307-4314, 1993
A;Title: Characterization of a cytochrome a-1 that functions as a ubiquinol oxidase in A
A;Recession: A36885; MUID:93322308; PMID:8392509
A;Accession: A36885
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytochrome O ubiquinol oxidase chain II (ЕС 1.10.3.-) [imported] - Yersinia pestis (stra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CjAccession: AD0384
R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rttherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Tele: Genome sequence of Yersinia pestis, PMID:11586360
                                                                                                                                                                                                                                                                                   A;Gene: cyoA; BU472
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; respiratory chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: terminal oxidase for ethanol oxidation
C; Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C; Keywords: copper; electron transfer; heterotetramer; membrane-associated complex; oxid
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-307/Product: bo-type ubiquinol oxidase chain II #status predicted <MAT>
F;89-105/Domain: transmembrane #status predicted <TM1>
                                 gb.
                           A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: A84985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bo-type ubiquinol oxidase (EC 1.10.3.-) chain II precursor - Acetobacter aceti
N;Alternate names: cytochrome al chain II
C;Species: Acetobacter aceti
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C'Species: Yersinia pestis
C'Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Residues: 1-307 <FUK>
Cross-references: GB:D13185; NID:g409064; PIDN:BAA02480.1; PID:g433186
Experimental source: isolate 1023
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   90.2%; Score 37; DB 2; 83.3%; Pred. No. 74; ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complex: heterotetramer; chains I, II, III and IV
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                                                                                                                                                                                           A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37;
Pred. No.
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1es 5; Conservative
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Best Local Similarity
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135 LDWKWL 140
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125 LDWKWL 130
81-86, 2000
                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-296 <STO>
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                                                                                                               A;Statue: preliminary
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K.; Lim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: cyoA; PA1317
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; respiratory chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytochrome o ubiquinol oxidase chain II (EC 1.10.3.-) [imported] - Brucella melitensis C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 22-Mar-2002 C;Datesion: A3489 B;Accession: A3489 Brucella melitens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: I
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; res;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-331 <STO>
A;Cross-references: GB:AE004561; GB:AE004091; NID:g9947253; PIDN:AAG04706.1; GSPDB:GN00
cytochrome o ubiquinol oxidase subunit II PA1317 [imported] - Pseudomonas aeruginosa (Species: Pseudomonas aeruginosa (C;Species: Pseudomonas aeruginosa (C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 (S;Stcession: D83480 R;Stcession: D83480 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Li Lory, S.; Olson, M.V.
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A;Realdudes: L-344 «KMS)
A;Crosa-references: GB:AE008917; PIDN:AAL53082.1; PID:g17983945; GSPDB:GN00190
A;Experimental source: strain 16M
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Pred. No. 83;
1; Mismatches
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Similarity 83.3%;
5; Conservative
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133 LDWKWL 138
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Best Local Similarity
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R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;bescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome strn
A;Reference number: A75001
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A, Status: preliminary
A, Molecule type: DA
A, Residues: 1-379 < KAW>
A, Cross-references: GB: AJ248284; GB: AL096836; NID: G5457730; PIDN: CAB49237.1; PID: G545774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable cytochrome o ubiquinol oxidase chain II protein (EC 1.10.3.-) [imported] - Sinc CiSpecies: Sinorhizobium meliloti
CiSpecies: Sinorhizobium meliloti
CiDate: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
CiAccession: C96006
RiFinan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. US.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-4k pSymB megaplasmid from the N2-fixing endc A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: C96006
A;Status: preliminary
A;Molecule type: DNA
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A;Cross-references: GB:AL591985; PIDN:CAC49715.1; PID:g15141202; GSPDB:GN00167
A;Cross-references: GB:AL591985; PIDN:CAC49715.1; PID:g15141202; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F., L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
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C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; resī
chain beta (soxb) PAB0214 - Pyrococcus abyssi (strain Orsay)
                                          C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: F75144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 379;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 2;
Pred. No. 96;
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100.0%; Pred. No. >v,
... 0; Mismatches
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Job time : 6.5921 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Gene: soxB; PAB0214
C,Superfamily: sarcosine oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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A;Gene: cyoA; SMb21487
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    sarcosine oxidase,
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A; Pitle: Complete sequence and gene organization of the genome of a hyper-thermophilic a A; Reference number: A71000; MUID:98344137; PMID:9679194
A; Accession: B71184
A; Accession: B71184
A; Residues preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-377 < KAWA
A; Residues: 1-377 < KAWA
A; Residues: 1-377 < KAWA
A; Residues: 1-377 < KAWA
A; Residues: Lis accession replaces an interim accession for a sequence replaced by GenBank
C; Genetics:
A; Note: this accession replaces an interim accession for a sequence replaced by GenBank
C; Superfamily: sarcosine oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: 20.Apr-2001 #sequence_revision 20-Apr-2001 #text_change 24-May-2001
C;Accession: A87469
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon In, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87469
A;Accession: A87469
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C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
                                                                                Gaps
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83.3%; Pred. No. 89;
ive 1; Mismatches 0; Indels
    Length 344;
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DB 2;
87;
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    Score 37;
Pred. No.
90.2%;
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Best Local Similarity 100.C
Matches 5; Conservative
                                      Best Local Similarity 83.3
Matches 5; Conservative
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141 LDWKWL 146
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LDWEW 358
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Sequence 939, App Sequence 939, App Sequence 46514, A Sequence 19572, A Sequence 32800, A Sequence 3354, Ap Sequence 6, Appli Sequence 2, Appli

Appl Appl Appl Appl Appl

Sequence 2, A Sequence 33, Sequence 37, Sequence 38, Sequence 38, Sequence 38, Sequence 29,

OM protein

Run on:

Searched:

Database

Sequence:

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OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
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APPLICANT: May, Michael J.
APPLICANT: Ghosh, Sankar
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/847,940B
CURRENT APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
SUPPRIOR FILING DATE: 2000-08-22
SUPPRIOR PLILING DATE: 2000-08-22
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                                  US-09-864-761-46514
US-10-369-493-19572
US-10-369-493-3354
US-10-369-493-3354
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US-09-847-9468-2
US-09-847-9468-3
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US-09-847-946A-148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/09847940B Patent No. US20020156000A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 17, Application US/09847946A; Publication No. US20030054999A1; GENERAL INFORMATION: APPLICANT: May, Michael J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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Query Match
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118, App
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                                                                                                                                          February 18, 2004, 14:36:10; Search time 16.6974 Seconds (without alignments) 75.239 Million cell updates/sec
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1: \cgn2_6/prodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: \cgn2_6/prodata/1/pubpaa/PCT_RW PUB.pep:*

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                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-847-946A-115
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Maximum Match 100%
Listing first 45 summaries
                                                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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SEQ ID NO 121
LENGTH: 7
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Matches 6; Conservative
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                  APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FELLING DATE: 2001-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 166
SOFFWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 45, Application US/09847946A

Bublication No. US20300549991

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Findeis, Mark A

APPLICANT: Pindeis, Mark A

APPLICANT: Pindeis, Mark A

APPLICANT: Hannig, Gerhard

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REPERENCE: PPI-119

CURRENT FILING DATE: 2001-05-02

PRIOR PAPLICATION NUMBER: 60/201,261

PRIOR PAPLICATION NUMBER: 60/201,261

PRIOR PAPLICATION NUMBER: 09/643,260

PRIOR PILING DATE: 2000-08-22

PRIOR PILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTHARE: PATENTIN VET: 2.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence:NEMO binding OTHER INFORMATION: sequence
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                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
Ghosh, Sankar
Findeis, Mark A
Phillips, Kathryn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 6; Conservative
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APPLICANT: PRINCIPS, MARK A
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FILE OF INVENTION AND APPLICANT
FOR THIN OWNERS: 0/00/10/5-02
FILE REPRENCE: PRINCIPS APPLICANT
FOR FILINO DATE: 0/00-10/5-02
FILE MARK APPLICANTON NORMER: 0/00/44/360
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Sequence 116, Application US/09847946A publication No. US20030054999A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 116
LENGTH: 9
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Publication No. US200300549991
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Findeal, Mark A
APPLICANT: Findeal, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
ITILE OF INVENTION ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT FILING DATE: 2001-05-02
FRIOR APPLICATION NUMBER: 09/643,260
FRIOR APPLICATION NUMBER: 09/643,260
FRIOR APPLICATION NUMBER: 09/643,260
FRIOR APPLICATION NUMBER: 09/643,260
FRIOR APPLICATION NUMBER: 09/643,260
FRIOR PLING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PALENTING DATE: 2000-08-22
                                                                   APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Ghosh, Sankar
APPLICANT: Pindeis, Mark A
APPLICANT: Pindeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
ITLE OF INVENTION: ANTI-INFLAWMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT PILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/641,261
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR PILING DATE: 2000-06-02
PRIOR PILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 100.0%; Score 41; DB 11; Length 8; Similarity 100.0%; Pred. No. 7e+05; 6; Conservative 0; Mismatches 0; Indels
Sequence 114, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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LENGTH: 8
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Sequence 113, Application US/09847946A

Publication No. US200300549991

GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillibb, Kathryn
APPLICANT: Phillibb, Kathryn
APPLICANT: Phillibb, Kathryn
APPLICANT: Phillibb, Kathryn
APPLICANT: Phillibb, Kathryn
APPLICANT: Phillibb, Kathryn
APPLICANT: Phillibb, ANIT-INFLAMMATORY COMPOUNDS AND USES THEREOF
ITIE REFERENCE: PPI-119
CURRENT PLIING DATE: 2001-05-02
RRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 2000-06-02
SPRIOR APPLICATION NUMBER: 2000-06-05
SPRIOR PLING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Findels, Mark A
APPLICANT: Findels, Mark A
APPLICANT: Hannig, Gerharyn
APPLICANT: Hannig, Gerharyn
APPLICANT: Hannig, Gerharyn
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR PILING DATE: 2000-05-02
PRIOR PLING DATE: 2000-06-03
PRIOR PLING DATE: 2000-06-03
PRIOR FILING DATE: 2000-08-22
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US-09-847-946A-113
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US-09-847-946A-116
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100.0%; Score 41; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels
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Indels

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Sequence 115, Application US/09847946A

Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Ghosh, Sankar

APPLICANT: Findeis, Mark A

APPLICANT: Fhillips, Kathryn

APPLICANT: Phillips, Carhard

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REPRENCE: PPILOR: 2001-05-02

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR FILING DATE: 2000-08-22

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: Patentin Ver. 2.0
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Sequence 118, Application US/09847946A

Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Hannig, Gerhard

TITLE OF INVENTION: ANTI-INFLAWMATORY COMPOUNDS AND USES THEREOF

TITLE OF INVENTION: ANTI-INFLAWMATORY COMPOUNDS AND USES THEREOF

CURRENT FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 05/201,261

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR PLING DATE: 2000-08-02

PRIOR PLING DATE: 2000-08-02

PRIOR PLING DATE: 2000-08-02

PRIOR PLING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: PATENTIN VET: 2.0
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ORGANISM: Artificial Sequence
PERATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
OTHER INFORMATION: sequence
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Best Local Similarity 100.0%; Pred. No. 7e+05; Matches 6; Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 6; Conserv
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2 LDWEWL 7
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US-09-847-946A-115
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US-09-847-946A-118
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Publication No. US2003005499A1

GENERAL INFORMATION;

APPLICANT: May, Michael J

APPLICANT: Pindeis, Mark

APPLICANT: Pindeis, Mark

APPLICANT: Pindeis, Mark

APPLICANT: Pindeis, Mark

APPLICANT: Pindeis, Mark

APPLICANT: Pindeis, Mark

APPLICANT: Pindeis, Mark

APPLICANT: Pindeis, Mark

TITLE OF INVENTION ANTI-INFLAWMATORY COMPOUNDS AND USES THEREOF

FILE REFERENCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT APPLICATION NUMBER: 60/201,261

PRIOR PILING DATE: 2000-05-02

PRIOR PILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: PATENTIN UNC: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: Description of Artificial Sequence:NEMO binding; OTHER INFORMATION: sequence
US-09-847-946A-119
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 6; Conservative
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; OTHER INFORMATION:
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US-09-847-946A-120
                                                                     LDWEWL 6
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LENGTH: 9
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APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: DATE: 1051-02-28
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12414
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APPLICANT: Ghosh, Sankar
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
ITILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT APPLICATION NUMBER: 60/201,261
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 160
SEQ ID NOS: 160
SEQ ID NO 112
LENGTH: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: NEMO binding OTHER INFORMATION: sequence US-09-847-946A-112
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Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      5-09-847-946A-112
Sequence 112, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
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ORGANISM: Aspergillus nidulans
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                                           Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
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Matches 6; Conservative
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US-09-847-946A-118
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; LOCATION: (1)..(471)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-12414

Query Match

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Best Local Similarity 83.3%; Pred. No. 4.78+02;

Matches 1. LDWEWL 6

| LDWEWL 6

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Db 119 IDWEWL 124

Search completed: February 18, 2004, 15:42:01

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; ORGANISM: Y1aX2
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35.929 Million cell updates/sec
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-168-629-15
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Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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No.
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APPLICANT: Marc J. Rubenfield et al.
TITLE OP INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OP INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE OP INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-07-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22395
LENGTH: 334
TYPE: PRT
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 Sequence 9, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 123, App
Sequence 121, App
Sequence 55, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 31, Appl
Sequence 33, Appl
Sequence 33, Appl
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Sequence 1275, Ap
Sequence 1275, Ap
Sequence 161, App
Sequence 162, App
Sequence 20614, A
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US-08-910-820-9
US-09-109-986-2
US-09-109-986-2
US-09-844-908-9
US-09-868-758-4
US-09-417-197-121
US-08-417-197-121
US-08-417-134-55
US-08-273-685-55
US-08-273-685-55
US-09-175-928-33
US-09-175-928-33
US-09-107-532A-4517
US-09-199-637A-162
US-09-199-637A-162
US-09-199-637A-162
US-09-199-637A-162
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Sequence 14, Application US/09172952
Patent No. 6368793
GENERAL INFORMATION;
APPLICANT: Hoch, James
APPLICANT: Dartois, Veronique
TITLE OF INVENTION: METABOLIC SELECTION METHODS;
FILE REFERENCE: 234/191
CURRENT APPLICATION NUMBER: US/09/172,952
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FRASESQ for Windows Version 3.0
                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                      ; Sequence 22395, Application US/09252991A; Patent No. 6551795; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22395
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Local Similarity 83.3%;
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                            US-09-252-991A-22395
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LENGTH: 745 amino acids
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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US-08-890-853-4
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US-09-023-321-3
; Sequence 3, Application US/09023321
; Sequence 3, Application US/09023321
; Patent No. 5844073
; GENERAL INFORMATION:
    APPLICANT: Rothe, Mike
    APPLICANT: Wu, Lin
    APPLICANT: Wu Lin
    APPLICANT: Wu Lin
    APPLICANT: Wu Lin
    APPLICANT: SAN FRANCISCO
    STATE: CALIFORNIA
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                                                                                                                                                                                                            Sequence 3, Application US/08887518
Patent No. 5843721
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
Score 36; DB 4; Length 439; Pred. No. 3.1e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 2; Length 745;
Pred. No. 5.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
CLASSTPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REFERENCE/DOCKET NUMBER: 197-008
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFEX: (415) 343-4341
TELEFEX: (415) 343-4341
TELEFEX: (415) 343-4341
TELEFEX: (415) 343-4341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
87.8%;
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 87.8
Best Local Similarity 83.3
Matches 5; Conservative
                                      5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                CITY: SAN FRANCISCO STATE: CALIFORNIA
                                                                                                                  171 LDWRWL 176
Query Match
Best Local Similarity
Matches 5; Conserv
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TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 83.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: Bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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   GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                         FILING DATE
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US-09-099-124A-4
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Pactent No. 5844003

GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Wothe, Mike
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
CORRESPONDENCE ADDRESS:
ADDRESSEE: ACHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
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                                                                                                                        Score 36; DB 2; Length 745;
Pred. No. 5.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 2; I
Pred. No. 5.1e+02;
0; Mismatches 1;
                                                                                                                                          5.16+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEFANDE: (415) 343-4341
TELEFAX: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-099-125A-4; Sequence 4, Application US/09099125A; Patent No. 5916760
                                                                                                                        87.8%;
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Best Local Similarity 83.3%;
Matches 5; Conservative
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
 745 amino acide
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Best Local Similarity 83.3
Matches 5; Conservative
                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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LENGTH:
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PERICONT: Geodedia, buyld V.
APPRICONT: Geodedia, buyld V.
APPRICONT: Wordletz John
TITLE OF THEWRITON: IKK. Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDER AND SEGUENCES: 4
CORRESPONDER AND SEGUENCES: 4
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CORRESPONDER AND SEGUENCES: 4
COMPUTER TRADABLE FORM:
MADUM TYPE: FLORDY disk
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| Sequence 4, Application US/08990854
| Patent No. 623512
| GENERAL INFORMATION:
| APPLICANT: Rothe, Mike
| APPLICANT: Rothe, Mike
| APPLICANT: Rother: Catherine
| TITLE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods
| INVENTION: IKK-' Proteins, Nucleic Acids and Methods
| ORRESPONDENCE ADDRESS:
| ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
| STREET: 268 BUSH STREET, SUITE 3200
| CITY: SAN FRANCISCO
| STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09023324
Patent No. 6235513
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
APPLICANT: R gnier, Catherine
TITLE OF INVENTION:
INVENTION: IKK-' Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                 Length 745;
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MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,854
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Pred. No. 5.1e+02;
                 Score 36; DB 3; Pred. No. 5.1e+02;
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                                                              0; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: OSWAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFRENCE/DOCKET NUMBER: 197-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                    87.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.3%;
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
                                   Best Local Similarity 83.3
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
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                                                                                                                                              738 LDWSWL 743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                        1 LDWEWL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-09-023-324-4
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US-08-890-854-4
                      Query Match
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Patent No. 6235492

APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rotherine
APPLICANT: Solication Methods
CORRESPONDENCES: 5
CORRESPONDENCES: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 2; Length 745
Pred. No. 5.1e+02;
0; Mismatches 1; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,476
                                                                       ATTORNEY AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 197-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEPHONE: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 anning acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 197-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 349-4341
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                87.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 87.8
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: peptide US-09-099-124A-4
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MOLECULE TYPE: peptide
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CITY: SAN FRANCISCO
STATE: CALIFORNIA
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CLASSIFICATION:
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738 LDWSWL 743
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; Sequence 2, Application US/09168629
; Patent No. 6242253
; GENERAL INFORMATION:
   APPLICANT: Karin, Michael
; APPLICANT: Dibonato, Joseph A.
   APPLICANT: Hayakawa, Makio
; APPLICANT: Randi, Ebrahim
; TITLE OF INVENTION: IRB Kinase, Subunits Thereof, and Methods of Using Same
; TITLE OF INVENTION: IRB Kinase, Subunits Thereof, and Methods of Using Same
; TITLE OF INVENTION NUMBER: US/09/168,629
; CURRENT APPLICATION NUMBER: 60/061,470
; EARLIER PILING DATE: 1997-10-09
; SOFTWARE: PALENTION DATE: 1997-10-09
; SOFTWARE: PALENTI Ver. 2.0
; SEQ ID NO 2
; LENGTH: 745
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                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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83.3%; Pred. No. 5.1e+02;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSYAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 34341
                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 343-437-
TELEPAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
1.ENGTH: 745 amino acids
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Best Local Similarity 83.5.
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
SAN FRANCISCO
: CALIFORNIA
RY: USA
                                                      ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
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US-09-168-629-2
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Patent No. 6479266

GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: A gnier, Catherine
TITLE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BIM PC COMPACIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/109,986
FLING DATE:
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                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIN Release #1.0, Version #1.25
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,131A
FILIANDEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 9-UD 2408
FELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: AT5 amino acid
TYPE: amino acid
TYPE: ATTORNATION COMPANIER
TYPE: TABLED ATTORNATION:
TELEPHONE: (749) 535-8949
TYPE: ATTORNATION COMPANIENCE CHARACTERISTICS:
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NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-006-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEPHONE: (415) 343-4342

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 08/890,854
FILING DATE:
United States
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Best Local Similarity 83.3
Matches 5; Conservative
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MOLECULE TYPE: protein

US-08-810-131A-2
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US-09-109-986-4
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i LENGTH: 745 amino acids

i TYPE: amino acid

i STRANDEDESS: single

i TOPOLOGY: linear

i TOPOLOGY: linear

i MOLECULE TYPE: peptide

US-09-109-986-4

Cuery Match

Best Local Similarity 83.3%; Pred: No. 5.18+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps

Cy 1 LDWEWL 6

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Db 738 LDWSWL 743

Search completed: February 18, 2004, 14:41:51
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015111 h inhibitor 060680 m inhibitor 014920 homo sapien 088351 mus musculu 09477 rattus norv 005047 catharanthu P43112 salmonalla P32563 saccharomyc 08693 buchnera ap P57544 buchnera ap P5053 acetobacter 090wri pseudomonas P79209 ovis aries P20937 mus musculu 060657 mus musculu P50900 clostridium 060677 mus musculu P50913 mus musculu P50913 mus musculu P50913 mus musculu P50914 homo sapien P29474 homo sapien
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                                                                                                          ; Search time 3.55263 Seconds (without alignments) 79.423 Million cell updates/sec
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gallus
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Q57596
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Q9v877
P38081
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P29318
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                   127863 seqs, 47026705 residues
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IKKB HUAN
IKKB MOUSE
IKKB RAT
EVET CATRO
VENT SALTI
VPHI YEAST
CYOA BUCAP
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Maximum Match 100%
Listing first 45 summaries
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                                                                      OM protein - protein search, using sw model
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EPB5_CHICK
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Maximum DB
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1 GUNB_CALSA P10474 c endogluca 1 VG41_BPML5 · Q05252 mycobacteri 1 VG41_BPMD2 · O64231 mycobacteri	BASI_HUMAN P35613	NOSO_BACSU O34453	ZDH4 MOUSE	ZDH4_HUMAN Q9npg8	GCST SYNEL Q8dkv6	1 APJ MACMU O97666 macaca mula 1 MANA_RHIME P29954 rhizobium m	ALIGNMENTS		PRT; 745 AA. 092467:	eated)	st sequence update) st annotation update)	a subu	(IkBKA) (IKK-alpha) (IKK-A) (IkappaB 1) (Conserved helix-loop-helix ubigu	inhibitor kinase alpha)		data; Craniata; Vertebrata; Euteleostomi;			FROM N.A., AND MUTAGENESIS OF LYS-44.		Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;	ог ан ткаррав		AND PARTIAL SEQUENCE.	arf D.M., Zandi E.,	"A cytokine-responsive IkappaB kinase that activates the transcription			IAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND	in the second se		y B.W., Shevchenko A., Benn Ba M Mann M., Manning A	-activated IkappaB kinases e		_		D.: L. 0012230.	_	-beta genes are coexpressed in adult	to different human chromosomes.
.5 1039 .0 83	269	336	ა ნ 4 გ ლაგ	344	366	387			STANDARD; O13132: 092467:	1. 40, Cre	1. 40, Las	of nuclear fact	kinase alpha) kinase 1) (IKK	(Nuclear factor NFkappaB	(Human).	zoa; Chordata;	ria, Prima	į	.A., AND M	IISSUE=1-CEII; MEDLINE=97386461; PubMed=9244310	ong H.Y.,	(1997)		SEQUENCE FROM N.A., AND PARTIAL S MENTINE-07294469. BubMod-0252196.	Hayakawa M	ponsive Ik	iactor Nr-Kappab."; Nature 388:548-554(1997).		.A., PARTIAL	carcinoma	3; PubMed=9346484;	Mercurio F., Zhu H., Murray B.W., Li J.W., Young D.B., Barbosa M.,	2: cytokin	NF-kappaB activation.";	Science 278:860-866(1997). [4]	. A.		>-		ייטר זוול מפ
3 82. 2 80.	8 8	8 6	2 6	80	80	8 8			AN 014666;	001 (Re	001 (Re	r of nu	-B kina -B kina	(Nuclea	OR IKKA. sapiens (H	a; Meta	; Euthe ID=9606		FROM N	-cerr; 9738646	C.H., S	373-383		FROM N	J.A.,	ine-res	r-Kappa 88:548-		FROM N	ervical	9800881	F., Zh Young	nd IKK-	Bactiv	7 8:00	FROM N	eart;	T., Wan	kinase	r tigan
ммм	m m	ገጠ	.	m	m (m m		HUMAN	IKKA HUMAN STI 01511: 014666: 0	6-0CT-2(16-UCT-2001 15-SEP-2003	Inhibitor o	(I kappa-B kinase (I-kappa-B kinase	(e)	CHUK OR 1 Homo sapi	ukaryota	Mammalia; Eutheria; NCBI TaxID=9606;	. [I]	SEQUENCE	EDLINE=	egnier (ell 90:	[2]	EQUENCE	Donato	A cytok:	actor N	[3]	SEQUENCE FROM N.A.,	TISSUE=Cervical	MEDLINE=98008813;	ercurio	IKK-1 aı	F-kappal	Science (4)	SEQUENCE FROM N.A	TISSUE=Heart;	Hu M.C7	IkappaB	embryonic tiggines but
3.5 3.5 3.5 3.5	37	9 6 6	4 4 0 L	42	43	4 4 5		ฐีฐ'		TO I) OE	_	SS H						RA RA			RP S		RT "			RP S			RA Ed					RC F Z			

TISSUE=Cervical carcinoma;
MEDLINE=56258427; PubMed=8777433;
Connelly M.A., Marcu K.B.;
CONNELLY, a new member of the helix-loop-helix and leucine zipper families of interacting proteins, contains a serine-threonine kinase catalytic domain.";

SEQUENCE OF 32-745 FROM N.A.

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Nemoto S., Dibonato J.A., Lin A., Inases by mitogen-activated protein Kinase kinase kinase land NF-kappaB-inducing kinase."; Mol. Cell. Biol. 18:7336-7343(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Preferentially found as a heterodimer with IXK-beta but also as an homodimer. Directly interacts with IKK-GAWMA/NEWO. Heterodimers form the active complex. The tripartite complex can also bind to MAPBKI4/NIK, MEKKI, IKAP and IKB-alpha-P65-P50 complex. A weak interaction with TRAP2 cannot be excluded. Part of a complex composed of NCOA2, NCOA3, IKKB, IKBKG and CREBBP.

TISSUE SPECIFICITY: Widely expressed.

PTM: Phosphorylated by MAPSKA-MIK, AKT and to a lesser extent by MEKKI, and dephosphorylated by PP2A. Autophosphorylated.

SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21968797; Pubmed=11971985; NCOA2; NCOA3; IKKB AND IKEKG. MEDLINE-21968797; Pubmed=11971985; Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J., O'Malley B.W.; Regulation. of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator activity by I kappa B kinase."; Mol. Cell. Biol. 22:3549-3561(2002).

**Non: Cell. Biol. 22:3549-3561(2002).

-!-FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates
                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99212141; PubMed=10195894; Delhase M., Hayakawa M., Chen Y., Karin M.; Papakawa M., Chen Y., Karin M.; Papakawa M., Chen Y., Karin M.; Mand negative and negative regulation of IkappaB kinase activity through Science 284:309-313(1999).
                                                    AND SER-180.
MEDLINE=88188283; PubMed=9520446;
Ling L., Cao Z., Goeddel D.V.;
"NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENZYME REGULATION: Activated when phosphorylated and inactivated
                                     PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179
                                                                                                                                                                                                                                                            "NF-kappaB activation by tumour necrosis factor requires the Akt serine-threonine kinase.";
Nature 401:82-85(1999).
                                                                                                                                                                                    PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23. MEDINE=99413720; PubMed=10485710; OZES O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M., Donner D.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jobin C., Sartor R.B.;
"The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";
Am. J. Physiol. 278:C451-C462(2000).
                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998)
Cell. Mol. Biol. Res. 41:537-549(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WEDLINE=99038238; PubMed=9819420;
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TKKA_MOUSE STANDARD; PRT; 745 AA.

000680, Q9D2X3;

16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-Kappa-B kinase alpha (IkBKA) (IKK-alpha) (IKK-A) (Ikappa-B kinase)
(I-kappa-B kinase alpha) (IKK) (Conserved helix-loop-helix ubiquitous (Nuclear factor NFkappa-B inhibitor kinase alpha) (NFKBIKA).
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Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K->A: LOSS OF KINASE ACTIVITY.
K->A: LOSS OF AUTOPHOSPHORYLATION.
S->A: LOSS OF PHOSPHORYLATION AND OF ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S->E: FULL ACTIVATION.
T->A: NO CHANGE IN PHOSPHORYLATION.
S->A: NO CHANGE IN PHOSPHORYLATION.
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                                                                                                                                                                                                                                                                                                        R InterPro; IPR002019; Prot_kinase.
R InterPro; IPR002019; Prot_kinase.
R InterPro; IPR001296; Ser thr pkinase.
R InterPro; IPR001296; Ser thr pkinase.
R Ffan; PF00006; Pkinase; I.
R PRINTS; PR00109; Prot_kinase; I.
R PRODOM; PR00109; Prot_kinase; I.
R PROSTIE; S000107; Prot_kinase; I.
R PROSTIE; PS00107; PROTEIN KINASE ATP; I.
R PROSTIE; PS00101; PROTEIN KINASE ATP; I.
R PROSTIE; PS00101; PROTEIN KINASE_DOM; I.
I Transferase; Serine/threonine-protein kinase; ATP-binding; I Phosphorylation.
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BY SIMILARITY.
PHOSPHORYLATION (BY PKB/AKT1).
EMBL; AF012890; AAC51662.1; -...
EMBL; AF00225; AAC51671.1; -...
EMBL; AF00025; AAC50713.1; -...
EMBL; AC50713.1; -...
HSSP; Q63450; LA06
Gonew, HGMC:1974; CHUK.
MIM; 600664; -...
GO; GO:000537; C:Cytoplasm; TAS.
GO; GO:000384; F:IkappaB kinase activity; TAS.
GO; GO:0007345; P:embryogenesis and morphogenesis; GO; GO:0007365; P:embryogenesis and morphogenesis; GO; GO:0007255; P:l-kappaB phosphorylation; TAS.
GO; GO:0007855; P:immune response; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.5%; Score 37; DB 1; Length 745; 83.3%; Pred. No. 76;
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L -> R (IN REF. 5).

TS -> AY (IN REF. 5).

P -> A (IN REF. 3 AND 5).

TS -> DL (IN REF. 5).
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IKAPPAB KINASE SUBFAMILY.

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Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Saito R., Kiuell P., Lewis S., Matsuo Y., Nikaido I., Rochiwa H., Kuell P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoco N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whithaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                      Mock B.A., Connelly M.A., McBride O.W., Kozak C.A., Marcu K.B.; "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome 10 and mouse chromosome 19.";
                                                                                                                                                                    Connelly M.A., Marcu K.B.; "CHUK, a new member of the helix-loop-helix and leucine zipper families of interacting proteins, contains a serine-threonine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20198447; PubMed=10733566; McKenzie F.R., Connelly M.A., Balzarano D., Mueller J.R., Geleziunas R., Marcu K.B.; "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking Leucine zipper and helix-loop-helix domains reveal that IKKalpha and IKKbeta have different activation requirements."; Mol. Cell. Biol. 20:2635-2649(2000).
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Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
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Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
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                                                                                                                                                                                                                             Cell. Mol. Biol. Res. 41:537-549(1996).
[3]
                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Colon;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99212141; PubMed=10195894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKK PHOSPHORYLATION.
MEDLINE-99038238; PubMed=9819420;
                                        MEDLINE=9604444; PubMed=7558004;
                                                                                                                                                        MEDLINE=96258427; PubMed=8777433;
[1]
SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION BY MAP3K14/NIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:685-690(2001).
                                                                                                Genomics 27:348-351 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKA-IKKB BINDING.
                                                                                                                                                                                                                 domain."
                                                                                                                                           STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Okumura K.;
                                                                                                                                                                                                                 catalytic
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this tatement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
REVIEW.
MEDLINE=20178139; PubMed=10712233;
Jobin C., Sartor R.B.;
"The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";
Am. J. Physiol. 278:C451-C462(2000).
-!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and the dissociation of the inhibitor. Also phosphorylates ultimately the degradation of the inhibitor. Also phosphorylates
                                                                                                                                                                                                                                                                                                                                                         when dephosphorylated.
SUBUNIT: Preferentially found as a heterodimer with IKK-beta but also as an homodimer. Directly interacts with IKK-gamma/NEMO. Heterodimers form the active complex. The tripartite complex can also bind to MAP3K14/NIK, MEKK1, IKAP and IKB-alpha-P65-P50 complex. A weak interaction with TRAF2 cannot be excluded. Part of a complex composed of NCOA2, NCOA3, IKKB, IKBKG and CREBBP (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=2; Synonyme=belta LH;
IsoId=Q66680-2; Sequence=VSP_004866, VSP_004867;
Name=3; Synonyme=belta H;
Name=3; Synonyme=belta H;
IsoId=Q6680-3; Sequence=VSP_004868, VSP_004869;
TISSUE SPECIFICITY: Ubiquitous only for isoform 1, isoforms 2 and are expressed predominantly in brain and T-lymphocytes.
DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by E11, E15 and E17 days. In the limb development, its expression predominates in the limb buds at E12.5 day.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by MEKK1, and dephosphorylated by PP2A. Autophosphorylated.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. IKAPPAB KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE;
PRODOM; PD000001; PTCK Kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE DAT; 1.
PROSITE; PS50011; PROTEIN KINASE DM; 1.
TXANSE PS50011; PROTEIN KINASE DM; 1.
TXANSE PS50011; PROTEIN KINASE DM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (BY PKB/AKT1)
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PHOSPHORYLATION (BY MAP3K14)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phosphorylation, Alternative splicing.

DOMAIN
15 300 PROTEIN KINASE.

DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q60680-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI: 99484; Chuk.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR001245; Tyr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AK018671; BAB31335.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U12473; AAC52589.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; 149101; 149101.
HSSP; Q63450; 1A06.
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ACT SITE
MOD_RES
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4LSLLRYNANLTKMKNTLIS -> IFRKNVKSMERNGRKGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             014920; 075327;
116-0CT-2001 (Rel. 40, Created)
116-0CT-2001 (Rel. 40, Last sequence update)
115-SEP-2003 (Rel. 42, Last annotation update)
115-SEP-2003 (Rel. 42, Last annotation update)
115-SEP-2003 (Rel. 42, Last annotation update)
116-SEP-2003 (Rel. 42, Last annotation update)
117-SEP-2003 (Rel. 42, Last annotation update)
117-SEP-2003 (Rel. 42, Last annotation update)
117-SEP-2003 (Rel. 40, Last annotation update)
118-SEP-2003 (Rel. 40, Las
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
"Assignment of IkappaB kinase beta (IKBKB) to human chromosome band
8p12-->p11 by in situ hybridization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
TISSUE-Cervical carcinoma;
MEDLINE-98008813; PubMed-9346484;
                                                                   Missing (in isoform 2).
/FIId=VSP 004867.
DHINSDST - GATLQSQY (in isoform 3).
/FIId=VSP 004868.
Missing (in isoform 3).
/FIId=VSP 004869.
K -> E (IM REP. 3).
S -> Y (IN REP. 3).
S -> Y (IN REP. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L., Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.; IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for NP-kappaB activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hu M.C.-T., Wang Y.-P.; "IkappaB kinase-alpha and -beta genes are coexpressed in adult and embryonic tissues but localized to different human chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                      DB 1; Length 745;
                                                                                                                                                                                                                                                                                                                                                                                            Indels
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
                        SLF (in isoform 2).
/FTId=VSP 004866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           756 AA.
                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                               Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                    Score 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytogenet. Cell Genet. 82:32-33(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99032998; PubMed=9813230;
                                                                                                                                                                                                                                                                                      84728 MW;
                                                                                                                                                                                                                                                                                                                                      92.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 278:860-866(1997).
                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 83...
From S; Conservative
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                                                                             745
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LDWSWL 743
                                                                                                                                                                                                                                                                                      745 AA;
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                                                                                                                                                                                                                                                         CONFLICT
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                                                                           VARSPLIC
                                                                                                                             VARSPLIC
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                                                                                                                                                                                                                                 CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M. R. C., Olin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
A. O'Malley B.W.;
T. "Requilation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
T. "Requilation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
T. activity by I kappa B kinase.";
Mol. Cell. Biol. 22:3549-3561(2002).
I. PONCTION: Phosphorylates inhibitors of NP-kappa-B thus leading to the dissociation of the inhibitor of NP-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates
NCOA3 (By similarity).
C. !- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but also as a homodimer. Directly interacts with IKK-gamma/NEMO.
Heterodimers form the active complex. The tripartite complex can also bind to MEKKI, MAP3KI4/NIK, IKAP and IKB-alpha-P65-P50
Complex. Phosphorylated IKB-alpha is further released from the complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKBKG
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Raha S.S., Loquin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquin T.B., McDwan P.J., McDwan P.J., McDwan P.J., McDwan P.J., McDwan P.J., McDwan P.J., McDwan F.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Waton D.K., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Rodrigues A.C., Grimwood J., Schmutz J., Marra M.A.; Richard M.A., Rodrigues A.C., Grimwood J., Schmutz J., Myers R.M., Generch A., Schein J.E., Jones S.J.M., Marra M.A.; Rodrigues A.C., Grimwood J., Schmutz J., Marra M.A.; Rodrigues A.C., Grimwood J., Schmutz J., Marra M.A.; Rodrigues A.C., Grimwood J., Schmutz J., Marra M.A.; Rodrigues A.C., Grimwood J., Schmutz J., Marra M.A.; Rodrigues A.C., Grimwood J., Schmutz J., Marra M.A.; Rodrigues A.C., Grimwood J., Schmutz J., Marra M.A.; Rodrigues A.C., Grimwood J., Schmutz J., Marra M.A.; Rodrigues A.C., Grimwood J., Schmutz J., Marra M.A.; Rodrigues A.C., Grimwood J., Schmutz J., Marra M.A.; Rodrigues A.C., Grimwood J., Schmutz J., Marra M.A.; Rodrigues A.C., Grimwood J., Schmutz J., Marra M.A.; Rodrigues A.C., Grimwood J., Schmutz J., Marra M.A.; Rodrigues A.C., Grimwood J., Schmutz J., Marra M.A.; Rodrigues A.C., Grimwood J., Schmutz J., Marra M.A.; Rodrigues A.C., Grimwood J., Schmutz J., Marra M.A.; Rodrigues A.C., Grimwood J., Schmutz J., Marra M.A.; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nemoto S., DiDonato J.A., Lin A.; "Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase kinase kinase kinase (1 nd NP-kappaB-inducing kinase."; Mol. Cell. Biol. 18:7336-7343 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [8]
IDENTIFICATION IN A COMPLEX WITH CREBBP; NCOA2; NCOA3; IKKA AND IKBKG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              skeletal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
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-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
IKAPPAB KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20178139; PubMed=10712233;
Jobin C., Sartor R.B.;
"The I kappa B/NF-kappa B system: a key determinant of mucosal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Physiol. 278:C451-C462(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKK PHOSPHORYLATION.
MEDLINE=99038238; Pubmed=9819420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouse cDNA sequences.
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EMBL; AF080158; AAD08997.1; -.
EMBL; AF01416; AAC64675.1; -.
EMBL; BC06231; AAH06231.1; -.
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SEQUENCE FROM N.A.
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PHOSPHORYLATION.
R->A: LOSS OF KINASE ACTIVITY AND NO
EFECT ON BINDING TO NIK.
S->A: DECREASE OF ACTIVITY.
S->B: FULL ACTIVATION.
S->B: FULL ACTIVATION.
WHSKYRQKSEVDIVYSEDLANTYV.
CNPSTLGGRGRMI (IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IKKB MOUSE STANDARD; PRT; 757 AA.
088351; 09R1J6;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
1nhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
(I-kappa-B-kinase beta) (IKKBRB) (IKK-beta) (IKK-B) (I-kappa-B kinase
2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIKB)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Differential regulation of IkappaB kinase alpha and beta by two uperream kinases. NF kappaB-inducing kinase and mitogen-activated protein kinase/ERK kinase kinase-1.";
Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
                                            GO; GO:0005737; C:cytoplasm; NAS.
GO; GO:0005524; F:ATP binding activity; NAS.
GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.
GO; GO:0004668; F:protein serine/threonine kinase activity; NAS.
GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
InterPro; IPR00719; Prot kinase.
InterPro; IPR002290; Ser Ehr pkinase.
Pfam; PF00069; pkinase; I.
Pfam; PF00040; ubiquitin; 1.
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PHOSPHORYLATION (BY SIMILARITY).
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Pred. No. 77;
                                                                                                                                                                                                                                                                                    Iransferase; Serine/threonine-protein kinase; ATP-binding;
Phosphorylation.
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LEUCINE-ZIPPER (POTENTIAL).
NEMO-BINDING.
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F9CADF671AE9E14E CRC64;
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ATP (BY SIMILARITY).
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STRAIN=C57BL/6; TISSUE=Spleen;
MEDLINE=98188238; PubMed=9520401;
                                                                                                                                                                                            Pfam; PF00240; ubiquitin; 1.
ProDom; PD000001; Proc kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00109; PROTEIN KINASE ST; 1.
PROSITE; PS0011; PROTEIN KINASE DOM; 1.
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83.3%;
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                HGNC:5960; IKBKB
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Rest Local Similarity
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H. M. C.-T., Wang Y.-P., Minhill A., Old W. R.;

H. M. C.-T., Wang Y.-P., Minhill A., Old W. R.;

H. Wintine IR kinase-B, a developmentally regalated protein kinase that reconstitutively bloosphoryleas serior sessions of IRB.;

B. Submitted (Md-1998) to the EMELORESHMEND of IRB.;

B. Submitted (Md-1998) to the EMELORESHMEND of IRB.;

H. M. C.-T., Wang Y.-P., Old W. R.; Mishall A., Meyer C.F., Tan T.-H.; Wenther C.F., Wang Y.-P., Old W. R.; Mishall A., Meyer C.F., Tan T.-H.; Wenther C.F., Wang Y.-P., Old W. R.; Mishall A., Meyer C.F., Tan T.-H.; Membrane C.F., Mishall A., Meyer C.F., Tan T.-H.; Membrane C.F., Mishall A., Meyer C.F., Tan T.-H.; Membrane C.F., Mishall A., Meyer C.F., Tan T.-H.; Membrane C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Meyer Meyer B., Mishall A., Meyer C.F., Mishall A., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer C.F., Meyer
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Vetter H.-P., Mangold U., Schroeder G., Marner F.-J., Vetter H.-P., Mangold U., Schroeder G., Marner F.-J., Werck-Reichhart D., Schroeder J., "Molecular analysis and heterologous expression of an inducible cytochrome P-450 protein from periwinkle (Catharanthus roseus L.).", Plant Physiol. 100:998-1007(1992).
 ELLULAR LOCATION: Cytoplasmic.
Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
                                                                                                                                                                                                                                                                                                                                     PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           524 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                               InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR01245; Tyr_pkinase.
                                                                                                                                                                        EMBL; AF115282; AAF21978.1; -. HSSP; Q63450; 1A06.
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SEQUENCE OF 469-524 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 83.3 es 5; Conservative
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757 AA;
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AC Q05047;
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MEDLINE=99038238; PubMed=9819420;
Nemcto S., DiDonato JA., Lin A.;
"Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase 1 and NP-kappaB-inducing kinase.";
Mol. Cell. Biol. 18:7336-7343(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jobin C., Sartor R.B.;
"The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";
Am. J. Physiol. 278-C451-C462(2000).
-!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but also as a homodimer. Directly interacts with IKK-gamma/NEMO. Heterodimers a homodimer active complex. The tripartite complex can also bind to MEKKI, MAPSKI4/NIK, IKAP and IKB-alpha-P65-P50 complex. Phosphorylated IKB-alpha is further released from the complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKBKG and CREBBP (By similarity).
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last sequence update)
17-01 (Rel. 41, Last annotation update)
17-02 - FEB-2003 (Rel. 41, Last annotation update)
17-02 - FEB-2003 (Rel. 41, Last annotation update)
17-03 - (Ir.Kappa-B-kinase beta) (IKBK) (IKK-beta) (IKK-beta) (Ir.Kappa-B kinase
17-03 (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIKB)
17-03 - (IKKB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                           N -> D (IN REF. 2).
N -> D (IN REF. 2).
K -> E (IN REF. 2).
L -> F (IN REF. 2).
F -> Q (IN REF. 2).
K -> R (IN REF. 2).
TLDWSWLQMEDEERCSLEQACD -> VTA (IN REF.
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                                                                        SIMILARITY)
                                                                                     SIMILARITY)
SIMILARITY)
                                                                                                                                                                                                                                    92.5%; Score 37; DB 1; Length 757; 83.3%; Pred. No. 77;
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PROTEIN KINASE.
LEUCINE-ZIPPER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Zhang Y., Sun S., Ravid K.;
"IKK beta in megakaryocyte differentiation.";
Submitted (DEC-1998) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                            FED962F095449CSE CRC64;
                                                                        (BY
(BY
(BY
                                     (BY SIMILARITY)
(BY SIMILARITY)
                        NEMO-BINDING.
ATP (BY SIMILARITY
ATP (BY SIMILARITY
BY SIMILARITY.
PHOSPHORYLATION (6)
                                                                                    PHOSPHORYLATION PHOSPHORYLATION
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                                                                                                                                                                                                             86690 MW;
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Matches 5; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae, lamiids; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae;
Catharanthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-2003 (Rel. 41, Last annotation update)
Cytochrome P450 72A1 (EC 1.3.3.9) (CYPLXXII) (Secologanin synthase)
Weakly autophosphorylated.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
IKAPPAB KINASE SUBFAMILY.
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Probom; PR00109; TYRKINASE.
Probom; PD000001; TYRKINASE.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation.
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Pred. No. 77;
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3AFFE46A7DF91F9C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                                                                                                                                   Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R., Mitch N., Farrar J., Feltwell T., Hamlin W., Hadre A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; amultiple drug resistant Salmonella enterica serovar Typhi CT18.";
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01-0CT-1993 (Rel. 27, Last sequence update)
15-DEC-1998 (Rel. 37, Last annocation update)
Vacuolar ATP synthase 95 kDa subunit (Vacuolar ATPase 95 kDa subunit).
VPH1 OR YOR270C.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                   SEQUENCE FROM N.A.
STRAINS-GIFU 10007;
MEDLINE-9332224; bubMed-8331073;
Hashimoto Y., Li, N., Yokoyama H., Ezaki T.;
"Complete nucleotide sequence and molecular characterization of ViaB region encoding Vi antigen in Salmonella typhi.";
"Bacteriol. 17:4456-4465(1993).
                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol. 185:2330-2337(2003).
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SEQUENCE 656 AA; 73652 MW; 26097F9D6F51ECED CRC64;
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                                                                                                                                                                                                                                                                                                                 MEDLINE=21534947; PubMed=11677608;
                                          Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL627283; CAD06771.1; -. EMBL; AE016848; AAO71797.1; -.
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    Salmonella typhi
                                                           NCBI_TaxID=601;
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ID VPH1_YEAST
AC P32563;
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K -> R.

S -> T.

V -> I.

K -> E.

S -> T.

W -> I.

K -> E.

MW; EFSD864E43C75IE8 CRC64;
                                                                                                                                                                                                     Irmler S., Schroeder G., St. Pierre B., Crouch N.P., Hotze M., Schndtd J., Strack D., Matern U., Schroeder J.; Strack D., Matern U., Schroeder J.; Strack D., Matern U., Schroeder J.; Schnidt alkaloid biosynthesis in Catharanthus roseus: new enzyme activities and identification of cytochrome P450 CYP72Al as secologanin synthase."; Plant J. 24:797-804 (2000).
-!- FUNCTION: Converts loganin into secologanin.
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InterPro; 1PR001128; Cytochrome_P450.

Pfam; PF00067; p450; 1.

PRINTS; PR00385; P450.

PROSITE; PS00086; CYTOCHROME P450; 1.

Oxidoreductase; Monooxygenase; Electron transport; Transmembrane; NADP; Heme; Alkaloid metabolism.

TRANSMEM 12 32 POTENTIAL.
               MEDLINE-93283641; PubMed-8507838;
Meijer A.H., Souer E., Verpoorte R., Hoge J.H.C.;
"Isolation of cytochrome P-450 cDNA clones from the higher plant Catharanthus roseus by a PCR strategy.";
Plant Mol. 8iol. 22:379-383(1993).
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-1. SUBCELLULAR LOCATION: Vacuolar membrane (Probable).
-1. TISSUE SPECIFICITY: Upper and lower leaf epidermis.
-1. SIMILARITY: Belongs to the cytochrome P450 family.
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100.0%; Pred. No. 77;
ive 0; Mismatches (
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01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
VEXE OR STY4651 OR T4344.
                                                                                                                                                                   STRAIN=cv. CP3A;
MEDLINE=20575722; PubMed=11135113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92332542; PubMed=1385813; Manolson M.F., Proteau D., Preston R.A., Stenbit A., Roberts B.T., Hopt M.A., Preuss D., Mulholland J., Botstein D., Jones E.W.; "The VPH1 gene encodes a 95-kDa integral membrane polypeptide required for in vivo assembly and activity of the yeast vacuolar
                                                                                                                                                                                                                                                                                                                                                                                                Cheret G., Bernardi A., Sor F.J.; "DNA sequence analysis of the VPHI-SNF2 region on chromosome XV of Saccharomyces cerevisiae."; east 12:1059-1064(1996).
                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDIJINE=93147685; PubMed=1491220;

Manolson M.F., Proteau D., Jones E.W.;

Manolson A.F., Proteau D., Jones E.W.;

"Evidence for a conserved 95-120 kbs subunit associated with and essential for activity of V-ATPases.";

J. Exp. Biol. 172:105-112(1992).
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M89778; AAA35211.1; -
EMBL; X89633; CAA61776.1; -
EMBL; Z75178; CAA99494.1; -
EMBL; Z75179; CAA99496.1; -
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                 Saccharomycetales; Saccharomycetaceae; Saccharomyces
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                                                                                                                                                                                        J. Biol. Chem. 267:14294-14303(1992)
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97051594; PubMed=8896271;
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                            NCBI_TaxID=4932;
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MEDLINE-22084549; PubMed=12089438;

Tamas I., Klasson L., Canbaeck B., Moran N.A., Andersson S.G.E.;

Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;

"50 million years of genomic stasis in endosymbiotic bacteria.";

Science 296:3376-2379 (2002).

-! FUNCTION: Cytochrome O terminal oxidase complex is the component

of the aerobic respiratory chain that predominates when cells are

grown at high aeration (By similarity).

-! CATALYTIC ACTIVITY: Ubiquinol-8 + H(2)O.

-! SUBCELULAR LOCATION: Integral membrane protein (By similarity).

-! SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.

BUT LACK HEME-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE014121; AAM67999.1; -.

InterPro; IPR001505; Copper CuA.

InterPro; IPR001843; CyA_II.

InterPro; IPR001843; Prok_Iipoprot.

Pfam; PF00116; COX2, 1.

Probom; PF001013; Copper CuA; 1.

Probom; PF001013; Copper CuA; 1.

Probom; PF001013; Copper CuA; 1.

Probom; PF001013; CyA, 1.

Prostrar, PR001013; CyA, 1.

PROSTR; PS00013; PROKKA LIPOPROTBIN; PALSE NEG.

Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome subbunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase constant 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
                         (POTENTIAL) (POTENTIAL)
                                                                                                                                                                            ö
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                                                                                                                       90.0%; Score 36; DB 1; Length 840; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLUAR (POTENTIAL).
                                                                         95528 MW; 77709A914410CD4D CRC64;
  (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                     290 AA
                         N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome
24 POTENTIAL
     N-LINKED
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25 25 N.J
25 25 N.J
43 63 POT
64 87 CYT
88 108 POT
109 EXT
290 AA, 33730 MW; 3
                                                                                                                                                                            5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290
252
422
63
108
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113 1
280 2
324 3
840 AA;
                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                        518 LDWAW 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=98794;
                                                                                                                                                                                                                        1 LDWAW 5
                                                                                                                                                                                                                                                                                                                                                                                                     BUCAP
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DOMAIN
SEQUENCE
                         CARBOHYD
CARBOHYD
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DOMAIN
TRANSMEM
                                                                            SEQUENCE
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08K993
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Gaps

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Indele

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0; Mismatches

83.3%;

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5; Conservative
  Best Local Similarity
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                                                                                                                                P50653:
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               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                DATURE 407:81-86 (2000).

-1- FUNCTION: CYTOCHROME O TERMINAL OXIDASE COMPLEX IS THE COMPONENT OF THE AEROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE GROWN AT HIGH AERATION (BY SIMILARITY).

-1- CATALYTIC ACTIVITY: Ubiquinol-8 + 0(2) = Ubiquinone-8 + H(2)0.

-1- SUBCELLULAR LOCATION: Intregral membrane protein (By similarity).

-1- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.

BUT LACK HEME-BINDING DOMAIN.
                                                                                                                                                                                                                                                       Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probon, PD000131, Copper CuA; 1.
TIGRRAMs; TIGR01433, CyOA; 1.
PROSITE; PS0013; PROKAR_LIPOPROTEIN; FALSE_NEG.
Oxidoreductase; Respiratory chain; Blectron transport; Transmembrane; Signal; Lipoprotein; Complete proteome.
                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome (Bubunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase CYOA OR BU472.
                                     Gaps
                                                                                                                                                                                                                                                                          Bacteria, Protecobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Buchnera.
NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                      STRAIN=TOKYO 1998,
MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
UBIQUINOL OXIDASE POLYPEPTIDE
N-ACYL DIGLYCERIDE (POTENTIAL)
EXTRACELLULAR (POTENTIAL).
               Length 290;
                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
1AB2B4F0408FFBAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
             DB 1;
                                                                                                                                              296 AA.
             Score 35; DB :
Pred. No. 63;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP, P18400; ICYW.
InterPro; IPR001505; Copper CuA.
InterPro; IPR00533; Cyca II.
InterPro; IPR002429; Cyc cox 2.
InterPro; IPR00647; Prok Ippoprot.
Pfam; PF00116; COX2; 1.
                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP001119; BAB13169.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34180 MW;
            87.5%;
Query Match
Best Local Similarity 83.5-
                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Lipoprotein; SIGNAL 1
                                                                                  134 LDWRWL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 AA;
                                                          1 LDWAWL 6
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          Buchnera sp. APS.
                                                                                                                                             CYOA BUCAI
P57544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                CYOA_BUCAI
                                                                                                                      RESULT 10
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87.5%; Score 35; DB 1; Length 296;

Query Match

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                                                                                                                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome Al subunit 2) (Oxidase BA(3) subunit 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fukaya M., Tayama K., Tamaki T., Ebisuya H., Okumura H., Kawamura Y., Horinouchi S., Beppu T.;
Kawamura Y., Horinouchi S., Beppu T.;
Characterization of a Cytochrome al that functions as a ubiquinol oxidase in Acetobacter aceti.";
J. Bacteriol. 175:4307-4314(1993).
-!- PATHWAY: TERMINAL OXIDASE FOR ETHANOL OXIDATION.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SUBCELLULAR TY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
BUT LACK HEME-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Acetobacteraceae; Acetobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.5%; Score 35; DB 1; Length 307; 83.3%; Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PROIDE; CYCOXIDASEII.
PRODOM; PRO1013; Copper CuA; 1.
TRGRAMA; TIGRO1433; CypA; 1.
PROSITE; PSO0013; PROKAK LIPDPROYEIN; 1.
Oxidoreductase; Transmembrane; Respiratory chain; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 AA; 33921 MW; E66734B84410996D CRC64;
                                                                                                                                                                                            307 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93322308; PubMed=8392509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP, P18400; ICYW.
InterPro, IPR001505; Copper_CuA.
InterPro, IPR006333; CyoA_II.
InterPro, IPR002429; Cyt_c_ox_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D13185; BAA02480.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
307
24
66
107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A36885; A36885.
                                                  125 LDWKWL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 LDWKWL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
9
                                                                                                                                                                                                                                                                                                                                                                                                                              Acetobacter aceti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LDWAWL 6
1 LDWAWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lipoprotein
SIGNAL
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TRANSMEM
SEQUENCE
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type

RESULT 12 CYOA_PSEPU

SEQUENCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nitric oxide + N NADP(+).
COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN VASCULAR SMOOTH WUSCLE RELAXATION THROUGH A CGMP.MEDIATED SIGNAL TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
T-cell surface glycoprotein YEI/48 (T lymphocyte antigen Al) (LY49-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR004030; NO_synthase.
Pfam; PF02898; NO_synthase; 1.
PR0SITE; PS60001; NOS; PARTIAL.
Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Calcium-binding; Heme; Multigene family.
               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, III) (NOSIII) (Endothelial NOS) (CONStitutive NOS) (CNOS)
                                                                                                                                                                                                                   Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                         NOS3 OR ENOS.
Ovis aries (Sheep).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                     developing fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE ENZYME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       brain of sheep; a studies on the expression pattern of constitutive forms of nitric oxide synthase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 AA; 11034 MW; 82C3C765557031DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 1;
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                               Aguan K., Weiner C.P.; "Effect of hypoxia on the microvasculature of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: Homodimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U76738; AAB40705.1; -. HSSP; P29473; 1D0C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.0%;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Endothelial cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||||:
DWAWI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DWAWL 6
                                                                                                                                                                                                                                                       NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LY4A MOUSE
P20937;
                                                                                                                                (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
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                                                                                                  30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase subunit 2).
                                                                                                                                                                                                                                                                                                                                                                                                                         Hirayama H., Takami H., Induce A., Horikoshi K.;

"Isolation and characterization of toluene-sensitive mutants from Pseudomonas putida IH-2000.";

"Isolation and characterization of toluene-sensitive mutants from Pseudomonas putida IH-2000.";

-I-STMCTION: CYTOCHROWE O TERMINAL OXIDASE COMPLEX IS THE COMPONENT OF THE ABROBIC RESPIRATORY CHAIN THAT PREDOMINATES WHEN CELLS ARE GROWN AT HIGH ARRATION (BY SIMILARITY).

-I-CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.

-I-SIMILARITY: SOME, TO MITOCHOUDRIAL OR BACTERIAL COXZ SUBUNITS.

BUT LACK HEME-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRPAMS; TIGR01433, Cyoā, 1.
PROSTE; BSO013; PROKAR LIPDPROTEIN; 1.
Oxidoreductase; Respiratory chain; Electron transport; Transmembrane;
Inner membrane; Signal; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UBIQUINOL OXIDASE POLYPEPTIDE N-ACYL DIGLYCERIDE (POTENTIAL) PERIPLASMIC (POTENTIAL).
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                                                              314 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99085656; PubMed=9868765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001505; Copper CuA.
InterPro; IPR006333; CyoA II.
InterPro; IPR002429; Cyt_cox_2.
Pfam; PF00116; COX2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD000131; Copper_CuA; 1.
                                                                                                                                                                                                                                                                                                    Pseudomonadaceae; Pseudomonas.
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                                                            STANDARD;
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                                                                                                                                                                                                                                                           Pseudomonas putida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDIATE.#93109828; PubMed=2787364;
MEDIATE.#93109828; PubMed=2787364;
"A mutine T lymphocyte antigen belongs to a supergene family of type II integral membrane proteins", "I mutiol. 143:1379-1386(1989).
"I mmunol. 143:1379-1386(1989).
"I mmunol. RECEPTOR ON NATURAL KILLER (NK) CELLS FOR H-2D ALLELES. INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                            MEDLINE-89140367; PubMed=2783949;
Chan P.-Y., Takei F.;
"Molecular cloung and characterization of a novel murine T cell
Burface antigen, YEJ/48,";
J. Immunol. 142:1727-1736(1989).
                                                                                                                                                                                                                                                                                 -!- SUBUNIT: Homodimer; disulfide-linked.
-!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- TISSUE SPECIFICITY: HIGH, IN T LYMPHOMA LINES, VERY LOW IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 1; Length 262;
Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> R (IN REF. 2).
3C3328D265F71B5E CRC64;
           KLRAI OR LY49A OR LY-49A OR LY49 OR LY-49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M25775; AAA40578.1; ALT_SEQ.
EMBL; M25812; AAA37242.1; -.
EMF; A30573; A30573.
PIR; A45813; A45813.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDB; 1Q03; 02-JAN-00.
MGD; MGI:101907; Klral.
InterPror; IFR001304; Lectin C.
Pfam; PF00059; lectin C; 1.
SMART; SM00034; CLECT; 1.
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80.0%;
                                                                                                                                                                                                                                                                                                                        NORMAL LYMPHOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 ;
262 AA;
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE FROM N.A.
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138
1167
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CARBOHYD
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CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR CLASS I MHC.
-1- SUBUNT: Homodimer; disulfide-linked.
-1- SUBCELLULAR LOCATION: Type II membrane protein.
-1- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CS7BL/6;
MEDLINE=96421544; PubMed=8824161;
Silver E.T., Elliott J.F., Kane K.P.;
"Alternatively spliced Ly-49D and H transcripts are found in IL-2-
                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
TIRA MOUSE STANDARD; PRT; 263 AA.

G0651, 078026; Q9ERAS;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
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16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last 
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM D2).
STRAIN=C57BL/6; TISSUE=Spleen;
MEDLINE=94300068; PubMed=8027540;
Smith H.R.C., Karlhofer F.M., Yokoyama W.M.;
"Ly-49 multigene family expressed by IL-2-activated NK cells.";
J. Immunol. 153:1068-1079(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=NOD, and NOR;
MEDLINE=20384764; PubMed=10925254;
Silver E.T., Gong D.-E., Chang C.S., Amrani A., Santamaria P.,
Kane K.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; 149049; 149049.

MGD; MGI:101904; Khra4.
InterPro; IPR001304; Lectin_C.
PR00159; lectin_C; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS0041; C_TYPE_LECTIN_2; 1.
T-Cell; Glycoprotein; Antigen; Transmembrane; Cell adhesion; Signal-anchor; Lectin; Receptor; Multigene family; Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Ly-49P activates NK-mediated lysis by recognizing H-2Dd."; J. Immunol. 165:1771-1781(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isold=060651-2; Sequence=VSP 003068; SIMILARITY: Contains 1 C-type Tectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q60651-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM D1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [mmunogenetics 44:478-482(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, U10090; AAA50218.1; -.
EMBL, 178247; AAG32667.1; -.
EMBL, AF218079; AAF99592.1; -.
EMBL, AF218078; AAF99592.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activated NK cells."
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=D1;
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CYTOPLASMIC (POTENTIAL).	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)	(POTENTIAL).	EXTRACELLULAR (POTENTIAL).	C-TYPE LECTIN (LONG FORM).	BY SIMILARITY.	BY SIMILARITY.	N-LINKED (GLCNAC) (POTENTIAL)	N-LINKED (GLCNAC) (POTENTIAL)	N-LINKED (GLCNAC) (POTENTIAL)	N-LINKED (GLCNAC) (POTENTIAL)	Missing (in isoform D2).	/FTId=VSP 003068.	E -> K (IN STRAINS NOD AND NOR)	R -> W (IN STRAINS NOD AND NOR)	E -> Q (IN STRAINS NOD AND NOR)	R -> G (IN STRAINS NOD AND NOR)	L -> F (IN STRAINS NOD AND NOR)	T -> I (IN STRAINS NOD AND NOR)	K -> Q (IN STRAINS NOD AND NOR)	Y -> S (IN STRAINS NOD AND NOR)	L -> F (IN STRAINS NOD AND NOR)	MW; D0A940A089A9F42D CRC64;		k; Pred. No. 82;	
44	65		263	258	254	246	87	104	170	222	41		2	29	32	35	45	9	79	132	189	30872 MW;	85.0%;	80.0%;	מרדים
H	45		99	139	168	233	87	104	170	222	39		S	29	32	35	45	09	79	132	189	263 AA;		milarity 80.	
DOMAIN	TRANSMEM		DOMAIN	DOMAIN	DISULFID	DISULFID	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD	VARSPLIC		VARIANT	SEQUENCE	Query Match	Best Local Similarity	, 4 ,								
FŢ	FI	FT	FŢ	FT	FT	FT	FT	FT	FT	FI	FT	FT	FT	FT	FT	FT	FT	FT	FŢ	FT	FŢ	ÖS	8	B Z	01.7

Search completed: February 18, 2004, 14:28:13 Job time : 3.55263 secs

2 DWAWL 6 ||||: 208 DWAWI 212

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GenCore version 5.1.6
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OM protein - protein search, using sw model

February 18, 2004, 14:12:09; Search time 6.5921 Seconds (without alignments) 87.531 Million cell updates/sec Run on:

US-09-643-260-16 40 1 LDWAWL 6 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	conserved helix-lo	purine phosphoribo	probable phosphotr	probable cytochrom	hypothetical prote	dipeptide ABC tran	cytochrome P450 (C		probable cytochrom	Vi polysaccharide	Vi polysaccharide	H+-exporting ATPas	probable two-compo	lysobactin synthet	hypothetical prote		bo-type ubiquinol	cytochrome o ubiqu	hypothetical prote	bo-type ubiquinol	0	0	hypothetical prote		cytochrome o ubiqu	ubiquinol oxidase	probable cytochrom	hypothetical prote	
SUMMARIES	_	I49101	D75215	E70521	F83632	AB2931	D98351	T10000	T09999	T09944	A56975	AF1040	A42970	F83153	T18545	C70829	C83748	JC5900	A84985	B83243	A36885	AD0384	D83480	AG2946	C98336	AG3489	A87469	C96006	C85064	D85064
	Length DB	:	215 2					516 2				656 2		1212 2					296 2				331 2						394 2	
di	Query Match I	92.5	90.0	90.0	0.06	0.06	90.0	90.0	90.0	0.06	0.06	90.0	90.0	90.0	90.0	87.5		•	87.5	•	•	ζ.	٠	۲.	87.5	۲.	۲.	۲.	87.5	7.
	Score	37																											35	
	Result No.	-	7	m	4	S	ø	7	ω	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	29

probable sugar tra	probable potassium	Ly-49D-GE antigen	natural killer cel		T-cell surface gly	LGL-1 - mouse	NADH2 dehydrogenas	NADH ubiquinone ox	NADH dehydrogenase	hypothetical prote	hypothetical prote	type I restriction	nitric-oxide synth	nitric-oxide synth	nitric-oxide synth
AE0309	AI0379	149049	149361	A30573	A45813	155686	A13395	AE2733	G97514	E90438	B96610	C69226	S71424	A47501	A38943
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443	1139	260	262	262	262	267	322	348	348	395	395	919	1202	1203	1205
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87	87	85	85	85	85	85	85.0	85	85	82	82	85	85.0	82	82
35	35	34	34	34	34	34	34	34	34	34	34	34	34	34	34
0	_	~	س	4	'n	G	7	38	6	_	_	~	_		

ALIGNMENTS

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C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Cocession: 149101
R;Mock, B.A.; Connelly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.
Genomics 27, 348-351, 1995
A;Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome A;Reference number: 149101; MUID:96044444; PMID:7558004
A;Reference number: 149101
A;Statuus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-745 <RES>
A;Residues: 1-745 <RES>
A;Cross=references: EMBL:U12473; NID:g1079492; PIDN:AAC52589:1; PID:g1079493
A;Gene: CHUK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homolocikoywords: ATP; phosphotransferase
C:Koywords: ATP; phosphotransferase
F:13-283/Domain: protein kinase homology <KIN>
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                                         conserved helix-loop-helix ubiquitous kinase (BC 2.7.1.-) CHUK - mouse
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149101
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|||:|| 738 LDWSWL 743 1 LDWAWL 6 ઠ В

purine phosphoribosyltransferase PAB2405 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: D75215
R;anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A;Bescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome strn A;Reference number: A75001
A;Accession: D75215
A;Accession: D75215
A;Accession: D75215
A;Accession: D75215
A;Accession: D75215
A;Accession: Carain Data
A;Residues: 1-215 < KAW>
A;Accession: Carain Orsay
C;Genetics: A;Coss-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49171.1; PID:e15150
A;Experimental source: strain Orsay
C;Genetics: A;Gene: gptA; PAB2405

Gaps ö 90.0%; Score 36; DB 2; Length 215; 66.7%; Pred. No. 57; ive 2; Mismatches 0; Indels Query Match Best Local Similarity 66.7 Matches 4; Conservative

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C;Accession: AB2331
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, J. erage, G.; Gilet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell'; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C'Accession: D98351

A. Scodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, R.; Goodner, B.; Hinkle, G.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001

Science 294, 2323-2328, 2001

A; Fittle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tun A; Reference number: A97359; MUID:21608551; PMID:11743194

A; Accession: D98351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytochrome P450 (CYP72C) - Madagascar periwinkle (fragment)
C;Species: Catharanthus roseus (Madagascar periwinkle)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001
C;Accession: T10000
R;Mangold, U.; Eichel, J.; Batschauer, A.; Lanz, T.; Kaiser, T.; Spangenberg, G.; Werck-Plant Sci. 96, 129-116, 1994
A;Title: Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from Catharanth A;Reference number: 216915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dipeptide ABC transporter, dipeptide-binding protein PAB0092 [imported] - Agrobacterium C;Species: Agrobacterium tumefaciens C;Species: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                     ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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A;Molecule type: DNA
A;Residues: 1-316 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK90334.1; PID:g15160371; GSPDB:GN00170
                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-316 KKUR>
A;Cross-references: GB:AE008689; PIDN:AAL43864.1; PID:g17741409; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
";Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 316;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
84;
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A;Molecule type: mRNA
A;Residues: 1-516 <MAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.0%; Scor.
100.0%; Pred. No. ...
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A,Map position: linear chromosome
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A;Map_position: linear chromosome
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Best Local Similarity 100.0
Matches 5; Conservative
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Best Local Similarity
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A, Status: preliminary
A, Molecule type: DNA
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C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C; Accession: F83632
R; Stover C. K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bz adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patholasterence number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                          C,Accession: E70521
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Connor, R.; Davies, R.; Perkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Naturnes: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Arlitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A7050; MulD:98295987; PMID:9634230
A; Accession: E7051
A; Molecule type: DNA
A; Residues: 1-251 <COL>
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A;Cross-references: GB:AE004449; GB:AE004091; NID:g9945928; PIDN:AAG03503.1; GSPDB:GN001
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:Z97188; GB:AL123456; NID:G3261805; PIDN:CAB10016.1; PID:G2224828
A;Experimental source: strain H37Rv
C;Genetics:
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C;Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable cytochrome c oxidase assembly factor PA0113 [imported] - Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                   C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                   probable phosphotransferase - Mycobacterium tuberculosis (strain H37RV)
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67;
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C;Superfamily: kanamycin kinase
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C;Superfamily: heme O synthase
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141 IDWAWI 146
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                                1 LDWAWL 6
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A; Status: preliminary
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Vi polygaccharide capsule transporter VexE - Salmonella typhi
C;Species: Salmonella typhi
C;Species: O3-Oct-1995 #sequence_revision O3-Oct-1995 #text_change 11-Jan-2000
C;Accession: A56975
R;Hashimoto, Y.; Li, N.; Yokoyama, H.; Ezaki, T.
B. Bacteriol. 175, 4456-4465, 1993
A;Title: Complete nucleotide sequence and molecular characterization of ViaB region enc
A;Reference number: A36892; MUID:93322324; PMID:8331073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Genetics:
C;Genetics:
C;Genetics:
C;Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat h
F;284-317/Domain: tetratricopeptide repeat homology <TT1>
F;318-351/Domain: tetratricopeptide repeat homology <TT2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFIGNO.

Vi polysaccharide export protein [imported] - Salmonella enterica subsp. enterica servov

Vi polysaccharide export protein [imported] - Salmonella enterica servova Typhi

A; Note: this species has also been called Salmonella typhi

C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C; Accession: Arlo40

C; Accession: Arlo40

C; Date: 09-Nov-2001 #text_change 18-Nov-2002

C; Accession: Arlo40

C; Date: 09-Nov-2001

C; Date: 09-Nov-2001

C; Date: 09-Nov-2001

C; Date: 09-Nov-2001

C; Date: 09-Nov-2002

C; Date: 09-Nov-2001

C; Date: 09-Nov-2002

C; Date: 09-Nov-2002

C; Date: 09-Nov-2003

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C; Date: 09-Nov-2003

C; Date: 09-Nov-2003

C; Date: 09-Nov-2003

C; Date: 09-Nov-2003

C; Date: 09-Nov-2003

Notered: 0-Nov-2003

A; Davis, N.; Finmonds, M.; Skelton, J.; Stevens, K.

A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
A; Accession: AP1040

A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-656 < PAR>
A; Residues: 1-656 < PAR>
A; Cross-references: GB:AL513382; PIDN:CAD06771.1; PID:g16505421; GSPDB:GN00176
A; Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const. Const.
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C,Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat h
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        Similarity 100.0%; Score 36; DB 2; Length 524; Similarity 100.0%; Pred. No. 1.4e+02; 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                      28 LDWAW 32
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Cypecies: Catharanthus roseus (Madagascar periwinkle)
Cypecies: Catharanthus roseus (Madagascar periwinkle)
Cypecies: 16-Uul-1999 #sequence_revision 16-Uul-1999 #text_change 16-Feb-2001
Cypecesion: T09999
RyMangold, U.; Eichel, J.; Batschauer, A.; Lanz, T.; Kaiser, T.; Spangenberg, G.; Werck-Plant Sci. 96, 129-136, 1994
AyTitle: Gene and CDNA for plant cytochrome P450 proteins (CYP72 family) from Catharanth A;Reference number: 216915
AyAccession: T09999
AyStatus: preliminary; translated from GB/EMBL/DBJ
AyRetus: preliminary; translated from GB/EMBL/DBJ
AyRetus: preliminary;
AyMolecule type: DNA
AyErose-references: EMBL:119074; NID:9404687; PID:9404688
AyErose-references: EMBL:119074; NID:9404687; PID:9404688
AyExperimental source: cv. cp3
CyGenetics:
AyGene: CYP72B
AyIntrons: 96/1; 170/3; 252/2; 381/3
CySuperfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology
CyKeywords: heme; iron; metalloprotein
F;329-492/Domain: cytochrome P450 homology <P45>
F;470/Binding site: heme iron (Cys) (axial ligand) #status predicted
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NyAlternate names: CYP72 protein
NyAlternate names: CYP72 protein
Cypecias: Catharanthus roseus (Madagascar periwinkle)
Cypecias: Catharanthus roseus (Madagascar periwinkle)
Cypecias: 16-701-1999 #sequence_revision 16-701-1999 #text_change 16-Feb-2001
CyAccession: T09944
NyCeter, H.P.; Mangold, U.; Schroeder, G.; Marner, F.J.; Werck-Reichhart, D.; Schroeder
Plant Physiol. 100, 9994-1007, 1992
A; Reference number: 216902
A; Reference number: 216904
A; Reference number: 216904
A; Residus: preliminary; translated from GB/EMBL/DDBJ
A; Residus: 1-524 < VET>
A; Residus: 1-524 < VET>
A; Residus: 1-524 < VET>
A; Crosser-references: EMBL:L10081; NID:g167483; PID:g167484
A; Gene: CYP72
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A;Experimental source: cv. cp3
C;Genetics:
A;Gene: CYP2C
C;Superfamily: unassigned cytochrome P450; cytochrome P450 homology
C;Keywords: heme; iron; metalloprotein
F;318-481/Domain: cytochrome P450 homology <P45>
F;459/Binding site: heme iron (Cys) (axial ligand) #status predicted
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100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0;
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Best Local Similarity 100..
Best Local Si Conservative
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.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path.
A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                        A;Residues: 1-1212 <STO>
A;Cross-references: GB:AE004812; GB:AE004091; NID:g9950125; PIDN:AAG07333.1; GSPDB:GN001
A;Experimental source: strain PAO1
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A. Description: Identification of genes encoding for peptide synthetases from Gram-negatul
A;Reference number: Z18962
A;Accession: T18545
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A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title. Deciphering the biology of Mycobacterium tuberculosis from the complete genom A; Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Species: Lysobacter sp.
A;Variety: ATCC 53042
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 01-Dec-2000
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Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 28-Jul-2000
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A,Molecule type: DNA
A,Residues: 1-1575 <BER>
A,Cross-references: EMBL:X96558; NID:e991096; PID:e236566; PIDN:CAA65394.1
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C.Suberfamily: acrl carrier protein homology; acetate-CoA ligase homology
C.Keywords: carrier protein; phosphopantetheine; phosphoprotein
F;468-924/Domain: acetate-CoA ligase homology <ACL>
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F;974/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h Similarity 100.0%; Score 36; DB 2; Length 1212; Similarity 100.0%; Pred. No. 3.2e+02; 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: PA3946
C;Superfamily: evgS protein; response regulator homology
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Best Local Similarity
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A, Status: preliminary
A, Molecule type: DNA
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R, Bernhard, F.
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H+-exporting ATPase (EC 3.6.3.6) 95K chain, vacuolar - yeast (Saccharomyces cerevisiae) N;Alternate names: protein 05430c; protein YOR270c C;Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevisiae C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 03-Jun-2002 C;Accession: A42970; S67167; S67172; S72041 K;Manolson, M.F.; Proteau, D.; Preston, R.A.; Stenbit, A.; Roberts, B.T.; Hoyt, M.A.; Pr J. Biol. Chem. 267, 14294-14303, 1992 A;Title: The VPH1 gene encodes a 95-kDa integral membrane polypeptide required for in vi A;Reference number: A42970; MUID:92332542; PMID:1385813
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C; Superfamily: vacuolar ATP synthase 95K chain
C; Superfamily: vacuolar ATP synthase 95K chain
C; Reywords: ATP; glycoprotein; hydrogen ion transport; hydrolase; membrane-associated cf 7407-441/Domain: transmembrane #status predicted <TM2>
P; 457-478/Domain: transmembrane #status predicted <TM3>
P; 559-558/Domain: transmembrane #status predicted <TM3>
P; 655-591/Domain: transmembrane #status predicted <TM3>
P; 635-656/Domain: transmembrane #status predicted <TM5>
P; 733-795/Domain: transmembrane #status predicted <TM6>
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R;Cheret, G.: Sor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Cheret, G.; Bernardi, A.; Sor, F.
Seast 12, 1059-1064, 199
A;Title: DNA sequence analysis of the VPH1-SNF2 region on chromosome XV of Saccharomyces
A;Reference number: S72039; MUID:97051594; PMID:8896271
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| Cross-references: EMBL:275178; NID:g1420605; PIDN:CAA99494.1; PID:g1420606; GSPDB:GNOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: F83153 C;Accession: F8153 Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description: hydrogen ion transport; hydrolase; required for assembly and activity of Superfamily: vacuolar ATP synthase 95K chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A). Cross-references: EMBL:X89633; NID:g1279694; PIDN:CAA61776.1; PID:g1279697
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
C,Genetics:
A,Gene: SGD:VPH1; MIPS:YOR270c
A,Cross-references: MIPS:YOR270c, SGD:S0005796
A,Map position: 15R
C,Function:
A,Description: hydrogen ion transport; hydrolase; required for assembly and activi
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-840 cMAN>
A; Residues: 1-840 cMAN>
A; Cross-references: GB: M89778; NID: g173172; PIDN: AAA35211.1; PID: g173173
A; Experimental source: strain X2180-1b; vacuolar acidification-defective mutants A; Note: sequence extracted from NCBI backbone (NCBIN:108529, NCBIP:108530)
B; Jauniaux, J.C.; Polrey, R.
submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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2.2e+02;
thes 0;
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submitted to the Protein Sequence Database, July 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable two-component sensor PA3946 [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Experimental source: strain S288C
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A;Accession: S67167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reference number: S67169
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                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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A, Experimental source: strain H37Rv C, Genetics: A, Gene: Rv0471c C, Superfamily: Mycobacterium tuberculosis hypothetical protein Rv0471c Query Match 87.5%; Score 35; DB 2; Length 162; Best Local Similarity 83.3%; Pred. No. 62; Matches 5; Conservative 0; Mismatches 1; Indels

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Search completed: February 18, 2004, 14:38:52 Job time : 7.5921 secs

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                                                                  (without alignments)
35.929 Million cell updates/sec
                                                         February 18, 2004, 14:16:39; Search time 7.06579 Seconds
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/cgn2_6/ptodata/1/iaa/SB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/GA_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-887-518-3
US-08-887-518-3
US-08-897-85-3
US-09-032-475-3
US-09-032-475-4
US-09-032-476-4
US-09-032-476-4
US-09-03-125A-4
US-09-03-125A-4
US-09-03-125A-4
US-09-03-131A-2
US-09-109-986-4
US-09-844-908-10
US-09-844-908-10
US-09-03-321-4
US-09-032-321-4
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US-09-168-629-15
US-08-910-820-9
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Maximum Match 100%
Listing first 45 summaries
                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                          US-09-643-260-16
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Match Length
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                                                         Run on:
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No.
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Sequence 5762, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                       Sequence 4, Appli
Sequence 123, App
Sequence 121, App
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Sequence 20395, A
Sequence 21655, A
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Sequence 14, App
Sequence 2, Appl
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
US-09-844-908-9
US-09-868-758-4
US-09-417-197-121
US-09-417-197-121
US-09-252-991A-21055
US-09-252-991A-21055
US-09-252-991A-21055
US-09-252-991A-21055
US-09-172-952-14
US-07-908-245-2
US-08-319-866-10
US-09-123-708-6
US-09-123-708-6
US-08-123-64-6
US-08-123-64-6
US-08-123-64-6
US-08-113-64-6
US-08-241-633-28
US-08-241-633-28
US-08-241-633-28
US-08-850-917-28
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COMPUTER: PC
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COMPUTER: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAMM: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
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; LOCATION: (B) LOCATION 1...23
; SEQUENCE DESCRIPTION: SEQ ID NO: 5762:
US-09-107-532A-5762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
COUNTRY: USA
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US-08-899-853-4
; Sequence 4, Application US/08990853
; Patent No. 5851812
; GENERAL INFORMATION:
    APPLICANT: Goeddel, David V.
    APPLICANT: Woronicz, John
    TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
    STREET: 268 BUSH STREET, SUITE 3200
    CITY: SAN FRANCISCO
    STATE: CALIFORNIA
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PILING DATE: US/09/023,321
FILING DATE: US/09/023,321
FILING DATE: US/08/887,518
PRIOR APPLICATION NUMBER: US/08/887,518
FILING DATE: ATTORNATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 2; Ler
Pred. No. 3.4e+02;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
                               ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                   NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T9'
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.5%;
                                                                                                                                                                                                                                                                                                                                                                                (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.5
Lag 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
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CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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                                                       Gaps
                                                                                                                                                                                                                    Sequence 3, Application US/08887518

Patent No. 5843721

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STRATE: CALIFORNIA
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Patent No. 5844073
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
               DB 4; Length 223;
80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.5%; Score 37; DB 2; Length 745; 83.3%; Pred. No. 3.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
               Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
ATTORNEY/ACBNT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
               95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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                             Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                              amino acid
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Best Local Similarity
Matches 5; Conserv
                                                                                          1 LDWAWL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94104
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                                                                                                                                                                                                     US-08-887-518-3
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                 Query Match
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Gaps

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GENERAL INFORMATION:
APPLICANT: Geeddel, David V.
APPLICANT: Geeddel, John
TITLE OF INVENTION: IKK-
NUMBER OF SEQUENCES:
ACCRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09099124A
Patent No. 5939302
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Pred. No. 3.4e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                         COMPUTER: FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,125A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTOMNEY/AGENT INFORMATION:
NAME: CLASSI INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,124A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.5%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 83.3'
                                                                                                                                                     STREET: 268 BUSH STRE
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        738 LDWSWL 743
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APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                       Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.5%; Score 37; DB 2; Length 745; 83.3%; Pred. No. 3.4e+02;
                                                                                                                                                                                           0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,475
                                                                                                                                                     Score 37; DB 2; 1
Pred. No. 3.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSWAN, RICHARD A
REGISTRATION NUMBER: 36,627
REPERRINGE/OCKET WUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 4, Application US/09099125A
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Patent No. 5854003
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 343-4341
TELEPAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
                                                                                                                                                     92.5%;
                  l: 745 amino acids
amino acid
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                      single
                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-890-853-4
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                                                      STRANDEDNESS:
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US-09-099-125A-4
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Gaps

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APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
APPLICANT: R gnier, Catherine
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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APPLICANT: Rothe, Mike
APPLICANT: Cao, Zalodan
APPLICANT: R gnier, Catherine
APPLICANT: R gnier, Catherine
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APPLICANT: R gnier, Catheri
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                                                        Score 37; DB 3; Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,854
                                                                                             Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 3;
Pred. No. 3.4e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08890854
Patent No. 6235512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-09-033-324-4
Sequence 4, Application US/09023324
; Patent No. 6235313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REFERENCE/DOCKET NUMBER: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                                                           92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       745 amino acids
                                                        Query Match 92.5
Best Local Similarity 83.3
Matches 5; Conservative
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LENGTH: 745 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                              738 LDWSWL 743
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                             1 LDWAWL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94104
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US-08-890-854-4
US-09-032-476-4
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Patent No. 6235492
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rotherine
APPLICANT: Sequence: Standard
APPLICANT: IKC-' Proteins, Nucleic Acids and Methods
CORRESPONDENCES: 5
CORRESPONDENCE ADMENS:
ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 2;
Pred. No. 3.4e+02;
1; Mismatches 0
                                                                               APPLICALLOW.

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
REFERENCE/DOCKET NUMBER: T97-006-1
TELEPAN: (415) 343-4341
FELEPAN: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
LENGTH: amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REPRENCE/DOCKET NUMBER: T97-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 738 LDWSWL 743
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Sequence 2, Application US/08810131A
Patent No. 6268194
GENERAL INFORMATION.
APPLICANT: Karin, Michael
APPLICANT: DiDonato, Joseph A.
APPLICANT: DiDonato, Joseph A.
APPLICANT: HAYAkawa, Makio
APPLICANT: APANATK, Eardim
TITLE OF INVENTION: 1-kappa-B Kinase and Methods of Using
TITLE OF INVENTION: Same
CORRESPONDENCES: 9
CORRESPONDENCES. 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.5%; Score 37; DB 3; Length 745; 83.3%; Pred. No. 3.4e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                      APPLICANT: Zhu, Hengyi
APPLICANT: Zhu, Hengyi
APPLICANT: Li, Giban
APPLICANT: Li, Giban
APPLICANT: Mirray, Brion W.
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,820
FILING DATE: 12-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.413C1
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                             Sequence 10, Application US/08910820; Patent No. 6258579; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3.
                                                                                                                                                                                                                                                                                                                                                                     CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
US-08-910-820-10
     738 LDWSWL 743
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                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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                                                                             US-08-910-820-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-08-810-131A-2
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Sequence 2, Application US/09168629;
Sequence 2, Application US/09168629;
Patent No. 6242233;
GENERAL INFORMATION:
APPLICANT: BiDonato, Joseph A.
APPLICANT: DiDonato, Joseph A.
APPLICANT: Application Makio
TITLE OF INVENTION: IEE Kinase, Subunits Thereof, and Methods of Using Same;
FILE REFERENCE: P-UD 3295;
CURRENT APPLICATION NUMBER: US/09/168,629;
CURRENT FILING DATE: 1998-10-08;
EARLIER APPLICATION NUMBER: 60/061,470
SARALIER FILING DATE: 1997-10-09;
NUMBER OF SEQ ID NOS: 20;
SOFTWARE PRESENCE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 745;
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Pred. No. 3.4e+02;
1; Mismatches 0; Indels
                                                                                                                                                                          ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
       STREET: 26 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTY: USA ZIP: 94104
                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.5%;
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Best Local Similarity 83.3'
Matches 5; Conservative
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; MOLECULE TYPE: peptide
US-09-023-324-4
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738 LDWSWL 743
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LENGTH: 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mercary,
Zhu, Hengyi
Barbosa, Miguel
Li, Gian
Murray, Brion W.
TITLE OF INVENTION: STIMULS-INDUCIBLE PROTEIN KINASE
COMPLEX AND METHODS OF USE THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: FIORPY disk
COMPUTER: IND PC Compatible
COMPUTER: PLAN PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/99/844,908
FILING DATE: 27-Apr-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION: cUnknown>
PRIOR APPLICATION NUMBER: US/08/910,820
FILING DATE: 12-AUG-1997
ATTORNEY/AGENT INPORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                    Score 37; DB 4; Length 745;
Pred. No. 3.4e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.5%; Score 37; DB 4; Length 745; 83.3%; Pred. No. 3.4e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 860098.413C1
TELECOMMUNICATION INFORMATION:
TELEFONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/09844908
Patent No. 6576437
GENERAL INFORMATION:
APPLICANT: Mercurio, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 745 amino acids TYPE: amino acid
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                                                                                                                                                                         92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
                                                                                                                                                                    Query Match
Best Local Similarity 83..3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: peptide
US-09-109-986-4
                                                                                                                                                                                                                                                                                      738 LDWSWL 743
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738 LDWSWL 743
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Best Local Similarity
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; Sequence 4, Application US/09109986
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: IKK-N Proteins, Nucleic Acids and Methods
; TITLE OF INVENTION: IKK-N Proteins, Nucleic Acids and Methods
; TORRESPONDENCE ADDRESS:
; SORRESPONDENCE ADDRESS:
; STREET: 268 BUSH STREET, SUITE 3200
; STREET: CALIFORNIA
; STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.5%; Score 37; DB 3; Length 745; 83.3%; Pred. No. 3.4e+02; Live 1; Mismatches 0; Indels
                                                                                                                                     CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/810,131A

TILING DATE: 25-FBE-1997

FILING DATE: 25-FBE-1997

TLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: P-UD 2408

TELEPARATION OF SEQ 1D NO: 2: SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

TYPE: AMINO ACID

TYPE: AMINO ACID

TOPLICULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,986
                                                         COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
PPLICATION NUMBER: 08/890,854
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEPAX: (415) 343-4341
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
California
: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83...
5; Conservative
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738 LDWSWL 743
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Search completed: February 18, 2004, 14:41:51 Job time : 7.06579 BecB

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMedt G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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Enterobacteriaceae; Escherichia.
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EcoGene; EC13361; ydaS.
Hypothetical protein; Signal; Complete proteome.
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AR12_CABE10
AR12_CABE10
AR12_MOUSE
AR12_MOUSE
AR12_MOUND
AR10_MOUND
CPAA_BACTU
CCPAA_BACTU
TOKI_YEAST
ATX1_ARATH
V131_MSTUA
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239 LDWSYV 244
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                                                                                                     RESULT 3
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                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                    A Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Barviss R., Boursler L., Brans A., Braun M., Brignell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Broinsot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T.,

R. Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

R. Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

R. Hibert H., Holsappel S., Hagach J., Harwood C.R., Henaut A.,

R. Hibert H., Holsappel S., Hagas K., Haiech J., Harwood C.R., Henaut A.,

R. Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

R. Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

Modina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

R. Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

R. Sekiguchi J., Sekwaka A., Seror S.J., Serror P., Shin B.S., Soldo B.,

R. Sekiguchi J., Sekwaka A., Seror S.J., Serror P., Shin B.S.,

R. Josato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

Hinters P., Wanbutt R., Wedler E., Wedler K., Yasumoto K., Yata K.,

Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,

The complete genome sequence of the Gram-positive bacterium Bacillus

The Control of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.7%; Score 33; DB 1; Length 330;
83.3%; Pred. No. 51:
                                                          Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7C6C65F1EDB276B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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POTENTIAL.
POTENTIAL.
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Hypothetical transport protein yetK.
                                                                                                                                                           MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35758 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z99107; CAB12540.1; -. PIR; H69798; H69798.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Subtilist, BG12867; yetK.
InterPro, IPR000620; DUF6.
Pfam; PF00892; DUF6; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vature 390:249-256(1997).
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                                                                                                                      SEQUENCE FROM N.A.
                                       Bacillus subtilis.
                                                                          NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical
                                                              Bacteria;
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TRANSMEM
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TRANSMEM
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Gaps

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Indels

Pred. No. 51; 1; Mismatches

Conservative

Best Local Similarity Matches 5; Conserv

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MEDLINES-11898401; PubMed=11859360;

WEDLINES-12948401; PubMed=11859360;

Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Squros J., Peat N., Hayles J., Baker S., Basham D., Bowaman S.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J.,

A James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA James K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E.,

A Noney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Nitherford K., Rutter S., Saudres R., Seeger K., Sharp S.,

Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Borzym K., Langer I., Beck A., Lehzer E., Moestl D., Hilbert H.,

Borzym K., Langer I., Beck A., Lehzer E., Moestl D., Hilbert S.,

Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

Goffeau A., Cadieu E., Dimenez J., Sanchez M., Gel Rey F., Benito J.,

Bominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

Certutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

Shakovski G.V., Ussery D., Barrall B.G., Nurse P.,

Nather G. M., Nather B., Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 415:871-880(2002).
-!- FUNCTION: ADEN'LATES FWN TO FAD (BY SIMILARITY).
-!- CATALYTIC ACTIVITY. APTP + FWN = diphosphate + FAD.
-!- SIMILARITY: BELONGS TO THE PAPS REDUCTASE FAMILY. FAD1 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                      30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable FAD synthetase (EC 2.7.7.2) (FWN adenylyltransferase) (FAD pyrophosphorylase) (Flavin adenine dinucleotide synthetase).
SPCC1235.04C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase; NucleoLidyltransferase; FAD; FWN.
SEQUENCE 265 AA; 30608 MW; BC6C662E6F43A6F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
    265 AA
                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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InterPro; IPR002500; PAPS_reduct.
Pfam; PF01507; PAPS_reduct; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL031764; CAA21108.1; -.
                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T40878; T40878
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4896
FAD1_SCHPO
074841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=972;
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212
394
469
476 AA;
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                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                    similarity)
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ACT_SITE
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANGE AND A RANG
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                                                                                                                                                                                                                                                                                                                                                                        Quirk P.G., Krulwich T.A.,
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
--- COFACTOR: Pyridoxal phosphate (Potential).
--- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthase)
CLS OR CLSD OR CPE1430.
Clostridium perfringens.
Bacteria; Firmicutes; Clostridia, Clostridiales; Clostridiacese;
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STRAIN-NCTC 8237 / ATCC 13124 / CN 1491 / Type A;
BEDLINE-2004836, PubMed=10585141;
Koyama M., Katayama S., Kaji M., Taniguchi Y., Matsushita O.,
Minami J., Morita S., Okabe A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 280 PYRIDOXAL PHOSPHATE (POTENTIAL).
445 AA, 48849 MW; 5C921199BC2E24BC CRC64;
                                                                                                                                                                                         01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Probable aminotransferase in katA 3'region (EC 2.6.-.-) (ORF Bacillus firmus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cardiolipin synthetase (EC 2.7.8.-) (Cardiolipin synthase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.9%; Score 32; DB 1; Length 445; 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, P12995, 1033.
InterPro; IPR005614; Aminotrans_3.
Pfam, PF00202; aminotran_3; 1.
PROSITE, PS00600; AA_TRANSFER_CLASS_3; 1.
Hypothetical protein; Aminotransferase; Transferase;
                                                                                                                                                          445 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                476 AA
                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L02548; AAA22560.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          aminotransferases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S27492; S27492.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                    173 LDWSY 177
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ø
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1399;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1502;
                LDWSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 DWSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLS CLOPE
Q9ZNC6;
                                                                                                                                                      YKAB BACFI
P30268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
                                                                                                                                   BACFI
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NCBI_TaxID=6239;
                                                                                                                                                   STRAIN=13 / Type A;
MEDLINE=21664373; PubMed=11792842;
Shimizu T., Ohtenin K., Hirakawa H., Ohshima K., Yamashita A.,
Shibizu T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                 flesh-eater.",
Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
-!- FUNCTION: Catalyzes the reversible phosphatidyl group transfer
from one phosphatidylglycarol molecule to another to form
cardiolipin (CL) (diphosphatidylglycerol) and glycerol (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: 2 Phosphatidylglycerol = diphosphatidylglycerol + glycerol. SUBCELLULAR LOCATION: Membrane-bound (By similarity). SINGCELLULAR ELONGS TO THE PHOSPHOLIPASE D FAMILY. CARDIOLIPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
cysG(B)
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"A Clostridium perfringens hem gene cluster contains a homologue that is involved in cobalamin biosynthesis."; Microbiol. Immunol. 43:947-957(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biosynthesis; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T -> I (IN REF. 1).
BEC32FC113F0A9CB CRC64;
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PLD PHOSPHODIESTERASE
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16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    517 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB017186; BAA74786.1; --
EMBL; AP00130; BAB81136.1; --
PIR; T43863; T43863.
HAMAP; MF 00130; -1.
InterPro; TPR001736; PLD.
Pfam; PF00614; PLDC; 2.
SWART; SM00155; PLDC; 2.
PROSTIE; PS50035; PLD; 2.
Transferase; Phospholipid biosynt
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55040 MW;
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dentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Jones E., Jones M., Leather S., McDonald S., Jügels K., Jünes K., Jönes M., Jönes M., Leather S., McDonald S., McDean J., Money P., Moule S., Mungall K., Murphy L., Niblett D., Odeil C., Andrews R., Sauders D., Seeger K., Sharp S., Autherford K., Ritter S., Saunders B., Seeger K., Sharp S., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Meltjens I., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Puchs M., Fritz C., Holzer E., Moestl D., Hilbert H., Aeltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Amer S., Gabel C., Euchs M., Fritz C., Holzer E., Moestl D., Hilbert H., Berzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Goffeau A., Cadieu E., Dreano S., Gloux S., Leluure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Foreburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shak Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., When J. M., March J. C., March J., Lowe T., McCombie W.R., Paulse P., Miller S., M. M., Chiller M., M., Carlon C., Nosery D., Barrell B.G., Nurse P., M., Chiller M., M., Chiller M., M., Chiller M., M., Chiller M., M., Chiller M., M., Chiller M., M., Carlon C., Moreno S., Armstrong J., Foreburg S.L., The Genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified ann-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moon K.Y., Kong D., Lee J.K., Raychaudhuri S., Hurwitz J.;
"Identification and reconstitution of the origin recognition complex
from Schizosaccharomyces pombe.";
Proc. Natl. Acad. Sci. U.S.A. 96:12367-12372(1999).
-!- FUNCTION: COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC) THAT
BINDS ORIGINS OF REPLICATION. IT HAS A ROLE IN BOTH CHROMOSOMAL
REPLICATION AND MATING TYPE TRANSCRIPTIONAL SILENCING. BINDS TO
THE ARS CONSENSUS SEQUENCE (ACS) OF ORIGINS OF REPLICATION.
-!- SUBGELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- DEVELOPMENTAL STAGE: EXPRESSED CONSTITUTIVELY DURING THE CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA replication; Nuclear protein; DNA-binding; ATP-binding. NP BIND 368 375 ATP (POTENTIAL). SEQUENCE 707 AA; 80514 MW; D056018159A40A44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 707;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE ORC1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GeneDB_SPombe; SPBC29A10.15; -.
InterPro; IPR0013593; AAA_ATPase.
InterPro; IPR0013595; AAA_ATPase_centr.
InterPro; IPR000637; AT hook.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEDLINE=20006240; PubMed=10535928;
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100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U43392; AAB38247.1; -.
EMBL; U38522; AAC49129.1; -.
EMBL; AL034463; CAA22443.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR001025; BAH.
Pfam; PF0004; AAA; 1.
Pfam; PF02178; hock; 1.
Pfam; PF01426; BAH; 1.
SMART; SM00382; AAA; 1.
SMART; SM00344; AT hock; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U40378; AAC49141.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
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Best Local Similarity
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SEQUENCE
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             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                           -i- SUBCELLULAR LOCATION: Nuclear (By similarity).
-i- SIMILARITY: Belongs to the sestrin family.
-i- CAUTION: Ref.1 sequence differs from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgource J., Peat N., Hayles J., Baker S., Basham D., Bowann S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muzi-Falconi M., Kelly T.J.;
Orppi, a member of the Cdc18/Cdc6 family of S-phase regulators, is
homologous to a component of the origin recognition complex.";
Proc. Natl. Acad. Sci. U.S.A. 92:12475-12479(1995).
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.9%; Score 32; DB 1; Length 517; 66.7%; Pred. No. 1.2e+02; ive 2; Mismatches 0; Indels
                                                    Du H., Wohldmann P., Ames M.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D7BC041916D0E205 CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
28-FBB-2003 (Rel. 41, Last annotation update)
Crigin recognition complex subunit 1.
ORCI OR ORPI OR SPBC29A10.15.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaces;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96099401; PubMed=7502077;
Gavin K.A., Hidaka M., Stillman B.D.;
"Conserved initiator proteins in eukaryotes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            707 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006730; PA26.
Pfam; PF04658; PA26.1.
Hypochetical protein; Nuclear protein
SEQUENCE 517 AA; 60881 MW; D7BC041
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AC024206; AAF36051.1; ALT_SEQ. WormPep; Y74C9A.5; CE24663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                        Axelsen K., Bairoch A.;
Unpublished observations (MAR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21848401; PubMed=11859360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Query Match
Best Local Similarity 66./.,
Best Local 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 270:1667-1671 (1995)
                                                                                                                                                                                                                                               gene model prediction.
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                                                                                                                  CONCEPTUAL TRANSLATION.
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NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :[|||:
156 IDWSYM 161
                              STRAIN=Bristol N2;
Du H., Wohldmann P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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MEDLINE=88126353; PubMed=3137939;
A Mahreholz A.M., Votaw P., Roach P.J., Depaoli-Roach A.A.,
Zioncheck T.F., Harrison M.L., Geahlen R.L.;
Thosphorylation of glycogen synthase by a bovine thymus protein-
T tyrosine kinase, p40.";
Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem. Blochem
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"Effect of protesses on the structure and activity of rabbit skeletal muscle glycogen synthetase.";
PEBS Lett. 98:66-70(1979).
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MEDLINE=86242253; PubMed=3087361;
Cohen P., Holmes C.F.B.;
"Identification of the C-terminus of rabbit skeletal muscle glycogen
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id sequence
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Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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MEDLINE-80246030; PubMed=6772446;
RYJatt D.B., Aitken A., Bilham T., Condon G.D., Embi N., Cohen "Glycogen synthase from rabbit skeletal muscle. Amino acid sequat the sites phosphorylated by glycogen synthase kinase-3, and extension of the N-terminal sequence containing the site phosphorylated by phosphorylase kinase.";
Eur. J. Blochem. 107:529-537(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang W.M., Browner M.F., Fletterick R.J., DePaoli-Roach A.A.,
Roach P.J.;
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MEDLINE-85285012; PubMed-3928373;
Kuret J., Woodgett J.R., Cohen P.;
"Multisite phosphorylation of glycogen synthase from rabbit suuscle. Identification of the sites phosphorylated by casein kinase-I.";
                                                   GYS1_RABIT STANDARD; PRT; 734 AA. P13834; 021831; 0218817; 012817; 01-078-1390 (Rel. 13, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Glycogen (starch) synthase, muscle (EC 2.4.1.11). GYS1 OR GYS.
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STRAIN=New Zealand white; TISSUE=Skeletal muscle;
MEDLINE=90033911; PubMed=2509275;
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                                                                                                                                                                                                                                                          Oryctolagus cuniculus (Rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from cDNA clones.";
FASEB J. 3:2532-2536(1989).
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Allosteric enzyme; Phosphorylation.
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P -> S (IN REF. 2).
S -> P (IN REF. 2).
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SEQUENCE FROM N.A., AND VARIANT NIDDM SER-464.
MEDLINE=95385855; PubMed=7657035;
Orbo M., Nikula-Ijas P., Schalin-Jantti C., Permutt M.A., Groop L.C.;
Isolation and characterization of the human muscle glycogen synthase
                                                                                                                                                                                                                                       Browner M.P., Nakano K., Bang A.G., Fletterick R.J.; "Human muscle glycogen synthase cDNA sequence: a negatively charged protein with an asymmetric charge distribution."; Prote. Natl. Acad. Sci. U.S.A. 86:1443-1447(1989).
                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                             01-JAN-1990 (Rel. 13, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annocation update)
Glycogen [starch] synthase, muscle (EC 2.4.1.11).
GYS1 OR GYS.
            737 AA.
                                                                                                                                                                                                               TISSUE=Muscle;
MEDLINE=89160794; PubMed=2493642;
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              STANDARD;
                                                                                                                    Homo sapiens (Human)
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                                                                                                                                                                NCBI_TaxID=9606;
              HUMAN
                         P13807
GYS1_HUMAN
ID GYS1 F
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skeletal

TISSUE=Endometrium;
MEDLINE=97163531; PubMed=9010351;
Su X., Schuler L., Shapiro S.S.;
"Cloning and characterization of a glycogen synthase cDNA from human

endometrium.";
J. Steroid Biochem. Mol. Biol. 59:459-465(1996)

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                 nonreducing end of alpha-1,4-glucan.
-!- CATALYTIC ACTIVITY: UDP-glucose + { (1,4)-alpha-D-glucosyl} (N) = UDP + (1,4)-alpha-D-glucosyl} (N+1).
-!- ENZYME REGULATION: ALLOSTERIC ACTIVATION BY GLUCOSE-6-PHOSPHATE, AND PHOSPHORYLATION BY A CAMP-DEPENDENT KINASE.
-!- PATHWAY: Glycogen biosynthesis.
-!- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE
FUNCTION: Transfers the glycosyl residue from UDP-Glc to the
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Pred. No. 1.7e+02;
0; Mismatches 1; Indels
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Allosteric enzyme; Phosphorylation; Disease mutation;
Diabetes mellitus; Polymorphism.
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A -> D (IN REF. 1 AND 3).

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EMBL; Z33626; CAA83916.1;
EMBL; Z33610; CAA83916.1;
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Best Local Similarity 83.3
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C TISSUE=Skeletal muscle;
C TISSUE=Skeletal muscle;
TISSUE=Skeletal muscle;
A Ortmeyer H.K., Marciani K.R., Hansen B.C.;
Monkey skeletal muscle glycogen synthase sequence.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Transfers the glycosyl residue from UDP-Glc to the nonreducing end of alpha-1,4-glucan (By similarity).
-!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl} (N+1).
-!- ENZYME REGULATION: ALLOSTERIC ACTIVATION BY A CHAP DEPENDENT KINASE.
-!- BATHWAY: Glycogen biosynthesis.
-!- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycogen biosynthesis; Transferase; Glycosyltransferase;
Allosteric enzyme; Phosphorylation.
BINDING 39 39 0DP-GLUCOSE (BY SIMILARITY).
MOD_RES 8 8 PHOSPHORYLATION (BY SIMILARI MOD_RES 641 641 PHOSPHORYLATION (BY SIMILARI MOD_RES 645 645 PHOSPHORYLATION (BY SIMILARI MOD_RES 649 PHOSPHORYLATION (BY SIMILARI MOD_RES 653 653 PHOSPHORYLATION (BY SIMILARI MOD_RES 653 653 PHOSPHORYLATION (BY SIMILARI MOD_RES 657 657 PHOSPHORYLATION (BY SIMILARI MOD_RES 657 657 PHOSPHORYLATION (BY SIMILARI MOD_RES 657 657 PHOSPHORYLATION (BY SIMILARI MOD_RES 657 657 PHOSPHORYLATION (BY SIMILARI MOD_RES 657 657 PHOSPHORYLATION (BY SIMILARI
                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glycogen [starch] synthase, muscle (EC 2.4.1.11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION (BY PHOSPHORYLATION (BY B8B0B3114C58F56C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.9%; Score 32; DB 1; I
83.3%; Pred. No. 1.7e+02;
ive 0; Mismatches 1;
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   737 AA
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                                                                                                                                                                                                      Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
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GYS3 MOUSE
ID GYS3 MOUSE STANDARD;
AC P54859;
DT 01-OCT-1996 (Rel. 34, Created)
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   STANDARD;
                                                                                                                                                                                                                                                                                              Cercopithecinae; Macaca.
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737 AA;
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                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9544;
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GYS1 MACMU
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Gaps

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY).
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                                                                                                                                                                              Brain Res. Mol. Brain Res. 38:191-199(1996).
--- FUNCTION: Transfers the glycosyl residue from UDP-Glc to the nonreducing end of alpha-1,4-glucan.
---- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) = UDP + {(1,4)-alpha-D-glucosyl}(N+1).
---- BNZYME REGULATION: ALLOSTERIC ACTIVATION BY GLUCOSE-6-PHOSPHATE, AND PHOSPHORYLATION BY A CAMP-DEPENDENT KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metezoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                 -1- PATHWAY: Glycogen biosynthesis.
-1- SIMILARITY: BELONGS TO THE MAMMALIAN/FUNGAL GLYCOGEN SYNTHASE
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                                                                                                                             MEDILINE-96385248; Value 2011, MEDILINE-96385248; PubMed-8793107; Pellegri G., Rossier C., Magistretti P.J., Martin J.L.; "Cloning, localization and induction of mouse brain glycogen synthase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 737;
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X94616; CAA64322.1; -.
MGD; MGI:107378; Gya3.
Glycogen biosynthesis; Transferase; Glycosyltransferase;
Allosteric enzyme; Phosphorylation.
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  891A0614C8F6C085 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYSI MOUSE STANDARD; PRT; 738 AA. 1021E4; 16.0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Glycogen [starch] synthase, muscle (EC 2.4.1.11) GYSI OR GYS.
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glycogen (starch) synthase, brain (EC 2.4.1.11).
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                                                                                                                    STRAIN-OF1 Albinos; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83824 MW;
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                                                Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                737 AA;
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                                                                                NCBI_TaxID=10090;
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GYS1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
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MEDLINE-97039016; Pubmed-8884597;
Peterson M.D., Uriosote A.S., Titus M.A.;
"Dictyostelium discoideum myod; a member of a broadly defined myosin V class or a class XI unconventional myosin?";
Hammer J.A. III, Jung G.; "The sequence of the dictyostelium myo J heavy chain gene predicts novel, dimeric, unconventional myosin with a heavy chain molecular
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Glycogen biosynthesis; Transferase; Glycosyltransferase;
Allosteric enzyme; Phosphorylation.
BINDING 39 39 UDP-GLUCOSE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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NCBI_TaxID=44689;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.9%; Score 32; DB 1; I
83.3%; Pred. No. 1.7e+02;
iive 0; Mismatches 1;
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01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dictyostelium discoideum (Slime mold).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 271:7120-7127(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96215148; PubMed=8636147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83955 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U53218; AAD09457.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              738 AA;
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                                                                                                   Eukaryota; Merazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adama M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adama M.D., Celniker S.E., in P. W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutcon G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxer E.G., Helt G., Nelson C.R., Miklos G.L.G.
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                          -!- SUBCELLUTAR LOCATION: Mitochondrial (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE=99389723; PubMed=10458908;
Gao Q., Chess A.;
"Identification of candidate Drosophila olfactory receptors from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
               15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Potential mitochondrial 60s ribosomal protein L49 (MRP-L49).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                           Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF05046; Img2; 1.
Hypothetical protein; Ribosomal protein; Mitochondrion.
SEQUENCE 223 AA; 25862 MW; 2A8DC95C813CBA3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OR46A OR OR46F.1 OR DOR46F.1 OR AN9 OR CG17849.
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Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O46A_DROME STANDARD; PRT; 385 AA. P81919; Q9U6X9; Q9V5H3; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
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Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WormPep; R11D1.9; CE06314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics 60:31-39(1999).
                                                                       R11D1.9.
Caenorhabditis elegans
(Rel. 38, (Rel. 38, 1
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                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Steward C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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-!- SIMILARITY: Contains 1 dilute domain.
-!- SIMILARITY: Contains 3 IQ domains.
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Pfam; PF00612; IQ; 6.
Pfam; PF00612; IQ; 6.
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PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD003376; DIL; 1.
SMART; SM00015; IQ; 3.
SMART; SM00242; MYSC: 1.
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Indels

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Length 223;

EXTRACELLULAR (POTENTIAL)

Multigene family DOMAIN

1 (POTENTIAL). CYTOPLASMIC (POTENTIAL).

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Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Broketein P., Botelar P., Burtis K.C., Busam D.A., Butler H., Cadieu B., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., A de Pablos B., Defcher A., Dong Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Digan-Rocha S., Dunkov B.C., Dunn P., Dorbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Rolestor K.A., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Andlain M.E., Harvey D., Heiman T.J., Mernandez J.R., Houck J., Andlain M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalai M., Murbhy B., Murphy L., McPherson D., Lin X., Marteel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Link Y., Marteel B.B., McIntosh T.C., McLed M., Poherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Relson K.A., Nixon K., Nusskern D.R., Nelson D.E., Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rese M.G., Siden-Kiamos I., Simpson M., Strong R., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Smith T., A Shirskas R., Tector C., Trurer R., Venter E., Wang S., Yao Q.A., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Weinston S., Bohng X.H., Zhong F.N., Zhong W., Zhang G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zh
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-1- TISSUE SPECTFICITY: EXPRESED IN A SUBSET OF 17 OLFACTORY RECEPTOR NEURONS IN THE MAXILLARY PALE.
-1- SIMILARITY: BELONGS TO FAMILY DR-OR OF G-PROTEIN COUPLED
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MEDLINE=99166868; PubMed=10069338; Clyne P.J., Warr C.G., Freeman M.R., Lessing D., Kim J., Carlson J.R.; "A novel family of divergent seven-transmembrane proteins: candidate odorant receptors in Drosophila."; Neuron 22:327-338 (1999). MEDLINE=222456069; PubMed=12537572;
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Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Annotation of the Drosophila melanogaster euchromatic genome: a Senome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)

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Transmembrane, G-protein coupled receptor, Olfaction, Glycoprotein,

EMBL; AE003830; AAF58834.2; -. FlyBase, FBgn0026388; Or46a. InterPro; IPR004117; 7tm 6. Pfam; PF02949; 7tm 6; 1.

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6 4 3 2 1 1 0 0 9 8 7 6 5 8 4 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9		T 1 TAEIN YCFD HAEIN P44683; 01-NOV-1995 01-NOV-1995 28-FEB-20095	H10396. Haemophilus influenzae. Bacteria, Proteobacteria, Gammaproteobacteria, P Pasteurellaceae, Haemophilus. NCBI TaxID=727;	[1] SEQUENCE FROISTRAIN=RG STRAIN=RG STRAIN=RG STRAIN=RG STRAIN=RG STRAIN=RG STRAIN=RG STRAIN=RG STRAIN=RG STRAIN=RG STRAIN=RG STRAIN=RG STRAIN=RG STRAIN=RG STRAIN STRAIN=RG STRAIN=RG STRAIN=RG STRAIN=RG STRAIN=RG STRAIN=RG STRAIN=RG STRAIN=RG STRAIN=RG STRAIN=RG STRAIN=RG STRAIN=RG STRAIN STRAIN STRAIN=RG STRAIN STR	Vencer J.C.; Whole-genome random sec Rd."; Science 269:496-512(1999 [2]	IDENTIFICATION BY MASS SPECTROMBETRY. MEDLINE-2013748; Pubmed=10675023; Langen H., Takacs B., Evers S., Berndt P., Gray C., Fountoulakis M.; "Two-dimensional map of the proteome of HE Electrophoresis 21:411-429(2000).	This SWISS-Proceeds of the European use by non-modified and entities requests requests to the control of the co	EMBL; U32723 FIR; A641236 FIGR; H10396 InterPro; IPI SWART; SMOOS! Complete pro!	uery Match est Local Similarity
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Gaps
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Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
"Nucleotide sequence of the infectious cloned DNA components of
African cassava mosaic. virus (Nigerian strain).";
Nucleic Acids Res. 18:197-198(1990).
-! SIMILARITY: BELONGS TO GEMINIVIRUSES AL2 PROTEIN FAMILY.
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Indels
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InterPro; IPR000942; Gemini_AL2.
Pfam; PF01440; Gemini_AL2; \(\bar{1}\).
PRINTS; PR00230; GEMCGTAL2.
PRODOM; P0001117; Gemini_AL2; 1.
SEQUENCE 135 AA; 15159 MW; 75D24A8CD6368848 CRC64;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Stanley J., Gay M.R.;
"Nucleotide sequence of cassava latent virus DNA.";
Nature 301:260-262(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cassava latent virus (strain Nigerian).
Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=10819;
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Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
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Last annotation update)
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ALZ protein (15.2 kDa protein).
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                                              366 LDWAFL 371
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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MEDLINE-92024070; PubMed-1926771;
Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
Navot N., Bichersky E., Zeidan M., Zamir D., Czosnek H.;
Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
Ninalogy 185:151-161(1991).
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-!- SIMILARITY: BELONGS TO GEMINIVIRUSES AL2 PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                             88.6%; Score 31; DB 1; Length 135; 100.0%; Pred. No. 36; 0; Indels ive 0; Mismatches 0; Indels
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InterPro; IPR000942; Gemini AL2.
InterPro; PP01440; Gemini AL2; I.
PRINTS; PR00230; Gemini AL2; I.
PRODOM; PD001117; Gemini AL2; I.
SEQUENCE 135 AA; 15178 MW; 2825C2F42E5E1F49 CRC64;
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PIR, C40779; QQCVC4.
InterPro; IPRO00942; Gemini AL2.
PFam; PF01440; Gemini AL2; 1.
PRINTS; RR00230; GEMCOATAL2.
PRODOM; PD001117; Gemini AL2; 1.
SEQUENCE 135 AA; 15611 MW; F111C8C2F7E9DD32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tomato yellow leaf curl virus (TYLCV).
Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
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(Rel. 29, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CO-92 / Biovar Orientalis;
MEDLINE-21470413; PubMed=11586360;
Parkhil J., Warn B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B. Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.P., Quall M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Yersinia pestis, the causative agent of plague.",
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PHOSPHORIBOSYL-ATP PYROPHOSPHOHYDROLASE.
BF3328DF1COA8C79 CRC64;
                                                                                                                                                                                                                                                                        Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 184:4601-4611(2002)
-!- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl) -ATP + H(2)O = 1-(5-phosphoribosyl)-AMP + diphosphate
-!- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-AMP + H(2)O = 1-(5-phosphoribosyl)-AMP + H(2)O = 1-(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphoribosyl)-5-[(5-phosphorib
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-i- PATHWAY: Histidine biosynthesis; third step.
-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-i- SUBILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE PRA-CH
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
18-FEB-2003 (Rel. 41, Last annotation update)
19-FEB-2003 (Rel. 41, Last annotation his [Includes: Phosphoribosyl-APP cyclohydrolase (EC 3.5.4.19) (PRA-CH);
Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) (PRA-PH);
HISI OR HISIE OR YPO1542 OR Y2628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD002610; PRA-CH; 1.
ProDom; PD002611; Pra_PH/CH; 1.
Histidine biosynthesis; Multifunctional enzyme; Hydrolase;
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STRAIN-KIM5 / Biovar Mediaevalis;
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InterPro; IPR002496; PRA-CH.
InterPro; IPR002497; PRA-PH.
Pfam; PP01502; PRA-CH; 1.
Pfam; PP01503; PRA-CH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     Yersinia pestis
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=632;
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Length 204;

DB 1;

88.6%; Score 31;

Query Match

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AND ONE SACCHARIDE -- SACCHARIDE -- SACCHARIDE -- SIMILARITY: BELONGS -- SIMILARITY: BELONGS -- SIMILARITY: BELONGS -- SIMILARITY: BELONGS -- SIMILARITY: BELONGS -- SIMILARITY: BELONGS -- SIMILARITY: BELONGS -- SIMILARITY: BELONGS -- SIMILARITY: BELONGS -- SIMILARITY: BELONGS -- SIMILARITY: SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SIMILARITY: SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- SPRONGS -- 
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- SUBUNIT: HOMOTECERAMENT.
- TISSUB SPECIFICITY: Seed.
- TISSUB SPECIFICITY: Seed.
- TISSUB SPECIFICITY: Seed.
- THE HEPTASACCHARIDE ((BETA-XYLOSYL-1,2) (ALPHA-MANNOSYL-1,6) (ALPHA-MANNOSYL-1,3)]BETA-MANOSYL-1,4-GLCNAC-BETA-1,4-GLCNAC-BETA-1,4
[ALPHA-FUCOSYL-1,3] JGLCNAC. A SMALL PROPORTINO OF ALPHA CHAINS ARE PROTECLYTICALLY CLEAVED AT 114-115 INTO GAMMA AND BETA CHAINS ARE PROTECLYTICALLY CLEAVED AT 114-115 INTO GAMMA AND BETA CHAINS.
- HIS IS PROBABLY DEPENDENT ON THE DEGLYCOSYLATION OF N-111.
- MISCELLANGOUS: BINDS ONE MANGANESE (OR OTHER TRANSITION METAL) ION SAND ONE CALCIUM ION: THE METAL IONS ARE ESSENTIAL FOR THE SACCHARIDE-BINDING AND CELL-AGGLUTINATING ACTIVITIES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Calvete J.J., Santos C.F., Mann K., Grangeiro T.B., Nimtz M., Urbanke C., Sousa-Cavada B.;
"Amino acid sequence, glycan structure, and proteolytic processing of the lectin of Varairea macrocarpa seeds.";
FEBS Lett. 425:286-292(1998).
-!- FUNCTION: LECTIN THAT BINDS GALACTOSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I; Fabales, Fabaceae, Papilionoideae, Dalbergieae, Vatairea.
                                           Gaps
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Seed lectin (VML).
    ; Pred. No. 54;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             240 AA
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Similarity 100.
5; Conservative
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P81371;
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CXAS CANFA P33725;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98066770; PubMed=9403066;
Seul K.H., Tadros P.N., Beyer E.C.;
Seul K.H., Tadros P.N., Beyer E.C.;
"Mouse connexin40: gene structure and promoter analysis.";
Genomics 46:120-126(1997).
-!- FUNCTION: One gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell.
-!- SUBUNIT: A connexon is composed of a hexamer of connexins.
-!- SUBCELPULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Highly expressed in lung.
-!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
                Gaps
                                                                                                                                                                                                                             Eukaryota; Mětazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                       STRAIN=Sprague-Dawley,
MEDLINE=92112940, PubMed=1370487;
Haefliger J.-A., Bruzzone R., Jenkins N.A., Gilbert D.J.,
Copeland N.G., Paul D.L.,
"Four novel members of the connexin family of gap junction proteins.
Molecular cloning, expression, and chromosome mapping.";
J. Biol. Chem. 267:2057-2064(1992).
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93021055; PubMed=1328644;
Beyer E.C., Reed K.E., Westphale E.M., Kanter H.L., Larson D.M.;
"Molecular cloning and expression of rat connexin40, a gap junction
protein expressed in vascular smooth muscle.";
J. Membr. Biol. 127:69-76(1992).
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               Indels
                                                                                                                                                   01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Gap junction alpha-5 protein (Connexin 40) (Cx40)
GJA5 OR CXN-40.
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                                                                                                                              355 AA.
               0; Mismatches
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     Pred. No.
                                                                                                                             PRT;
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InterPro; IPR000500; Connexin.
Pfam; PF00029; connexin; 1.
100.08;
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                5; Conservative
                                                                                                                              STANDARD;
                                                                                                                                                                                                                   Rattus norvegicus (Rat).
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  Best Local Similarity
Matches 5; Conserv
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                                                              224 LDWSF 228
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                        1 LDWSF 5
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                                                                                                                            CXA5 RAT P28234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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                                                                                                                                                                                                Score 31; DB 1; Length 355;
Pred. No. 94;
                                                                                                                                                                                                                                      0; Indels
                                  EXTRACELLULAR (POTENTIAL).
                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                           CYTOPLASMIC (POTENTIAL).
4F859438686000B9 CRC64;
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.
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CYTOPLASMIC (POTENTIAL).
                                                                      CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Gap Junction alpha-5 protein (Connexin 40) (Cx40).
                                                                                                                                                                                                           100.0%; Pred. No.
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                                                                                         POTENTIAL.
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InterPro; IPR000500; Connexin.
Pfam; PF00029; connexin; 1.
PRINTS; PR00206; CONNEXIN.
SMART; SM00037; CNX; 1.
PROSITE; PS00400; CONNEXINS 1; 1.
PROSITE; PS00400; CONNEXINS 2; 1.
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INIT_MET 0 0
DOMAIN 1 22
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40
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Best Local Similarity
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SUBFAMILY
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Q01231;
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CXAS_MOUSE
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MEDINES-2138257; Pubmed=12477932;
MEDINES-2138257; Pubmed=12477932;
MEDINES-2138257; Pubmed=12477932;
MALEGNUI S.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Antechnia K., Farmer A.A., Rubin G.M., Hong L., Brapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ugdin T.B., Toshiyvik S., Carninci P., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Rhebar S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Nilalon D.K., Murany D.M., Sodergren E.J., Lu X., Gibbs R.A., Wilalon D.K., Murany D.M., Sodergren E.J., Lu X., Gibbs R.A., Wilalon D.K., Murany D.M., Sodergren E.J., Lu X., Gibbs R.A., Wilalon D.K., Murany D.M., Sodergren E.J., Lu X., Gibbs R.A., Anting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Anting B. M., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A., Schnerch A., Scher J., Skalaka U., Smailus D.E., Generation and initial analysis of more than 15,000 full-length D.C., Decondon Media Coll. Decondon Media Coll. Decondon Media Coll. Decondon Media Coll. Decondon Media Coll. Decondon Media Coll. Decondon Media Coll. Decondon Media Coll. Decondon Media Coll. Decondon Media Coll. Decondon Media Coll. Decondon Media Coll. Decondon Media Coll. Decondon Media Coll. Decondon Media Coll. Decondon Media Coll. Decondon Media Coll. Decondon Media Coll. Decondon Media Coll. Decondon Media Coll. Decondon Media Coll. Decondon Media Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. Decondon Coll. 
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-1- FUNCTION: One gap junction consists of a cluster of closely packed
pairs of transmembrane channels, the connexons, through which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haefliger J.-A., Goy J.J., Waeber G., "Sporadic cases of dilated cardiomyopathies associated with atrioventricular conduction defects are not linked to mutation within the connexins 40 and 43 genes."; Eubmitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95055780; PubMed=7966354;
Kanter H.L., Saffitz J.E., Beyer E.C.;
"Molecular cloning of two human cardiac gap junction proteins,
connexin(a and connexin(45.";
                                                  Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beyer E.C., Christensen E.A.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lin H.H., Jin N., Kiang D.T.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
356 CYTOPLASMIC (POTENTIAL).
39801 MW; C8431D65CF9E78FE CRC64;
                                                                                                                                                                                                                                                                                   OCT-2001 (Rel. 40, Last sequence update)
SEP-2003 (Rel. 42, Last annotation update)
junction alpha-5 protein (Connexin 40) (Cx40).
                                                  DB 1;
94;
                                                                                   Mismatches
                                                  Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Mol. Cell. Cardiol. 26:861-868(1994)
                                                   88.00.
100.0%; Pre-
                                                                                                                                                                                                                                                                 (Rel. 29, Created)
(Rel. 40, Last sequ
(Rel. 42, Last anno
                                                  88.64;
                                                                                    Conservative
                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
228 3
356 AA;
                                                  Query Match
Best Local Similarity
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16-OCT-2001 (
15-SEP-2003 (
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ID _CXAS_HUMAN
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                   SEQUENCE
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                                                                                   Matches
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materials of low mw diffuse from one cell to a neighboring cell. SUBUNIT: A connexon is composed of a hexamer of connexins. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Hennemann J., Suchyna T., Lichtenberg-Frate H., Jungbluth S.,
Dahl E., Schwarz J., Nicholson B.J., Willecke K.;
"Molecular cloning and functional expression of mouse connexin40,
second gap junction gene preferentially expressed in lung.";
J. Cell Biol. 117:1299-1310(1992).
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94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 121013; -. Gonnexon channel activity; TAS. GO; GO:0015285; P:intercellular junction assembly; TAS. GO; GO:0007085; P:intercellular junction assembly; TAS. GO; GO:0006936; P:muscle contraction; TAS.
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CYTOPLASMIC (POTENTIAL)
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01-APR-1993 (Rel. 25, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
Gap junction alpha-5 protein (Connexin 40) (Cx40).
GJAS OR CXN-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 AA.
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0; Mismatches
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Pred. No.
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PROSITE; PS00407; CONNEXINS_1; 1.
PROSITE; PS00408; CONNEXINS_2; 1.
                                                                                                                                                                                                                                                                                                                                                                              EMBL, U03486, AAA60457.2; -.
EMBL, 134994; AAA91833.1; -.
EMBL, AF151979; AAD37801.1; -.
EMBL, BC013313; AAH13313.1; -.
Genew, HGNC:4279; GJA5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000500; Connexin.
Pfam; PF00029; connexin; 1.
PRINTS; PR00206; CONNEXIN.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 AA;
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FUNCTION: One gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell. SUBUNIT: A connexon is composed of a hexamer of connexins. SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap junction proteins.",
J. Biol. Chem. 265:14439-14443(1990).
-!- FUNCTION: One gap junction consists of a cluster of closely packed
pairs of transmembrane channels, the connexons, through which
materials of low mw diffuse from one cell to a neighboring cell.
-!- SUBUNIT: A connexon is composed of a hexamer of connexins.
                                                                       in lung.
SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning and developmental expression of two chick embryo
                                            -i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- TISSUB SPECIFICITY: Kidney, heart and skin, but most abundant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.6%; Score 31; DB 1; Length 357; 100.0%; Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 7823CDA57A9C7C90 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
08-FBB-2003 (Rel. 41, Last annotation update)
Gap junction alpha-5 protein (Connexin 42) (Cx42).
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Preu. ...
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MGD; MGI:95716; Gja5.
InterPro; IPR000500; Connexin.
Pfam; PP00029; connexin; 1.
PRINTS; PR00206; CONNEXIN.
SMART; SM00037; CNX; 1.
PROSITE; PS00400; CONNEXINS 1; 1.
PROSITE; PS00400; CONNEXINS 1; 1.
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MEDLINE=90354434; PubMed=2167316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 40282 MW;
                                                                                                                                                                                                             EMBL; X61675; CAA43850.1; -.
                                                                                                                                                                                                                                                                                                                   Gap junction; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                357 AA;
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2 DWSFL 6
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                                                                                             SUBFAMILY.
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-!- CATALYTIC ACTIVITY: N(6)-(L-1,3-dicarboxypropyl)-L-lysine + NAD(+)
+ H(2)O = L-lysine + 2-oxoglutarate + NADH.
SUBCELLULAR LOCATION: Integral membrane protein.
INSSUE SPECIFICITY: Mostly in heart, and in the whole embryo,
liver, stomach, and pectoral muscle.
SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
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eighth (last) step.
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28-FEB-2003 (Rel. 41, Last annotation update)
Saccharopine dehydrogenase [NAD+, L-lysine forming] (EC 1.5.1.7)
(Lysine--2-oxoglutarate reductase) (SDH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=5476;
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Garrad R.C., Schmidt T.M., Bhattacharjee J.K.;
"Molecular and functional analysis of the LYS1 gene of Candida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUĞUNIT: Monomer (By similarity).
-i- SIMILARITY: TO OTHER FUNGAL SACCHAROPINE DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 368; 97;
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100.0%; Pred. No.
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PROSITE; PS00408; CONNEXINS 2; 1.
                                                                                                                                                                                                                                                                                                                                                                    EMBL; M35043; AAA48716.1; -.
PIR; B37819; B37819.
InterPro; IPR000500; Connexin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
28-FEB-2003 (Rel. 41, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00029; connexin; 1.
PRINTS; PR00206; CONNEXIN.
SMART; SM00037; CNX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Candida albicans (Yeast).
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Best Local Similarity
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INIT_MET
                                                                                                         SUBFAMILY
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WEDLINE=21848401; PubMed=11859360;
WOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros U., Peat N., Hayles U., Basham D., Bowman S., Brown D., Brown S., Chillingworth T., Churcher C.M., Gonlins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gonle A., Hamlin N., Harris D., Hidalo J., Hodgson G., Holroyd S., Horneby T., Howarth S., Huckle E.J., Hunt S., Jagels K., Anchory R., Jones L., Jones M., Leather S., McDonald S., McLean J., Monory P., Moule S., Murphy L., Niblett D., Odell C., Andonory P., Noule S., Margall K., Murphy L., Niblett D., Odell C., Ratherford K., Rutter S., Saunders D., Seeger K., Sharp S., Stevens K., Starp S., Stevens K., Starp S., Stevens K., Starp S., Stevens K., Starp S., Stevens K., Taylor R.G., Art R., Robben J., Grymonprez B., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vantereels E., Rieger M., Schaefer M., Mueller-Auer S., Bablien C., Phubs M., Fritz C., Holzer E., Moestl D., Hilbert H., Agel C., Phubs M., Fritz C., Holzer E., Moestl D., Hilbert H., Agel D., Lehrach H., Reinhardt R., Purnelle B., Lehrach H., Reinhardt R., Purnelle S., Lehrach M., Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Lucke M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Bada R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Aboninguez A., Revuelta J.L., Mooren S., Armetrong J., Porsburg S.L., Raderrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., SUBUNIT, SUBCELLULAR LOCATION, AND FUNCTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99365157; PubMed=10436019;
Gaits F., Russell P.;
"Vacuole fusion regulated by protein phosphatase 2C in fission
                                                                                                                                                                                                                                  Length 382;
                                                                                                                                                                                                                                 88.6%; Score 31; DB 1; Length 382
100.0%; Pred. No. 1e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  P2C4 SCHPO STANDARD; PRT; 383 AA. 014156; Q9UR02; 15-JUL-1998 (Rel. 36, Created) 116-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Protein phospherase 2C homolog 4 (EC 3.1.3.16) (PP2C-4).
                                                                                                        EMBL, U13233; AAA21362.1; -.
InterPro; IPRO0402; Alabh PNT.
Pfam; PF01262; Alabh PNT C; 1.
Pfam; PF05222; Alabh PNT N; 1.
Lysine blosynthesis; Oxidoreductase; NAD.
ACT SITE
217
SEQUENCE 382 AA; 42394 MW; A3620191DF04B88F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Biol. Cell 10:2647-2654 (1999).
                                                                                                                                                                                                                                                 Local Similarity 100.
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NCBI_TaxID=4896;
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01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FE2-2003 (Rel. 4), Last annotation update)
Gap junction alpha-8 protein (Connexin 45.6) (Cx45.6).
Gallus gallus (Chicken)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R PIR, T38772; T38772.

R GeneDB_SPombe; SPAC4A8.03c; -.

R GeneDB_SPombe; SPAC4A8.03c; -.

R InterPro; IPR001932; PP2C.

DR SMART; SM00313; PP2C; 1.

DR SMART; SM00312; PP2C; 1.

DR SMART; SM00312; PP2C; 1.

DR SMART; Manganee; Membrane; Multigene family.

KW Hydrolase; Magnesium; Manganese; Membrane; Multigene family.

FT METAL 308 MANGANESE 1 AND 2 (BY SIMILARITY).

FT METAL 308 MANGANESE 2 (BY SIMILARITY).

FT METAL 318 MANGANESE 2 (BY SIMILARITY).

A17 347 MANGANESE 2 (BY SIMILARITY).
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-!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. VACUOLAR.
-!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
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MELINE=94325667; PubMed=8049527;
Jiang J.X., White T.W., Goodenough D.A., Paul D.L.;
"Molecular cloning and functional characterization of chick lens
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
Nature 415:81-880(2002).
-!- FUNCTION: HAS A ROLE IN THE REGULATION OF VACUOLE FUSION.
-!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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TISSUBS_Lens fibers;
MEDLINE=96437509; PubMed=8840185;
Sawada K., Agata K., Eguchi G.;
"Characterization of terminally differentiated cell state by categorizing cDNA clones derived from chicken lens fibers.";
Int. J. Dev. Biol. 40:531-535(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.6%; Score 31; DB 1; Length 383; 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399 AA.
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Mol. Biol. Cell 5:363-373(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF140285; AAD27651.1; -.
EMBL; Z98762; CAB58554.1; -.
PIR; T38772; T38772.
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Search completed: February 18, 2004, 14:28:12
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                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
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-!- FUNCTION: One gap junction consists of a cluster of closely packed pairs of transmembrane channels, the connexons, through which materials of low mw diffuse from one cell to a neighboring cell.
-!- SUBGNIT: A connexon is composed of a hexamer of connexins.
-!- SUBGELIDIAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion.
Eukaryota, Viridiplantae, Chlorophyta, Trebouxiophyceae, Chlorellales,
Chlorellaceae, Prototheca.
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MEDILNE=94180393; PubMed=8133522;
WOlff G., Plante I., Lang B.F., Kueck U., Burger G.;
"Complete sequence of the mitochondrial DNA of the chlorophyte alga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.6%; Score 31; DB 1; Length 399; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
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30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last ennotation update)
NADH-ubiquinone oxidoreductase 49 kDa subunit (EC 1.6.5.3)
(EC 1.6.99.3) (NADH dehydrogenase subunit 7).
                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
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WP -> D (IN REF. 2).
IRR -> SEL (IN REF. 2).
4197392ADB6CB5CA CRC64;
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PROSITE; PS00408; CONNEXINS 2; 1.
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InterPro; IPR002266; Connexin50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45485 MW;
                                                                                                                                                                                                                                                                                  Pfam; PF03509; Connexin50; 1.
Pfam; PF00029; connexin; 1.
                                                                                                                                                                                                                  EMBL; L24799; AAA57134.1; -. EMBL; D26333; BAA05381.1; -. PIR; I50219; I50219.
                                                                                                                                                                                                                                                                                                                                                                 Gap junction; Transmembrane.
                                                                                                                                                                                                                                                                                                             PR00206; CONNEXIN. M00037; CNX; 1.
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Matches 5; Conservative
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233
399 AA;
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DWSFL 6
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                                                                                SUBFAMILY
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TRANSMEM
DOMAIN
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NUCM PROWI
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                                  J. Mol. Biol. 237:75-86(1994).
-!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
TO BE UBIQUINONE. COMPONENT OF THE IRON-SULFUR (IP) FRAGMENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
-!- SUBCELLULAR LOCATION: Mitochonfrial.
-!- SIMILARITY: BELONGS TO THE COMPLEX I 49 kDa SUBUNIT FAMILY.
Prototheca wickerhamii. Gene content and genome organization.";
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100.0%; Pred. No. 1.1e+02;
ive 0; Mismatches 0; Indels
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PR0S1TE; PS00535; COMPLEX1_49K; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
OXIGORNCE 400 AA; 45810 MW; 7227458PE80BC9D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@igb-sib.ch).
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Best Local Similarity 100...
5; Conservative
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; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants US-09-847-940B-14
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APPLICANT: May, Michael J.
APPLICANT: Ghosh, Sankar
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-117CP
CURRENT APPLICATION NUMBER: US/09/847,940B
CURRENT APPLICATION NUMBER: US/09/847,940B
PRIOR PILING DATE: 2001-05-02
PRIOR PILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE PATENTIN Ver. 2.0
SEQ ID NO 14
LENGTH: 6
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                                    US-10-438-537-4

US-10-295-207-1228

US-10-032-189-106

US-10-032-189-104

US-09-86-776-48

US-09-86-776-48

US-10-032-189-103

US-10-032-189-103

US-10-032-189-103

US-10-195-144-7

US-10-195-444-7

US-10-195-444-7

US-10-847-946A-33

US-09-847-946A-33

US-09-847-946A-33

US-09-847-946A-33

US-09-847-946A-33

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US-09-847-946A-33

US-09-847-946A-33
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US-09-847-946A-28
US-09-847-946A-132
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US-09-847-946A-35
US-09-847-946A-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 14, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
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GENERAL INFORMATION: APPLICANT: MAPLICANT: MAY, Michael J
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ORGANISM: Artificial Sequence
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US-09-847-946A-14
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 Query Match
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Sequence 10, Appl
Sequence 50, Appl
Sequence 91, Appl
Sequence 15, Appl
Sequence 1782, Appl
Sequence 1782, Appl
Sequence 1782, Appl
Sequence 1782, Appl
Sequence 1782, Appl
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Sequence 4783, Ap
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Sequence 86, Appl
Sequence 96, Appl
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Sequence 14, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                         February 18, 2004, 14:36:10; Search time 16.6974 Seconds (without alignments) 75.239 Million cell updates/sec
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| cgn2_6/ptodata/l/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/l/pubpaa/PCT NEW PUB.pep:*
3: /cgn2_6/ptodata/l/pubpaa/US06_DNEW PUB.pep:*
4: /cgn2_6/ptodata/l/pubpaa/US06_DNEW PUB.pep:*
5: /cgn2_6/ptodata/l/pubpaa/US07_NEW PUB.pep:*
6: /cgn2_6/ptodata/l/pubpaa/US07_NEW PUB.pep:*
7: /cgn2_6/ptodata/l/pubpaa/US07_NEW PUB.pep:*
8: /cgn2_6/ptodata/l/pubpaa/US08_NEW PUB.pep:*
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11: /cgn2_6/ptodata/l/pubpaa/US08_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/l/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/l/pubpaa/US10_NEW_PUB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 US-09-847-946A-14
2 US-00-863-776-50
2 US-09-981-151A-91
2 US-10-947-470A-26
0 US-09-847-946B-15
0 US-09-847-946A-15
0 US-09-746-817-1782
2 US-10-242-515-1782
2 US-10-42-515-1782
0 US-09-786-15
0 US-09-786-15
0 US-09-786-15
0 US-09-786-15
0 US-09-786-16
0 US-09-78-78-86
0 US-09-78-78-86
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                                                                                                                                                                                                                                             801455 segs, 209382283 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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DB
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Match Length
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Sequence Sequence Sequence Sequence

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Scoring table:

Searched:

Database

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Gaps

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Gaps
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US-10-032-189-107
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PRIOR APPLICATION NUMBER: 60/274,192
PRIOR FILING DATE: 2001-03-08
PRIOR PLILING DATE: 2001-03-08
PRIOR PLILING DATE: 2001-03-22
PRIOR PLILING DATE: 2001-03-22
PRIOR PILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/29,981
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/203,247
PRIOR PILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 260
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 107
LENGTH: 218
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Best Local Similarity 83.3
Matches 5; Conservative
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APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT APPLICATION NUMBER: 00/201,261
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR PILLING DATE: 2000-05-02
PRIOR PILLING DATE: 2000-08-22
PRIOR PILLING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOOFWWARE: PATENTIN Ver. 2.0
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APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Proceins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
CURRENT APPLICATION NUMBER: US/10/032,189
                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 35; DB 11; Length 6; 100.0%; Pred. No. 7e+05; ive 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: 60/257,495
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/258,171
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/269,940
PRIOR FILING DATE: 2001-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/10032189
o. US20030170630A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patturajan, Mema
Grosse, William M
Lepley, Denise M
Burgess, Catherine E
Shimkets, Richard A
Grosse, William M
Szekeres, Edward S
Vernet, Corine A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Casman, Stacie J
Boldog, Ferenc L
Gorman, Linda
Gangolli, Esha A
Fernandes, Blma R
Rieger, Daniel K
Edinger, Shlomit R
Gunther, Erik
Millet, Isabelle
Sciore, Paul
                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 6; Conservative
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PRIOR APPLICATION NUMBER: 60/242,152
PRIOR APPLICATION NUMBER: 60/242,152
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,611
PRIOR APPLICATION NUMBER: 60/242,612
PRIOR APPLICATION NUMBER: 60/242,612
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-10-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Connexin OTHER INFORMATION: Consensus Sequence US-09-981-151A-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.3%; Score 33; DB 12; Length 218; 83.3%; Pred. No. 3.8e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 12; Length 827;
Pred. No. 1.2e+03;
1; Mismatches 0; Indels
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US-10-347-470A-26

US-10-347-470A-26

Sequence 26, Application US/10347470A

Publication No. US20040002054A1

GENERAL INFORMATION:

APPLICANT: Hwang, Ho Yon

TITLE OF INVENTION: SQV NUCLEIC ACIDS AND POLYPEPTIDES

FILE REFREENCE: 01997/542003

CURRENT FILING DATE: 2003-01-17

PRIOR APPLICATION NUMBER: US 60/349,630

PRIOR APPLICATION NUMBER: US 60/349,630

PRIOR PILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-06-24

NUMBER OF SEQ ID NOS: 81

SGFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 26

LENGTH: 827
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; Patent No. US20020156000A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Drosophila melanogaster
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Best Local Similarity 83.3.
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Best Local Similarity 83.3
Matches 5; Conservative
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LENGTH: 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.3%; Score 33; DB 12; Length 218; 83.3%; Pred. No. 3.8e+02; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gorman, Linda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/981,151A
CURRENT FILING DATE: 2001-10-16
PRIOR PEDILOCATION NUMBER: 60/241,040
PRIOR FILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR PLING DATE: 2000-10-17
            PRIOR APPLICATION NUMBER: 60/210,060
PRIOR FILING DATE: 2000-06-07
PRIOR PELING DATE: 2000-06-07
PRIOR PELING DATE: 2000-07-20
PRIOR PILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: 60/221,337
PRIOR APPLICATION NUMBER: 60/221,337
PRIOR PILING DATE: 2000-07-31
PRIOR PILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 60/263,686
PRIOR PILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ 1D NOS: 155
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Patturajan, Meera
Taupier Jr, Raymond J
Burgess, Catherine E
Zerhusen, Bryan D
Kekuda, Ramesh
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Shimkets, Richard A
Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Edinger, Shlomit R
APPLICANT: Gerlach, Valerie
APPLICANT: MacDougall, John R
APPLICANT: Malyankar, Muriel M
APPLICANT: Smithson, Glemda
APPLICANT: Millet, Isabelle
APPLICANT: Stone, John A
APPLICANT: Stone, David J
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Gangolli, Esha A
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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FILING DATE: 2000-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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1 MDWSFL 6
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LENGTH: 218
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NUMBER OF SEQ ID NOS: 4031
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Best Local Similarity
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APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
TITLE OF ILLING DATE: 2001-05-02
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR PILING DATE: 2000-08-22
PRIOR PILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants US-09-847-940B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-15
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  TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 91.4%; Score 32; DB 10; Length 6; Best Local Similarity 83.3%; Pred. No. 7e+05; Matches 5; Conservative 1; Mismatches 0; Indels
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                       FILE REFERENCE: PPI-117CP
CURRENT APPLICATION NUMBER: US/09/847,940B
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
SUMMBER OF SEG ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
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83.3%;
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 5; Conserv
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1 LDWSYL 6
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1 LDWSYL 6
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WHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (56)
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005C1.
FILE REFERENCE: PC005C1.
CURRENT APPLICATION NUMBER: US/10/242,515
CURRENT FILING DATE: 2002-09-13
FRIOR PAPLICATION NUMBER: 06/179,065
FRIOR APPLICATION NUMBER: 06/180,628
FRIOR APPLICATION NUMBER: 06/180,628
FRIOR APPLICATION NUMBER: 06/214,886
FRIOR PILING DATE: 2000-02-04
FRIOR FILING DATE: 2000-06-07-11
FRIOR APPLICATION NUMBER: 06/217,487
FRIOR APPLICATION NUMBER: 06/225,758
FRIOR APPLICATION NUMBER: 06/225,758
FRIOR APPLICATION NUMBER: 06/225,758
FRIOR APPLICATION NUMBER: 06/225,447
FRIOR PILING DATE: 2000-08-14
FRIOR FILING DATE: 2000-07-11
FRIOR PILING DATE: 2000-07-14
FRIOR APPLICATION NUMBER: 60/217,496
FRIOR APPLICATION NUMBER: 60/225,447
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FRIOR APPLICATION NUMBER: 60/225,447
FRIOR FILING DATE: 2000-07-14
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FRIOR FILING DATE: DOO-07-14
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Pred. No. 1.8e+02;
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Pred. No. 1.8e+02;
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Publication No. US20040009488A1
GENERAL INFORMATION:
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83.3%;
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83.3%;
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1782
LENGTH: 56
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SEQ ID NO 1782
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                                                                                                                                                       ORGANISM: Homo sapiens
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Best Local Similarity
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27 LDWNFL 32
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Publication No. US20030003471A1
GENERAL INFORMATION
APPLICANT: Famodu, Omolayo O.
APPLICANT: Forge, Charlie
APPLICANT: Misso, Guo-Mua
TITLE OF INVENTION: CDNAS Encoding Polypeptides
FILE REFERENCE: BB-1365 US NA
 Mismatches
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CURRENT APPLICATION NUMBER: US/10/078,770
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/614,188
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,400
PRIOR PLICOR DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 60/153,534
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-10-22
PRIOR PLING DATE: 1999-10-15
PRIOR PLING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-15
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PILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
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US-09-738-626-4783
                                                                                                                                                                    Sequence 4783, Application US/09738626
Publication No. US20020197605A1
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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LENGTH: 157
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                       Sequence 2340. Application US/10104047

Publication No. US20030226392A1

GENERAL INFORMATION:

APPLICANT: HELLIX RESEARCH INSTITUTE

TITLE OF INVENTION:

FILE REFERENCE: H1-A0105

CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT APPLICATION NUMBER: US/02-03-25

PRIOR FILING DATE:

PRIOR FILING DATE:

NUMBER OF SEQ ID NOS: 4096

SOFTWARE: PACENTIN Ver. 2.1

SEQ ID NO 2340

LENGTH: 743
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Pred. No. 1.5e+03;
1; Mismatches 0; Indels
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100.0%; Pred. No. 5e+02;
1; Mismatches
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Patent No. US2002004941A1
GENERAL INFORMATION:
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Best Local Similarity 83.3
Matches 5; Conservative
5; Conservative
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; ORGANISM: Homo sapiens
US-10-104-047-2340
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Best Local Similarity
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98 VDWSFL 103
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27 LDWNFL 32
                                   1 LDWSFL 6
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OTHER INFORMATI
                                                                                                                                           -10-104-047-2340
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Matches
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; ORGANISM: Zea mays
US-10-078-770-96
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US-10-078-770-96
Sequence 96, Application US/10078770
Publication No. US20030003471A1
GENERAL INFORMATION:
APPLICANT: Forge, Charlie
APPLICANT: Forge, Charlie
APPLICANT: Forge, Charlie
APPLICANT: Mao, Guo-Hua
TITLE OF INVENTION: CDNAS Encoding Polypeptides
FILE REFERENCE: BB-1365 US NA
CURRENT APPLICATION NUMBER: 09/614,188
PRIOR PILING DATE: 2000-07-12
PRIOR PLING DATE: 1000-07-12
PRIOR PLING DATE: 1999-07-12
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-00-15
PRIOR FILING DATE: 1999-00-15
PRIOR PLING DATE: 1999-00-15
PRIOR PLING DATE: 1999-00-15
PRIOR PLING DATE: 1999-07-12
PRIOR PLING DATE: 1999-07-12
PRIOR PLING DATE: 1999-07-12
PRIOR PLING DATE: 1999-07-12
PRIOR PLING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-12
PRIOR PLING DATE: 1999-07-12
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Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 5; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/143,419
PRIOR FILING DATE: 1999-07-12
PRIOR PELING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Mccrosoft Office 97
LENGTH: 184
                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Zea mays
FBATURE:
NAME/KEY: UNSURE
LOCATION: (98)
NAME/KEY: UNSURE
LOCATION: (104)...(105)
NAME/KEY: UNSURE
LOCATION: (117)
NAME/KEY: UNSURE
LOCATION: (117)
NAME/KEY: UNSURE
LOCATION: (117)
NAME/KEY: UNSURE
LOCATION: (117)
NAME/KEY: UNSURE
LOCATION: (117)
NAME/KEY: UNSURE
LOCATION: (117)
NAME/KEY: UNSURE
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NAME/KEY: 1
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Ouery Match

Query Match

Best Local Similarity 100.0%; Pred. No. 8.66+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSF 5

Cy 26 LDWSF 30

Search completed: February 18, 2004, 15:42:00

Job time: 17.7529 secs
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                                                                                          February 18, 2004, 14:16:39; Search time 7.06579 Seconds (without alignments) 35.929 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, A Sequence 4, A Sequence 2, A Sequence 2, A Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, A
Sequence 4, A
Sequence 10,
Sequence 3, A
Sequence 4, A
Sequence 2, A
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Sequence 3, p
Sequence 4, p
Sequence 3, p
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Sequence
Sequence
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2: /cgn2 6/ptodata/1/laa/5B COMB.pep:*
3: /cgn2 6/ptodata/1/laa/6A COMB.pep:*
5: /cgn2 6/ptodata/1/laa/6B COMB.pep:*
5: /cgn2 6/ptodata/1/laa/PCTUS COMB.pep:*
6: /cgn2 6/ptodata/1/laa/PCTUS COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-107-532A-7054
US-08-118-273A-7054
US-08-118-27-68
US-08-30-68
US-09-328-352-63
US-09-328-352-7417
US-09-328-352-7815
US-09-328-352-7815
US-09-023-318-3
US-09-023-318-3
US-09-023-318-3
US-09-032-475-4
US-09-032-475-4
US-09-032-475-4
US-09-032-476-4
US-09-032-476-4
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US-09-032-332-4
US-09-032-332-4
US-09-08-758-3
US-09-08-758-3
US-09-08-758-3
US-09-08-758-3
US-09-08-758-3
US-09-08-33-32-4
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                                                                                                                                                                                                                                                                                328717 segs, 42310858 residues
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Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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35
1 LDWSFL 6
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Match Length DB
                                                                                                                                                             Title:
Perfect score:
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                                                                                                                                                                                              Sequence:
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Sequence 27150, Application US/09252991A

Sequence 27150, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT PELLOGATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
US-09-107-532A-7054
US-09-107-532A-7054
Sequence 7054, Application US/09107532A
Secont No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION:
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Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 9, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 12, Appli
Sequence 123, Appli
Sequence 123, Appli
Sequence 121, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 27, Appli
Sequence 27, Appli
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.4%; Score 32; DB 4; I
83.3%; Pred. No. 6.3e+02;
iive 1; Mismatches 0;
US-09-032-475-4
US-09-099-125A-2
US-09-099-125A-2
US-09-032-476-2
US-09-032-476-2
US-09-03-324-2
US-09-166-629-15
US-09-109-986-2
US-09-109-986-2
US-09-868-758-4
US-09-868-758-4
US-09-417-197-121
US-09-22-617A-12
US-08-22-617A-27
US-08-22-617A-27
US-08-22-617A-27
US-08-22-617A-27
US-08-22-617A-27
US-08-22-617A-27
US-08-22-617A-27
US-08-22-617A-27
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COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 100 Beaver Street CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27150
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Best Local Similarity 83.3
Matches 5; Conservative
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LDWSYL 491
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Sequence 68, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                            Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.6%; Score 31; DB 5; Length 277; 100.0%; Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08528

FILING DATE: 09-SEP-1993

PRIOR APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Townsend, Kevin G.

REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: MURPHY=2 PCT

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                          88.6%; Score 31; DB 1; L
100.0%; Pred. No. 3.1e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. No. 3.1 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                               TELEX: 248633
INFORMATION FOR SEQ 1D NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 24863
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acids
                        : 202-628-5197
202-737-3528
                                                                                                                                                                                                                                                                                                       Query Match . 88.6
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 5; Conservative
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TELEFAX: 202-737-3528
                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                     ; MOLECULE TYPE: peptide US-08-118-270-68
                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US93-08528-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US93-08528-68
                                                                                                                                                                                                                  TOPOLOGY:
                                                TELEFAX:
TELEX: 24
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| Sequence 64, Application US/08118270
| Patent No. 5508384
| GENERAL INFORMATION:
| APPLICANT: Murphy, Randall B. |
| APPLICANT: Schueter, David I. |
| TITLE OF INVENTION: POLYPEPIDES OF G-COUPLED PROTEIN TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF NUMBER OF SEQUENCES: 348
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: BROWDY AND NEIMARK STREET: 419 Seventh Street, N.W., Suite 300
| CITY: Mashington STATE: D.C. |
| STATE: D.C. |
| COUNTRY: USA |
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                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGRYI INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 47,489
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...86
SEQUENCE DESCRIPTION: SEQ ID NO: 7054:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 7054:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Gaps ; 0

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03P4
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7147
LENGTH: 365
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4918, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                               Gaps
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                                                             Length 177;
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Pred. No. 6e+02;
                                                             Score 30; DB 4; Length 177
Pred. No. 2.9e+02;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A PELLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 APPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: PC
COMPUTER: PC
COMPAND
CORRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                             US-09-328-352-7147
; Sequence 7147, Application US/09328352
; Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
, ORGANISM: Acinetobacter baumannii
US-09-328-352-5063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Acinetobacter baumannii
US-09-328-352-7147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.78;
                                                                85.7%;
66.7%;
                                               Query Match
Best Local Similarity 66.7
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Matches 4, Conservative
                                                                                                                                                                                           137 IDWTFL 142
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                                                                                                                                                            1 LDWSFL 6
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APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.6%; Score 31; DB 2; Length 382; 100.0%; Pred. No. 4.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                           APPLICANT: Johnson's K. Bhattacharjee
APPLICANT: Richard C. Garrad
APPLICANT: Raber C. Garrad
APPLICANT: Robert P. Peery
TITLE OF INVENTION: Methods and Reagents for
TITLE OF INVENTION: Detecting Fungal Pathogens in a
TITLE OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
                                                                                                                                                                                                                                                                                                                                     3: McDonnell Boehnen Hulbert & Berghoff
300 S. Wacker Drive Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM WORD 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0,904
CLASSIFICATION: 435
ATTONEN'AGENT INFORMATION:
NAME: BGTGATTON: WUMBER: 30,243
REFERENCE/DOCKET NUMBER: 30,243
REFERENCE/DOCKET NUMBER: 94,319
TELECHONE: (312)913-0001
TELEPHONE: (312)913-0001
TELEPHONE: (312)913-0001
TELEPHONE: CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.09-128-152-5063
Sequence 5063, Application US/09128352
Patent No. 6562958
                                                           Sequence 30, Application US/08360606B
Patent No. 5919617
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 382 amino acid residues
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 88.6
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
STATE: Illinoia
COUNTRY: U.S.A.
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 LDWSF 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 5063
LENGTH: 177
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Sequence 3, Application US/09023321
Patent No. 5644073
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB 2; 1
Pred. No. 1.2e+03;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 797-008
                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
                                                                                 CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFREENCE/DOCKET NUMBER: T97-CTELECOMMUNICATION INFORMATION:
TELEPRAX: (415) 343-4341
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-321-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.3
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide US-08-887-518-3
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738 LDWSWL 743
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US-09-023-321-3
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Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILLING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7815
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Patent No. 5843721
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCE: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAM FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.7%; Score 30; DB 4; Length 413; 66.7%; Pred. No. 6.8e+02; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
85.7%; Score 30; DB 4; Length 397
Best Local Similarity 66.7%; Pred. No. 6.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                        ), NAME/KEY: misc_feature

; LOCATION: (B) LÖCATION 1...397

; SEQUENCE DESCRIPTION: SEQ ID NO: 4918:

US-09-107-532A-4918
                                                                                                                                                                                                                              ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
TELEPHONE: (781)893-5007
                   TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4918:
SEQUENCE CHARACTERISTICS:
LENGTH: 397 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Acinetobacter baumannii
US-09-328-352-7815
                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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233 IDWTFL 238
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183 IDWTFL 188
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Best Local Similarity
Matches 4; Conserv
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ZIP: 94104
                                                                                                                                                                                                                                                     FEATURE
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Sequence 4, Application US/09099125A
Sequence 4, Application US/09099125A
Patent No. 5916760
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30; DB 2; Length 745;
Pred. No. 1.2e+03;
1; Mismatches 0; Indels
                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPY disk

COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT PAPLICATION DATA:

APPLICATION NUMBER: US/09/032,475

FILING DATE:

CLASSIFICATION DATA:

APPLICATION NUMBER: 08/087,518

FILING DATE:

ATORNEY AGENT INFORMATION:

NAME: OSWAN, RICHARD A

REFERENCE/DOCKET NUMBER: 35,627

REFERENCE/DOCKET NUMBER: 35,627

REFERENCE/DOCKET NUMBER: 343.4341

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF SEQ ID NO: 3:

SEQUIENCE CHARACTER STICS:

LENGTH: A43.4341

TELEGRA: (415) 343.4341

TELE
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/099,125A
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REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 197-006-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRICR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide US-09-032-475-3
    CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 738 LDWSWL 743
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                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
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                                                                                                                           Gaps
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| Patent No. 5651812
| GENERAL INFORMATION:
| APPLICANT: Goeddel, David V. APPLICANT: Woronicz, John | TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods | TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods | TOTE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods | TOTE OF INVENTION: IKK- PROTEINCE & TECHNOLOGY LAW GROUP | STREET: 268 BUSH STREET; SUITE 3200 | CITY: SAN FRANCISCO | STATE: CALIFORNIA | COUNTRY: USA | CALIFORNIA | COUNTRY: USA | CALIFORNIA | COUNTRY: USA | CALIFORNIA | COUNTRY: USA | CALIFORNIA | COUNTRY: USA | CALIFORNIA | COUNTRY: USA | CALIFORNIA | COUNTRY: USA | CALIFORNIA | COUNTRY: USA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALIFORNIA | CALI
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Batent No. 5854003

GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
                                          Length 745;
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Score 30; DB 2; Lengtn (22), Pred. No. 1.2e+03;
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COMPUTER READABLE FORM:
MEDIUDIER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy Size
COMPUTER: Floppy Size
COMPUTER: Floppy Size
COMPUTER: Floppy Size
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
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83.3%; Pred. No. 1.2e+03;
Micmatches 0;
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSNAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/POCKET NUMBER: 197-(TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                                  Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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INFORMATION FOR SEQ ID NO: 4:
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Best Local Similarity 83.3
Matches 5; Conservative
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US-09-099-124A-4
; Sequence 4, Application US/09099124A
; Patent No. 5939302
; GENERAL INFORMATION:
; APPLICANT: Gooddel, David V.
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; VORRESPONDENCE ADDRESS:
; ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; STATE: CALIFORNIA
; COUNTRY: USA
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Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                             Length 745;
                                                                                                                                                                                                                             Score 30; DB 2; Length 745
Pred. No. 1.2e+03;
1; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,124A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILLING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSNAN, RICHARD A
REGISTRATION NUMBER: 197-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEPHONE: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-099-125A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
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738 LDWSWL 743
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Search completed: February 18, 2004, 14:41:50 Job time : 7.06579 secs

2, Appli 3, Appli 5707

Sequence 1427, P Sequence 9, Appl Sequence 3, Appl Sequence 877, P Sequence 8, Appl

5707, Ap 8, Appli 7, Appli

Sequence 50, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1276, Ap Sequence 1276, Ap Sequence 1276, Ap Sequence 1276, Ap

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Sequence 13, Application US/09635872A

Sequence 13, Application US/09635872A

Patent No. 6534300

BERERAL INFORMATION:
APPLICANT: CANFIELD, WILLIAM

TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES

TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES

TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES

CURRENT RAPELICATION UNMBER: US/09/635,872A

PRIOR APPLICATION NUMBER: 60/153,831

PRIOR APPLICATION NUMBER: 60/153,831

PRIOR FILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 52

SOFTWARE: PATENTIN VERSION 3.0
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Patent No. 6537785

GENERAL INFORMATION:
TITLE OF INVENTION: METHODS OF TREATING LYSOSOMAL STORAGE DISEASE
FILE REFERENCE: 195612030

CURRENT APPLICATION NUMBER: US/09/636,077A

CURRENT PILING DATE: 1990-09-10

PRIOR APPLICATION NUMBER: 60/153,831

PRIOR APPLICATION NUMBER: 60/153,831

SOFTWARE: PatentIn version 3.0

SOFTWARE: PatentIn version 3.0

LENGTH: 502

TYPE: PRI
TYPE: PRI
CORGANISM: Discophila melanogaster
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Pred. No. 4.8e+02;
1; Mismatches 0; Indels
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                           US-09-413-814-50
US-09-13-814-50
US-09-036-987A-2
US-09-303-207-2
US-09-603-207-2
US-09-082-708-1276
US-09-082-779B-1276
US-09-082-779B-1276
US-09-082-779B-1427
US-09-082-779B-1427
US-09-040-285A-3
US-09-040-285A-3
US-09-1040-285A-3
US-09-040-285A-3
US-09-040-285A-3
US-09-040-285A-3
US-09-040-285A-3
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LENGTH: 502
TYPE: PRT
ORGANISM: Drosophila melanogaster
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Best Local Similarity 83.3%;
Matches 5; Conservative
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35.929 Million cell updates/sec
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/cgn2 6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2 6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-31-71A-240
US-08-311-71A-240
US-09-277-262-2
US-09-252-91A-32240
US-08-804-198-6
US-07-929-580B-5
US-07-708-88B-3
US-07-708-88B-3
US-07-708-88B-3
US-07-708-88B-3
US-07-708-88B-3
US-09-252-991A-30879
US-09-252-991A-29305
US-09-078-166-34
US-09-198-452A-702
US-09-252-991A-29305
US-09-252-991A-29305
US-09-252-991A-29305
US-09-252-991A-29305
US-09-252-991A-17687
US-09-252-991A-17687
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US-09-252-991A-31124
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Database :

Result . 9 Searched:

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Run on:

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Gaps

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
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Best Local Similarity 83.5
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Best Local Similarity 83.3
Matches 5, Conservative
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231 LDWSSL 236
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US-09-252-991A-32240
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                                                                                                                                                           Sequence 240, Application US/08311731A

Sequence 240, Application US/08311731A

Patent No. 6583266

GENERAL INPORMATION:
APPLICANT: SMITH, DOUGLAS

APPLICANT: MAO, JEN-II

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STRATE: MASSACHUSETTS

COUNTRY: USA
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APPLICANT: Gogos, Joseph A
TITLE OF INVENTION: OF SCHIZOPHRENIA, OR A DISEASE OR DISORDER RELATED
TITLE OF INVENTION: THERETO
FILE REFERENCE: 600-1-223 CIP
                  Gaps
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
 Pred. No. 4.8e+02;
1; Mismatches 0;
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83.3%; Pred. No. 1.6e+02;
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NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REPERBROKE DOCKETS NUMBER: 31,616
TELEPANNICATION INFORMATION:
TELEPANNICATION INFORMATION:
TELEPANNICATION SEQ 10 NO: 240: SEQUENCE CHARACTERISTICS:
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US-09-277-262-2
Sequence 2, Application US/09277262
Patent No. 6395482
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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amino acid
Best Local Similarity 83.3
Matches 5, Conservative
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Best Local Similarity
Matches 5; Conserv
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GENERAL INCORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield and AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PELICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32240
LENGTH: 735
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Pred. No. 7.3e+02;
1; Mismatches 0; Indels
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Patent No. 587691

GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          1; Mismatches
CURRENT APPLICATION NUMBER: US/09/277,262
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 09/229,530
EARLIER FILING DATE: 1999-01-13
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 2
LENGTH: 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32240, Application US/09252991A Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32240
                                                                                                                                                                                                                                                                                           90.9%;
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                                                                                                                                                               Sequence 5, Application US/07929580B

Patent No. 5426181

GENERAL INFORMATION:
APPLICANT: Lee, Tae Ho
APPLICANT: Lee, Gene W.
APPLICANT: Vilcek, Jan
TITLE OF INVENTION: Cytokine-Induced Protein, TSG-14,
TITLE OF INVENTION: DNA Coding Therefor and Uses Thereof
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
  Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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0; Mismatches 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/929,580B
FILING DATE: 19920814
CLASSIFTCATION ATA:
APPLICATION NUMBER: 07/640,492
FILING DATE: 14-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEANGY/COCKET NUMBER: 34,033
REPERENCE/DOCKET NUMBER: 34,033
REPERENCE/DOCKET NUMBER: 134,033
REPERENCE/DOCKET NUMBER: 14-DAN-1558
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 maino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.9%; Score 29; DB 1;
83.3%; Pred. No. 4.1e+02
  Mismatches
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CEA-Binding Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-708-885B-3
; Sequence 3, Application US/07708885B
; Sequence 3, Application US/07708885B
; Patent No. 5245017
; GENERAL INFORMATION:
; APPLICANT: Maswoswe, Sibusiaiwe M. APPLICANT: Toch, Carol A.; APPLICANT: Toch, Carol A.; APPLICANT: Thomas, Peter ; TILE OF INVENTION: Method for Isola ; TITLE OF INVENTION: CEA-Binding Prot.
                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 93.3'
  5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                               180 LDWQAL 185
                                        1 LDWSAL 6
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  Matches
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                                                                                                                                                                                                                                                                                                                                                                                         Score 30; DB 2; Length 1891;
Pred. No. 2.8e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Burgett, Stanley G.
APPLICANT: Ruhstoss, Stuart A.
APPLICANT: Rao, Magaraja R.
APPLICANT: Rao, Magaraja R.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: PAUL R. CANTRELL 1138
STREET: LILLY CORPORATE CENTER
          SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
FILING DATE: PEDATURY 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2499
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1891 and a acids
TYPE: amino acid
MOLECULE TYPE: peptide
US-08-004-227C-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REPRENCE/DOCKET NUMBER: P911:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08804198
Patent No. 5945320
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           90.9%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1891 amino acids
OPERATING SYSTEM: MS-DOS
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Best Local Similarity 83.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
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904 LDWAAL 909
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LDWSAL 6
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Length 223;
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     Diskette, 3.5 inch, 720kb storage
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COUNTRY: U.S.A.
ZIP: '02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Biskette, 3.5 inch, 720kb
MEDIUM TYPE: storage
COMPUTER: IBM XT
OPERATING SYSTEM: DOS 3.30
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/708,888A
FILING DATE: 19910531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/07708888A
Patent No. 5281697
GENERAL INFORMATION:
APPLICANT: Toth, Carol A.
APPLICANT: Thomas, Peter
APPLICANT: Maswoswe, Sibusisiwe M.
APPLICANT: Briggman, Joseph V.
TITLE OF INVENTION: and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE: Genomic Sequence for Human
TITLE: C.reactive Protein
JOURNAL: J. of Biological Chemistry
VOLUME: 260
MEDIUM TYPE: DIEGRAL
COMPUTER: IBM XT
OPERATING SYSTEM: DOS 3.30
SOFTWARE: Word Perfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/71/
FILING DATE: 19910531
CLASSIFICATION S30
PRIOR APPLICATION NUMBER:
FILING DATE:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: C-reactive protein
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          Liu, Teresa
Zon, Gerald
Soravia, Emilia
Liu, Teh-Yung
Goldman, Neil D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83...
5, Conservative
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AUTHORS:
AUTHORS:
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AUTHORS:
AUTHORS:
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US-07-708-888A-3
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                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720kb storage
COMPUTER: IBM XT
OPERATING SYSTEM: DOS 3.30
SOFTWARE: Word Perfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/708,885B
FILING DATE: 19910531
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-714-386-3

US-07-714-386-3

Sequence 3, Application US/07714386

Patent No. 5278200

GENERAL INFORMATION:
APPLICANT: Thomas, Peter
APPLICANT: Troch, Carol A.

APPLICANT: Maswoswe, Sibusisiwe M.
APPLICANT: Briggman, Joseph V.

TITLE OF INVENTION: Binding Protein for TITLE OF INVENTION: CEA and Uses Thereof NUMBER OF SEQUENCES:
ADDRESSED ADDRESSES: Lahive F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic Sequence for Human
C-reactive Protein
: J. of Biological Chemistry
260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUBLICATION

NAME/KEY: C-reactive protein
PUBLICATION INFORMATION:
AUTHORS: Liu, Teresa
AUTHORS: Zon, Gerald
AUTHORS: Soravia, Emilia
AUTHORS: Liu, Ten-Yung
AUTHORS: Liu, Ten-Yung
AUTHORS: Goldman, Neil D.
AUTHORS: Goldman, Neil D.
                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                FILING DATE:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
                                           ADDART: 60 CITY: BOSTON STATE: MASSACHUSELTS COUNTRY: U.S.A. TE: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 87.9
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 60 State Stree CITY: Boston STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02109 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATE: 25 OCT 1985
US-07-708-885B-3
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VOLUME: 24
ISSUE: 24
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0; Gaps

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| Sequence 34, Application US/08858003
| Sequence 34, Application US/08858003
| Patent No. 6060234
| GENERAL INFORMATION:
| APPLICANT: Stassi, Diane L.
| APPLICANT: Stassi, Diane L.
| APPLICANT: Ruan, Xiaoan
| APPLICANT: Ran, Xiaoan
| APPLICANT: Ran, Xiaoan
| APPLICANT: Ran, Xiaoan
| APPLICANT: ARAN'S Stassis Stephan J.
| APPLICANT: ARAN'S Stassis Stassis Stassis Stassis Stassis Stassis Stassis Stassis Stassis Stassis Stassis Stassis Stassis Stassis Stassis Stassis Stassis Stassis Stassis Stassis ADDRESSEE: Abbott Laboratories STREET: 100 Abbott Park Rd.
| STREET: 100 Abbott Park Rd.
                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                            87.9%; Score 29; DB 4; Length 297; 100.0%; Pred. No. 6.18+02; ive 0; Mismatches 0; Indels
                    APPLICANT: Hoch, James
APPLICANT: Hoch, James
APPLICANT: Dartois, Veronique
TITLE OF INVENTION: METABOLIC SELECTION METHODS
FILE REPERENCE: 234/191
CURRENT APPLICATION NUMBER: US/09/172,952
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRAESEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,003
FILING DATE: I6-MAY-1979
CLASSIFICATION: 435
PROR APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WITOKNEJ/ASSER
NAME: Dianne Casuco
REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 4952
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: No. 6060234e
US-08-858-003-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 345 amino acide
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (847)-938-2623
                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 LDWSA 63
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                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: YiaR-Ec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-08-858-003-34
                                                                                                                                                                                                                                                                                       US-09-172-952-30
                                                                                                                                                                                            SEQ ID NO 30
LENGTH: 297
                                                                                                                                                                                                                                                                                                                                   Query Match
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Sequence 30879, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 30879

LENGTH: 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.9%; Score 29; DB 1; Length 223; 83.3%; Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 4.56
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic Sequence for Human
C-reactive Protein
                                                    FILING DATE:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: C-reactive protein
PUBLICATION INFORMATION:
AUTHORS: Liu, Teresa
AUTHORS: Liu, Teresa
AUTHORS: Soravia, Emilia
AUTHORS: Liu, Teh-Yung
AUTHORS: Goldman, Neil D.
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US-09-172-952-30
; Sequence 30, Application US/09172952
; Patent No. 6368793
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jouranl of Biological
Chemistry
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ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 83.3
Matches 5; Conservative
                    FILING DATE: APPLICATION NUMBER:
APPLICATION NUMBER:
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US-09-078-166-34

Sequence 34, Application US/09078166

Patent No. 6053561

GENERAL INFORMATION:

APPLICANT: Rats, Leenard
APPLICANT: Stassi, Diane L.

APPLICANT: Stassi, Diane L.

APPLICANT: Ramers Jr. Richard G.

APPLICANT: Ramers Jr. Richard G.

APPLICANT: Ramers Jr. Richard G.

APPLICANT: Ramers Jr. Richard G.

APPLICANT: Rakavas, Stephan J.

TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES

TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSER: Abbott Park Rd.

STREET: 10A Abbott Park Rd.

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Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels
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SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: OCIDENTICS:
TOPOLOGY: linear
MOLECULE TYPE: No. 6063561e
US-09-078-166-34
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Search completed: February 18, 2004, 14:41:50 Job time : 8.06579 secs

43 LDWSVL 48

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QBnv16 staphylococ
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Query Match

94.4%; Score 34; DB 16; Length 241;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels

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MEDLINE=21311952; PubMed=11418146;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

Hattori M., Ogasawara N., Hayashi H., Hiramateu K.,

"Whole genome sequencing of meticillin-resistant Staphylococcus
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MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
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83.3%; Pred. No. 1.4e+02;
.ive 1; Mismatches 0; Indels
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EMBL. APO04828; BABS5809.1; -
Hypotherical protein; Complete proteome.
SEQUENCE 281 AA; 33223 MW; 824E3760C6698B42 CRC64;
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EMBL, AP003360; BAB56966.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 282 AA; 33281 MW; 3529EEF885F1B1A6 CRC64;
                                                                                                                                                                                                                     (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
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01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878;
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620;
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SAV0804.
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01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
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MEDINE=9825987; PubMed=9634230; Garnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Elgimmeier K., Gas S., Barry C.E. Ili, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Mature 393:537-544(1998). SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Gaps Whole genome comparison of Mycobacterium tuberculosis clinical and Mus musculus (Mouse). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI_TaxID=10090; [1] · 0 Last sequence update)
Last annotation update)
in (O-methyltransferase, putative). Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; 94.4%; Score 34; DB 16; Length 282; illarity 83.3%; Pred. No. 1.5e+02; Conservative 1; Mismatches 0; Indels laboratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; 295584; CAB09012.1; -. 282 AA; 30887 MW; 41760C508774154A CRC64; TIGR; MT1187;
Tuberculist; Rv1153c;
Tuberculist; Rv1153c;
Pfam; PF02409; Omt N; 1.
Hypothetical protein; Transferase; Methyltransferase; Complete proteone
SEQUENCE 282 AA; 30887 MW; 41760C508774154A CRC64; 01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Corynebacterineae; Mycobacteriaceae; Mycobacterium 195 AA 01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequency of TremBlrel. 23, Last sequency of TrEMBLrel. 23, Last annotating typochetical 30.9 kDa protein (O-methyllomT OR RV1153C OR MTCI65,20C OR WT1187. AE006996; AAK45444.1; -. Mycobacterium tuberculosis.

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             STEAIN=C57BL/63;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium.
The FANTOM Consortium.
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The RANTOM Consortium.
The RANTOM Consortium Research Group Phase I & II Team;
The RANTOM Consortium of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas.";
Nature 420:563-573(2002).
EMBL, AXO45045; BAC32196.1;
Hypothetical protein.
SEQUENCE 195 AA; 22669 MW; 6C33550846800762 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
17 days embryo head cDWA, RIKEN full-length enriched library,
clone:3322402L07 product:hypothetical protein, full insert sequence
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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91.7%; Score 33; DB 11; Length 195;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels
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"Growth suppression of Escherichia coli by induction of mammalian genes with transmembrane or ATPase domains.";
Biochem. Blophys. Res. Commun. 268:553-561(2000).
EMBL, AB030195; BAA92788.1; -...
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Unknown protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 AA.
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STRAIN=C57BL/6J; TISSUE=Head;
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1es 5; Conservative
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167 VDYSWL 172
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58 VDYSWL 63
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 1 LDYSWL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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SEQUENCE FROM N.A.

SEQUENCE TRAIN=C57BL/6J; TISSUE=Head;

X MEDINE=20530913; PubMed=11076861;

X ARDINE=20530913; PubMed=11076861;

XA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

XA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

XA Konno H., Ishii Y., Nakamura S., Hazama M., Nishine T., Kashiwagi K.,

XA Yanamoto R., Matsumoto H., Sakaguohi S., Ikegami T., Kashiwagi K.,

RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

RA Yoneda Y., Ishikawa T., Matsuura S., Kawai J.,

RA Yoneda Y., Ishikawa T., Matsuura S., Kawai J.,

RT "RIKEN integrated sequence analysis (RISA) system=384-format

Genome Res. 10:1757-171(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Head;
MEDI.INE=22354683; PubMed=12466851;
The FANTOM Consortium.
The RANTOM Consortium.
The RANTOM Consortium.
The Manalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
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SEQUENCE FROM N.A.
STRANLE-SOFFICE (ST. TISSUE=Head;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatau N., Hiramoto K., Hiraka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Sibaki K., Salto R., Sakai K., Sano H., Saasaki D., Shibata K., Shibata Y., Sahiagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y., Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
"Functional annotation of a full-length mouse cDNA collection.";
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Pred. No. 2.1e+02;
1; Mismatches 0; Indels
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STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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83.3%;
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nes 5; Conservative
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Q99KP5

099KP5

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Fortin N., Fulthorpe R.R., Allen D.G., Greer C.W.;
"Molecular analysis of bacterial isolates and total community DNA from kraft pulp mill effluent treatment systems.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF043240; AAC08952.1;
HSSP, 060099; IAAG.
InterPro; IPR005833; HIgnase/hydrlase.
InterPro; IPR005834; Hydrolase.
Pfam; PF00702; Hydrolase; 1.
                                                                                                                                                                       SEQUENCE FROM N.A.
Fang R., Luo Z., Zhao H.;
Fang R., Luo Z., Zhao H.;
Novel structure of the rice yellow stunt virus genome: a plant rhabdovirus encodes seven genes.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AB011257, BAA25159.1;
SEQUENCE 93 AA; 10543 MW; AlOCC3BD41F88305 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ancylobacter aquaticus.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Hyphomicrobiaceae; Ancylobacter.
                                                                                                                                                                                                                                                                                                                                    Score 32; DB 12; Length 93; Pred. No. 1.1e+02;
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Pred. No. 1.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                   Viruses; ssRNA negative strand viruses; Mononegavirales;
Rhabdoviridae; Nucleorhabdovirus.
NCBI_TaxID=59380;
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AVG-1998 (TrEMBLrel. 07, Created)
01-AVG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Haloacid dehalogenase (Fragment).
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Last sequence update)
Last annotation update)
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83.3%;
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
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Matches 4; Conservative
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nes 5; Conservative
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                                                                                        Rice yellow stunt virus.
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63 IDYSWI 68
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STRAIN=KIMS / Biovar Mediaevalis;
MEDLINE=22137863; Pubmed=12142430;
Deng W., Burland V., Plunkett G.
Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
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                                                                                                    Similar to cyclin I.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Enterobacteriaceae, Yersinia.
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Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC004071, AAH44071.1;
InterPro; IRR001669, WD40.
Ffam; PF00400; WD40; 3.
SMART; SM00320; WD40; 2.
PROSITE; PS50294; WD REPEATS_REGION; 1.
CYClin; Repeat; WD repeat.
SEQUENCE 392 AA, 44527 MW; 4B2E5CBA3A22075A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
EMBL, AE013914; AAM86682.1; -.
HYpotherical protein.
SEQUENCE 66 AA; 7780 MW; EE5586E890246D88 CRC64;
                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last annotation update)
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                     392 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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Pred. No.
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                     PRT;
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                     PRELIMINARY;
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384 VDYSWL 389
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h Similarity 83.3%; Score 32; DB 2; Length 138; Similarity 83.3%; Pred. No. 1.6e+02; 5; Conservative 1; Mismatches 0; Indels
SEQUENCE 138 **
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NCBI_TaxID=83334;
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Marchesi J.R., Weightman A.J.;
"Relating the cultivable gene pool with the metagene pool in activated
                                                                                                                                                                                    Marchesi J.R., Weightman A.J.; "Relating the cultivable gene pool in activated
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Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJS11306; CADS4036.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sludge.";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ511311; CAD54101.1; -.
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138 AA; 15643 MW; 3F31CE5C83979082 CRC64;
                                                  Putative halocarboxylic acid dehalogenase (Fragment)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative halocarboxylic acid dehalogenase (Fragment)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
11-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative halocarboxylic acid dehalogenase (Fragment)
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83.3%; Pred. No. 1.6e+02;
iive 1; Mismatches 0;
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                                                                                uncultured bacterium.
Bacteria; environmental samples.
NCBI_TaxID=77133;
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Bacteria, environmental samples.
NCBI_TaxID=77133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21074935; PubMed=11206551; Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evanne P.S., Gregor J., Kirkpatrick H.A., Grocheck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; Per G., Boutin A., Sheo Y., Miller L., Grocheck E.J., Buttner F.R.; Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; Apodaca J., Anautharaman T.S., Lin J., Yen G., Schwartz D.C., Mall W. Welch R.A., Blattner F.R.; Lin J., Well B., Schwartz D.C., Malure 409:529-533 (2001).
                                                                                                                                                                                                                 Escherichia coli O157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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EMBL; AP002552; BAB34029.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 153 AA; 17334 MW; 1AD056E0EAA29C65 CRC64;
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                MEDLINE=91139597; PubMed=1995594; Schneider B., Mueller R., Frank R., Lingens F.; "Complete nucleotide sequences and comparison of the structural genes of two 2-haloalkanoic acid dehalogenases from Pseudomonas sp. strain CBS3.";
        01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
2-haloalkanoic acid dehalogenase II (EC 3.8.1.2) (L-2-haloacid dehalogenase II) (Haloaciboxylic acid halidohydrolase II) (DEHCII).
Pseudomonas sp. (strain CBS3).
                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 173:1530-1535(1991).
-!- CATALYTIC ACTIVITY: (S)-2-haloacid + H(2)0 = (R)-2-hydroxyacid
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HAD XANAU
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Q60099; Q56757;
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-SEP-2003 (Rel. 42, Last annotation update)
2-haloalkanoic acid dehalogenase (EC 3.8.1.2) (L-2-haloacid
2-haloalkanoic acid dehalogenase (Rolladohydrolase).
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Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Xanthobacter.
NCBI TaxID=280;
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InterPro; IPR006388; HAD_SF_IA v2.
InterPro; IPR005833; H1gmase/hydrlase.
InterPro; IPR005834; Hydrolase.
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PRINTS; PR00413; HADHALOGNASE.
TIGRFAMS; TIGR01493; HAD-SF-IA-v2; 1.
TIGRFAMS; TIGR01428; HAD_type_II; 1.
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NCBI_TaxID=306;
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229 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Virology 262:104-113(1999).
-!- FUNCTION: ESSENTIAL FOR LYSIS OF THE BACTERIAL CELL WALL BY DISKUPTING THE CELL WALL. THEREBY GIVING HYDROLYTIC ENZYMES ACCESS TO THE CELL WALL. (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE LAMBDA PHAGE S PROTEIN FAMILY.
                EXTRACELULAR (POTENTIAL).

5 (POTENTIAL).

6 (POTENTIAL).

6 (POTENTIAL).

EXTRACELULAR (POTENTIAL).

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8 Y SIMILARITY.

N-LINKED (GLCNAC. ...) (POTENTIAL).

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NCBI_TaxID=106199;
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                                                                                                                                                                                                                                                                                                                                                   91.7%; Score 33; DB 1; Length 404; 83.3%; Pred. No. 36; cive 1; Mismatches 0; Indels
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative lysis protein S (P11).
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TIGRFAMs; TIGR01594; holin_lambda; 1.
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Acconservative 5; Conservative
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SEQUENCE 94 AA: 1
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404 AA;
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 NCBI_TaxID=602;
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                                                                                                                                                                                                                                                                                       formate.";
J. Biol. Chem. 272:33015-33022(1997).

J. Biol. Chem. 272:33015-33022(1997).

I. FUNCTION: CATALYZES THE HYDROLYTIC DEHALOGENATION OF SMALL L-2-HALOALKANOIC ACIDS TO YIELD THE CORRESPONDING D-2-HYDROXYALKANOIC ACIDS. ACTIVE WITH 2-HALOGENATED CARBOXYLIC ACIDS AND CONVERTS ONLY THE L-ISOMER OP 2-CHLOROPROPIONIC ACID WITH INVERSION OF CONFIGHRATION TO PRODUCE D-LACTATE. OFTIMAL ACTIVITY SEEN PH 9-15.

J.O. AND MAXIMAL ACTIVITY SEEN AT PH 9-5.

CATALYTIC ACTIVITY: ($)-2-haloacid + H(2)O = (R)-2-hydroxyacid +
                                                                                                                                                                                                                         MEDLINE-98070500; PubMed-9407083;
Ridder I.S., Rozeboom H.J., Kalk K.H., Janssen D.B., Dijkstra B.W.;
"Intree-dimensional structure of L.2-haloacid dehalogenase from
Xanthobacter autotrophicus GJ10 complexed with the substrate-analogue
                                                                                                            van der Ploeg J., Janssen D.B.; "Sequence analyais of the upstream region of dhlB, the gene encoding haloalkanoic acid dehalogenase of Xanthobacter autotrophicus GJ10."; Biodegradation 6:257-263(1995).
Characterization of the haloacid dehalogenase from Xanthobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: Homodimer.
-!- SIMILARITY: BELONGS TO THE 2-HALOALKANOIC ACID DEHALOGENASE
                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) AND REVISION TO 84.
          autotrophicus GJ10 and sequencing of the dhiB gene."; J. Bacteriol, 173:7925-7933(1991).
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InterPro; IPR006388; HAD_SF IA_v2.
InterPro; IPR005833; HIgnase/hydrlase.
InterPro; IPR005834; Hydrolase.
Pfam; PF00702; Hydrolase; 1
PRINTS; PR00413; HADHALOGNASE.
TIGREAMS; TIGR01493; HAD_SYP-IA-v2; 1.
                                                                                             MEDLINE=96066306; PubMed=7580000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M81691; AAA27590.1; -.
EMBL; X86084; CAA60039.1; -.
PIR; S52840; S52840.
                                                               SEQUENCE OF 1-122 FROM N.A.
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ACT_SITE 8 8
CONFLICT 84 84
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PDB; 1QQ5; 29-NOV-99.
PDB; 1QQ6; 20-DEC-00.
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MEDINNE=21534948; PubMed=11677609;
MEDINNE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtent L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional analysis of ssad and the ssak/U operon, 13 genes encoding components of the type III secretion apparatus of Salmonella pathogenicity island 2.";
                                                                                                                                         Gape
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Hensel M., Shea J.E., Raupach B., Monack D., Falkow S., Gleeson C.,
Kubo T., Holden D.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 413:852-856(2001).
-!- FUNCTION: PART OF A TYPE III SECRETION SYSTEM.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE FLIR/MOPE/SPAR FAMILY.
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                                                                 DB 1; Length 253;
                                                                                                                                         Indels
27469 MW; E2ABBDEED37A5716 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Secretion system apparatus protein ssaT.
                                                                                                 Pred. No. 34;
1; Mismatches
                                                             Score 32;
Pred. No. 3
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15-JUL-1998 (Rel. 36, Last seqn
28-FEB-2003 (Rel. 41, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WEDLINE=97426617; PubMed=9278503;
Blatthar F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blatthar F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Kriley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
"The complete genome sequence of Escherichia coli K-12.";
science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                    Pfam; PF01311; Bac export 1; 1.
PRINTS; PR00953; TYPE31MRPROT.
TIGREAMS; TIGR01401; flir like III; 1.
Transport; Protein transport; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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No. 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8E5F0734991373DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CTT-2001 (Rel. 40, Last annotation update)
Putative transcriptional regulator abgR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. w.
                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.9%; Score 32;
                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
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                                                                                                                                                             MEDLINE=97251357; PubMed=9097039;
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STRAIN=BN101;
MEDLINE-99047572; PubMed=9829935;
                                                                                                                                                EMBL; X99944; CAA68201.1; -.
EMBL; AE008761; AAL20345.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29218 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
nes 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABGR ECOLI
P77744;
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Proc. Natl. Acad. Sci. U.S.A. 92:3105-3109 (1995).

-!- FUNCTION: SPECIFICALLY BINDS TO THE UPSTREAM REGULATORY REGION OF TYPE I IFN AND IFN-INDUCIBLE MHC CLASS I GENES (THE INTERFERON CONSENSUS SEQUENCE (ICS)) AND ACTIVATES THOSE GENES (BY
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Hussein M.J., Green J.M., Nichols B.P.;
"Characterization of mutations that allow p-aminobenzoyl-glutamate utilization by Escherichia coli.";
J. Bacteriol. 180:6260-6268(1998).
-!- FUNCTION: COULD BE THE REGULATOR OF THE ABG OPERON.
-!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL.
REGULATORS.
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BEDLINE=95241433; PubMed=7536924;
Jungwirth C., Rebbert M., Ozato K., Degen H.J., Schultz U., Dawid I.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.9%; Score 32; DB 1; Length 302; 100.0%; Pred. No. 42; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the IRF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPRO05119; LysR_subst.
InterPro; IPR005119; LysR_subst.
Pfam; PP00126; HTH 1; 1.
Pfam; PP03466; LysR_substrate; 1.
PROSITE; PR00039; HTHLYSR.
PROSITE; PS00044; HTH LYSR FAMILY; 1.
Transcription regulation; DNA-binding; Complete proteome. DNA BIND SIND SPORTIAL).
SEQUENCE 302 AA; 34058 MW; 57C83FA6DF8ABA66 CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Interferon regulatory factor 1 (IRF-1).
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Best Local Similarity
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              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leguminosarum.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-'- CaraiyTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L-glutamate.
-!- COFACTOR: Pyridoxal phosphate (By similarity).
-!- SIMILARITY: BELONGS TO CLASS-1 OF PYRIDOXAL-PHOSPHATE-DEPENDENT
AMINOTRANSFERASES.
    as its content is in
                                                                                                                                                                                                                                                         PROSITE; PS00601; IRF; 1.
Transcribtion regulation; DNA-binding; Activator; Nuclear protein.
Transcribtion regulation; DNA-binding; Activator; Nuclear protein.
DNA BIND 7 109 TRYPTOPHAN PENTAD REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001176; ACC synthase.
InterPro; IPR004839; Aminotransf1/2.
InterPro; IPR004839; NHtransf1.
InterPro; IPR004839; NHtransf1.
InterPro; IPR00155; Aminotran 1 2; 1.
PRINTS; PR00753; ACCSYNTHASE.
PROSITE; PS00105; AA TRANSFER CLASS 1; 1.
Transferase; Aminotransferase; Pyridoxal phosphate.
BINDING 239 239 PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Aspartate aminotransferase (EC 2.6.1.1) (Transaminase A) (ASPAT).
ASPC OR AATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                          Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Sequence of an aspartate aminotransferase from Rhizobium
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                                                                                                                                                                                                                                                                                                                                                                                        88.9%; Score 32; DB 83.3%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
non-profit institutions as long
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                                                                                                                                                       InterPro; IPR001346; IRF.
Pfam; PF00605; IRF; 1.
PRINTS, PR00257; INTFRNREGFCT.
PRODOM; PD002355; IRF; 1.
SMART; SM00348; IRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ006709; CAA07198.1; -.
                                                                                                              EMBL; L39766; AAA62160.1; -. HSSP; P15314; 11F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
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086459;
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88.9%; Score 32; DB 1; Length 400;

Query Match

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Fodor I., Grabko V.I., Khozinski V.V., Selimov M.A.;
Fodor I., Grabko V.I., Khozinski V.V., Selimov M.A.;
Fodor I., Grabko V.I., Khozinski V.V., Selimov M.A.;
Fodor I., Grabko V.I., Khozinski V.V., Selimov M.A.;
Arch. Virol. 135:451-459(1994).
I. FUNCTION: THIS PROTEIN FORMS SPIKES ON THE SURFACE OF THE VIRION.
I. IS RESPONSIBLE BOTH FOR THE BINDING OF THE VIRIOS TO SUSCEPTIBLE
HOST CELLS AND FOR INDUCING THE UPTAKE OF THE VIRIOS BY THE CELL.
THE INTERACTION BETWEEN THE INTERNAL COMPONENTS OF THE VIRION AND
THE PORALON OF THE GLYCORROTEIN EXPOSED ON THE CYTOPLASMIC FACE OF
THE PLASMA MEMBRANE PROBABLY DIRECTS ENVELOPMENT AND VIRUS
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Pred. No. 74;
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; Lyssavirus.
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Pfam; PP00974; Rhabdo_glycop; 1.
Transmembrane; Envelope protein; Glycoprotein; Signal.
SIGNAL 1 19 BY SIMILARITY.
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Last annotation update)
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P40944;
01-FEB-1995 (Rel. 31, Created)
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                             Caldicellulosiruptor sp. (strain Rt8B.4).
Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;
Caldicellulosiruptor.
NCBI_TaxID=28238;
                                                                                                                                                                                                                                                                             Appl. Microbiol. Biotechnol. 45:86-93(1996).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic linkages in xylans.
-!- PATHMAX: Xylan degradation.
-!- PATHMAX: Xylan degradation.
-!- SIMILARITY: BELONGS TO CELLULASE FAMILY P (PAMILY 10 OF GLYCOSYL
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Enterobacteriaceae; Pectobacterium.
                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=97077616; PubMed=8920183;
Dwivedi P.P., Gibbs M.D., Saul D.J., Bergquist P.L.;
"Cloning, sequencing and overexpression in Escherichia coli of a xylanase gene, xynA from the thermophilic bacterium Rt8B.4 genus Caldicellulosiruptor.";
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REMBL, L18965; AAB42044.1; -...
REMBL, S41788; S41788.
RECPERCY, IPRO01000; GBM CenC.
RECPERCY, IPRO01000; GBM CenC.
REAM, PPO0318, CBM 49; 2...
REAM, PPO0311; GBM 49; 2...
REAM, PRO0311; GBM 49; 2...
REAM, PRO0311; GBM CenC.
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REAM, PRO0311;
01.FEB-1995 (Rel. 31, Last sequence update).
28-FEB-2003 (Rel. 41, Last annotation update)
Endo-1,4-beta-xylanase A precursox (EC 3.2.1.8) (Xylanase A)
(1,4-beta-D-xylan xylanohydrolase A).
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PROTON DONOR (BY SIMILARITY)
NUCLEOPHILE (BY SIMILARITY).
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Ferrichrysobactin receptor precursor.
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STRAIN=3937;
MEDLINE=96165286; PubMed=8576065;
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Sauvage C., Franza T., Expert D.;
"Analysis of the Erwinia chrysanthemi ferrichrysobactin receptor gene: resemblance to the Escherichia coli fepA-fes bidirectional promoter region and homology with hydroxamate receptors.";
J. Bacteriol. 178:1227-1231(1996).
-!- FUNCTION: INVOLVED IN THE INITIAL STEP OF IRON UPTAKE BY BINDING CHRYSOBACTIN, AN IRON CHELATIN SIDEROPHORE THAT ALLOWS THE BACTERIA TO EXTRACT IRON FROM THE ENVIRONMENT.
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                HSSP, P06971, 2FCP.
InterPro; IPR00531; TonB boxC.
Pfam; PF00593; TonB dep Rec; 1.
Pfam; PF00593; TonB dep Rec; 1.
PR05ITE; PS01156; TONB DEPENDENT REC 2; FALSE NEG.
PROSITE; PS01430; TONB DEPENDENT REC 1; 1.
Signal; Receptor; Transmembrane; Outer membrane; Iron transport;
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FERRICHRYSOBACTIN RECEPTOR.
TONB BOX.
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                                                                                                                                                                                                                                                                                                                                                EMBL; X87967; CAA61205.1; -.
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PERIPLASMIC (POTENTIAL).

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29 103
376 41
417 57
571 61
177 17
285 28
792 79
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                             HSSP; 006851;
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01-JUL-1989 (Rel. 11, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Endoglucanase/exoglucanase B precursor [Includes: Endoglucanase(EC 3.2.1.4) (Endo-1.4-beta-glucanase) (Cellulase)
(Cellobiohydrolase); Exoglucanase (EC 3.2.1.91) (Exocellobiohydrolase)
                                                                                                                                                                                                                                                                                                                                                                                          Caldocellum saccharolyticum (Caldicellulosiruptor saccharolyticus).
Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae; Caldicellulosiruptor.
NCBI_TaxID=44001;
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89098398; PubMed=2789517;

MEDLINE=89098398; PubMed=2789517;

Saul D.J., Williams L.C., Love D.R., Chamley I.W., Bergquist P.I.;

"Nucleotide sequence of a gene from Caldocellum saccharolyticum
encoding for exocellulase and endocellulase activity.";

Nucleic Acids Res. 17.439-439 (1989).

-I- FUNCTION: THIS PROTEIN IS MADE UP OF TWO DOMAINS: THE N-TERMINAL
DOMAIN HAS EXOGLUCANASE ACTIVITY WHILE THE C-TERMINAL DOMAIN IS
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                 ö
                                                                                                                                                                                             88.9%; Score 32; DB 1; Length 735; 83.3%; Pred. No. 1.1e+02; ive 0; Mismatches 1; Indels
          EXTRACELLULAR (POTENTIAL).
                                             EXTRACELLULAR (POTENTIAL)
                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                            3C37073E4538DC3C CRC64;
                                                                                                                     EXTRACELLULAR (POTENTIAL)
                           PERIPLASMIC (POTENTIAL).
                                                               PERIPLASMIC (POTENTIAL).
                                                                                                   PERIPLASMIC (POTENTIAL).
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                                                                                         POTENTIAL
                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                           (1,4-beta-cellobiohydrolase)].
                                                                                                                                                                           735 AA; 81055 MW;
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                  STANDARD;
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Matches 5; Conserv
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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MEDLINE=95350630; PubMed=7542800;
Releischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F. Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M. McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fitchman J.L., Fulrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 THR/PRO-RICH, TANDEM REPEATS OF T-P.
CELLUCSE-BINDING (BY SIMILARITY).
THR/PRO-RICH, TANDEM REPEATS OF T-P.
THR/PRO-RICH, TANDEM REPEATS OF T-P.
PROTON DONOR (POTENTIAL).
BS NUCLEOPHILE (BY SIMILARITY).
BY SIMILARITY.
117641 MW; 0E0378171594DDAE CRC64;
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
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-!- SIMILARITY: SOME, TO MYCOBACTERIOPHAGES D29 AND L5 GP10.
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01-NOV-1995 (Rel. 32, Last sequence update)
01-ROV-1995 (Rel. 31, Last sequence update)
Hypothetical protein HI1415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 AA
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EMBL; X13602; CAA31936.1;
PIR; S02711; S02711.
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SEQUENCE FROM N.A.
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               RESULT 15
IKKA HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A., III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B. "Analysis of the protein-coding content of the sequence of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytomegalovirus strain AD169.";
Curr. Top. Microbiol. Immunol. 154:125-169(1990).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -LINKED (GLCNAC. ..) (POTENTIAL) 34668FE7F908C657 CRC64;
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                                                        HSSP; P23951; 2BAA.
TIGR; H11415; -.
HYpothetical protein; Complete proteome.
SEQUENCE 200 AA; 22895 MW; 42199FDDA4859FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0262; G_PROTEÎN_RECEP_F1_2; UNKNOWN_1.
protein; Transmembrane.
                                                                                                                               86.1%; Score 31; DB 1;
.larity 83.3%; Pred. No. 42;
Conservative 1; Mismatches C
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16-OCT-2001 (Rel. 40, Last annotation update)
UL78.
                                                                                                                                                                                                                                                                                               431 AA.
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83.3%; Pred. No. 9
or send an email to license@isb-sib.ch)
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PROSITE; PS50262; G_PROTEIN_RECEP_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=90269039; PubMed=2161319;
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                           EMBL; U32821; AAC23066.1; -. PIR; H64028; H64028.
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les 5; Conserv
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les 5; Conserv
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P16751;
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SEQUENCE
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=97394468; PubMed=9252186;
DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
"A cytokine-responsive IkappaB kinase that activates the transcription
TKKA_HUMAN STANDARD; PRT; 745 AA.

01511; 014666; 013132; 092467;

16-077-2001 (Rel. 40, Last sequence update)

16-077-2003 (Rel. 40, Last annotation update)

15-SEP-2003 (Rel. 42, Last annotation update)

Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)

I kappa-B kinase alpha) (IKBKA) (IKK-alpha) (IKK-A) (IkappaB kinase)

(I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous kinase)

Kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKBIKA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Connelly M.A., Marcu K.B.; "CHUK, a new member of the helix-loop-helix and leucine zipper families of interacting proteins, contains a serine-threonine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98188283; PubMed=9520446;
Ling L., Cao Z., Goeddel D.V.;
"NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Cervical carcinoma;
MEDLINE=98008813; PubMed=9346484;
Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
I.J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
"IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
NP-kappaB activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hu M.C.-T., Wang Y.-P., "IkappaB kinase-alpha and -beta genes are coexpressed in adult and embryonic tissues but localized to different human chromosomes.";
                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                      MEDLINE=97386461; PubMed=9244310; Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe "Identification and characterization of an IkappaB kinase."; Cell 90:373-383(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          catalytic domain.";
Cell. Mol. Biol. Res. 41:537-549(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Cervical carcinoma;
MEDLINE-96258427; PubMed-8777433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99032998; PubMed=9813230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 32-745 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 278:860-866(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 388:548-554 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 222:31-40(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nemoto S., DiDonato J.A., Lin A.; "Coordinate activated protein "Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase 1 and NF-kappaB-inducing kinase."; Mol. Cell. Biol. 18:7336-7343(1998).
                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT OF A COMPLEX CONTAINING CREBBP; NCOA2; NCOA3; IKKB AND IKBKG. MEDLINE-21968797; Pubmed-11971985; Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J., Qo'Malley B.W.; Ragulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator activity by I kappa B kinase."; Mol. Call. Biol. 22:3549-3561(2002).

**NORTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates
                                            MEDLINE-99212141; PubMed=10195894;
Delhase M., Hayakawa M., Chen Y., Karin M.;
"Postive and negative regulation of IkappaB kinase activity through
IKKbeta subunit phosphorylation.";
Science 284:309-313(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENZYME REGULATION: Activated when phosphorylated and inactivated
                                                                                                                                                                                                                                                                                             Jobin C., Sartor R.B.;
"The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";
Am. J. Physiol. 278:C451-C462(2000).
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GO:0008384; F:IKappaB kinase activity; TAS.
GO:0007345; P:embryogenesis and morphogenesis; TAS.
GO:0007252; P:I-kappaB phosphorylation; TAS.
GO:0006955; P:immune response; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRO00719; Prot kinase.
InterPro; IPR002290; Ser Thr pkinase.
InterPro; IPR01245; Tyr pkinase.
Pfam; PF00069; pkinase; I.
                                                                                                                                                                                                                                                                             MEDLINE=20178139; PubMed=10712233;
                                                                                                                                             IKK PHOSPHORYLATION.
MEDLINE=99038238; PubMed=9819420;
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EMBL; AF080157; AAD08996.1; -...
EMBL; US2512; AAC50713.1; -...
HSSP; Q63450; 1A06.
Genew; HGNC:1974; CHUK.
MIM; 600664; -...
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Nature 401:82-85(1999)
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Gaps
                                                                                              BY SIMILARITY.
PHOSPHORYLATION (BY PKB/AKT1).
PHOSPHORYLATION (BY MAPSK14).
T-AR: LOSS OF PHOSPHORYLATION AND
DECREASE OF KINASE ACTIVITY.
K-AR: LOSS OF KINASE ACTIVITY.
K-AR: LOSS OF AUTOPHOSPHORYLATION.
S-AR: LOSS OF PHOSPHORYLATION AND OF
ACTIVITY.
                                                                                                                                                                           T->A: NO CHANGE IN PHOSPHORYLATION S->A: NO CHANGE IN PHOSPHORYLATION
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    86.1%; Score 31; DB 1; Length 745; 83.3%; Pred. No. 1.7e+02; rive 1; Mismatches 0; Indels
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-> A (IN REF. 3 AND 5).
5 -> DL (IN REF. 5).
7A90B59BC98A56C2 CRC64;
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L -> R (IN REF. 5).
TS -> AY (IN REF. 5)
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

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; Search time 6.5921 Seconds (without alignments) 87.531 Million cell updates/sec

US-09-643-260-12 36

1 LDYSWL 6 Perfect score: Sequence: Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 segs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:* Database

1: pirl: * 2: pir2: * 3: pir3: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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probable ont protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B7055
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Accession: B70555
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A;Residues: 1-282 cCOL>
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A;Coss-references: GB:Z95584; GB:AL123456; NID:g3261774; PIDN:CAB09012.1; PID:e317129; A;Genetics:
A;Genetics:
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ö 94.4%; Score 34; DB 2; Length 282; 83.3%; Pred. No. 36; tive 1; Mismatches 0; Indels Best Local Similarity 83.3 Matches 5; Conservative Query Match

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Gaps

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adrenomedullin receptor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: 34-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000 C;Accession: JC5784 R;Haenze, J.; Dittrich, K.; Doetsch, J.; Rascher, W. Biochem. Biophys. Res. Commun. 240, 183-188, 1997 Bjichem. Biophys. Res. Commun. 240, 183-188, 1997 A;Title: Molecular cloning of a novel human receptor gene with homology to the rat adression: JC5784, MUID:98042541; PMID:9367907

A Molecule type: mRNA

A, Residues: 1-404 < HAE>
A, Cross-references: GB: V13583; NID: g2652933; PIDN: CAA73910.1; PID: g2652934
A, Cross-references: GB: V13583; NID: g2652933; PIDN: CAA73910.1; PID: g2652934
C; Superfamily: vertebrate rhodopsin
C; Keywords: glycoprotein; receptor; transmembrane protein
F; 58-79/Domain: transmembrane #status predicted < TM1>
F; 11.13-149/Domain: transmembrane #status predicted < TM2>
F; 128-149/Domain: transmembrane #status predicted < TM3>
F; 171-193/Domain: transmembrane #status predicted < TM5>
F; 128-239/Domain: transmembrane #status predicted < TM5>

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Riperna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayheiller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Mature 409, 529-533, 2001
A.Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A.Reference number: A88480; MUD:21074935; PMID:11206551
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A;Cross-references: GB:AE004631; GB:AE004091; NID:g9948050; PIDN:AAG05438.1; GSPDB:GN001
A;Experimental source: strain PAO1
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A;Cross-references: EMBL:U61948; PIDN:AAB03148.1; GSPDB:GN00022; CESP:C46A5.8
A;Experimental source: strain Bristol N2; clone C46A5
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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R;Johnson, D.; Stellyes, L.
Rsidnson, D.; Stellyes, L.
R;Johnson, D.; Stellyes, L.
A;Description: The sequence of C. elegans cosmid C46A5.
A;Reference number: Z20690
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Molecule type: DNA
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A,Gene: CESP:C46A5.8
A,Map position: 4
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
B;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gency A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Status: preliminary
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C,Species: Escherichia coli
C,Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein ECs0606 [imported] - Escherichia coli (strain 0157:H7, substrain RI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Xanthobacter autotrophicus
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 11-Jan-2000
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Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
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A;Residues: 1-122 <VAN>
A;Cross-references: EMB::X86084; NID:g763396; PIDN:CAA60039.1; PID:g763399
C;Superfamily: Alcaligenes eutrophus phosphoglycolate phosphatase
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F;260-280/Domain: transmembrane #status predicted <TM6>
F;301-320/Domain: transmembrane #status predicted <TM7>
F;28,37/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 82;
1; Mismatches 0; Indels
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83.3%;
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115 LDYTWL 120
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Best Local Similarity
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LEYSWL 48
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R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Parrar, N. S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A, Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K. A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero. A; Accession: AG0696
A; Reference number: AB0502; MUD:21534947; PMID:11677608
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-259 < PAR>
A; Corosa-references: GB:AL513382; PIDN:CAD01944.1; PID:g16502786; GSPDB:GN00176
C;Genetics:
A;Gene: ssaT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable transcription regulator LYSR-type [imported] - Escherichia coli (strain 0157:H C;Species: Escherichia coli (c) Date: 18-Jul-2001 #text_change 24-Aug-2001 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession: C90869 (c) Accession
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A;Accession: F85749
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A;Coss-references: GB:AE005174; NID:g12515416; PIDN:AAG56458.1; GSPDB:GN00145; UWGP:Z2
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: ydaK
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A;Cross-references: GB:BA000007; PIDN:BAB35346.1; PID:g13361388; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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A,Gene: EC81923
C,Superfamily: regulatory protein ilvY
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Matches 5; Conserv
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R/Schneider, B.; Mueller, R.; Frank, R.; Lingens, F.
R/Schneider, B.; Mueller, R.; Frank, R.; Lingens, F.
R/Schneider, B.; Mueller, R.; Frank, R.; Lingens, F.
A/Title: Complete nucleotide sequences and comparison of the structural genes of two 2-h
A/Reference number: A18452; MUID:91139597; PMID:1995594
A/Reference number: A38452
A/Residues: DAA
A/Residues: 1-229 -62GH>
A/Residues: 1-229 -62GH>
A/Residues: 1-229 -62GH>
C/Superfamily: A/canligenes eutrophus phosphoglycolate phosphatase
C; Keywords: hydrolase
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F;Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res . 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUD:20512582; PMID:11058132
A;Accession: B84016
A;Status: preliminary
A;Molecule type: DNA
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A;Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BAB06649.1; GSPDB:GN0d
A;Experimental source: strain C-125
C;Genetics:
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.Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 24-Nov-1999
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A.Note: this species has also been called Salmonella typhi
C.Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein BH2930 [imported] - Bacillus halodurans (strain C-125) C; Species: Bacillus halodurans C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                          Length 195;
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                                                                                      DB 2;
59;
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83.3%; Pred. No. 70;
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100.0%; Pred. No. 77;
ive 0; Mismatches
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                                                                                      Score 32;
Pred. No.
                                                             88.9%; Scc.
100.0%; Pred
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Best Local Similarity 100.
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Matches 5; Conserv
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              A;Introns: 93/3; 122/3
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conserved hypothetical protein STY0359 (imported) - Salmonella enterica subsp. enterica C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi (C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                      C;Accession: AH0542
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, H. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Authors: Parry, C.; Quail, M.; Rutherford, R.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seron A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-379 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08784.1; PID:g16501600; GSPDB:GN00176
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: Streptomyces coelicolor hypothetical protein SCE15.16c
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88.9%; Score 32; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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A;Status: preliminary
A;Molecule type: DNA
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R;Blattner, P.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A)Cross-references: GB: AE000232; GB:U00096; NID:g1787600; PIDN:AAC74421.1; PID:g1787601; A)Experimental source: strain K-12, substrain MG1655 C;Genetics: A;Genetics: A;Genetics: C;Superfamily: regulatory protein ilvY C;Superfamily: regulatory protein ilvY C;Keywords: DNA binding; transcription regulation F;21-51/Region: regulatory protein lysR motif
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A;Cross-references: EMBL:U39849; NID:g1055041; PID:g1055044; PIDN:AAA81047.1; CESP:C06A8
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A;Gene: CESP:C06A8.6
A;Introns: 29/3; 202/3; 263/3; 316/3
A;Introns: 29/3; 202/3; 263/3; 316/3
C;Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T15422
R;Leimbach, D.
R;Leimbach, D.
R;Description: The sequence of C. elegans cosmid C06A8.
A;Reference number: Z18348
                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
                                                                                                                       Gaps
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                                                      DB 2; Length 302; 93;
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88.9%; Score 32; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                    Indels
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A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                   88.9%; Score 32; DB 100.0%; Pred. No. 93; Live 0; Mismatches
C;Superfamily: regulatory protein ilvY
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Best Local Similarity 100.
                                                                                                                 Conservative
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les 5; Conserv
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RESULT 15

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Gaps

Sequence 2, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 15, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 14, Appli Sequence 123, Appli Sequence 123, Appli Sequence 123, Appli

Sequence 6, Appli Sequence 7614, Ap

us-09-643-260-12.rai

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Sequence 2, Application US/08696770

Patent No. 5763218

GENERAL INFORMATION:

APPLICANT: Fujii, Ryo

APPLICANT: Hinuma Shuji

APPLICANT: Ruben, Steven

APPLICANT: Ruben, Steven

TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR

NUMBER OF SEQUENCES:

CORRESPONDENCES:

ADDRESSER: SmithKilne Beecham Corporation

STREET: 709 Swedeland Road
US-08-887-518-4
US-09-023-321-4
US-09-023-321-4
US-09-032-475-4
US-09-099-125A-2
US-09-099-124A-2
US-09-099-124A-2
US-09-032-476-2
US-09-032-324-2
US-09-10-820-9
US-09-10-820-9
US-09-10-80-9
US-09-10-80-9
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US-09-10-80-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: TAKSO001-2
TELECOMMINICATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPACIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 404 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-terminal
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CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 610-270-5090
    SIRAN....
TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-696-770-2
      Sequence 2, Appli
Sequence 2, Appli
Sequence 4133, Ap
Sequence 4599, A
Sequence 457, App
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                                                                                                                                                        (without alignments)
35.929 Million cell updates/sec
                                                                                                                                    February 18, 2004, 14:16:39; Search time 7.06579 Seconds
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Sequence 7, A
Sequence 11,
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Sequence 1
Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1: /cgn2_6/ptodata/1/iaa/5A COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-696-770-2
US-09-105-557-2
US-09-105-557-2
US-09-252-991A-24938
US-08-637-7558-457
US-08-637-7558-457
US-08-91-685-11
US-08-591-685-11
US-08-591-685-11
US-08-291-197C-59
US-08-291-197C-59
US-08-291-197C-59
US-08-282-197C-59
US-09-282-197C-59
US-09-282-197C-59
US-09-282-197C-59
US-09-282-197C-59
US-09-125-74A-43
US-09-09-125A-4
US-09-09-125A-4
US-09-03-125A-4
US-09-03-125A-4
US-09-03-125A-4
US-09-03-125A-4
US-09-03-125A-4
US-09-03-125A-4
US-09-03-125A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-844-908-10
US-09-868-758-3
                                                                                                                                                                                                                                                                                                                                                     328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued Patents AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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36
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Match Length
                                                                                                                                                                                                                                                     1 LDYSWL 6
                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence:
                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
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No.
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Sequence 4133, Application US/09107532A Patent No. 6583275
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                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                 Sequence 2. Application US/09015557

| Sequence 2. Application US/09015557
| Patent No. 5932702
| GENERAL INFORMATION:
| APPLICANT: Fujii, Ryo
| APPLICANT: Hunna, Shuji
| APPLICANT: Ruben, Steven
| APPLICANT: Roppet, Daniel
| TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR NUMBER OF SEQUENCES: 8
| CORRESPONDENCE ADDRESS: 8
| CORRESPONDENCE ADDRESS: 8
| CORRESPONDENCE ADDRESS: 8
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                                                                    91.7%; Score 33; DB 1; Length 404; 83.3%; Pred. No. 1.8e+02; ive 1; Mismatches 0; Indels
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Pred. No. 1.8e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FASTSEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,557
FILING DATE:
APPLICATION NUMBER: 08/696,770
FILING DATE:
APPLICATION NUMBER: 08/696,770
FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAWE: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKT NUMBER: 34,344
REFERENCE/DOCKT NUMBER: TAKSO01-2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1010-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                             Conservative
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                        |||:||
| 115 LDYTWL 120
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115 LDYTWL 120
                                                                    Query Match
Best Local Similarity
Matches 5; Conserv
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US-08-696-770-2
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RESULT 3

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GREERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
STENT NO. 030227.
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                              NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Magsachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.9%; Score 32; DB 4; Lv 100.0%; Pred. No. 1.4e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: PC
OPERATING SYSTEM: «Unknown»
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature;
;
;CATION: (B) LOCATION 1...217
;SEQUENCE DESCRIPTION: SEQ ID NO: 4133:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: GTC-012 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-09-252-991A-24998
; Sequence 24998, Application US/09252991A
; Patent No. 6551995
                                                                                                                                                                                                                                                                                        ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 4133:
SEQUENCE CHARACTERISTICS:
LENGTH: 217 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                           COUNTRY: USA
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                      88.9%; Score 32; DB 4; Length 228; 100.0%; Pred. No. 1.5e+02;
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88.9%; Score 32; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIREET: 1.101 WEST PERCETTES SIREET
CITY: ALIANG
COUNTRY: USA
ZIP: 30309-3450
ZONPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: PREENTIN Release #1.0, Version #1.30
SOFTWARE: PREENT Release #1.0, Version #1.30
SOFTWARE: OB-MAY-1996
CLASSIFICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION: 435
RILNG DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: PRADER, PRACE AL.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
THE FERENCE/DOCKET NUMBER: RPMS 101
TELECOMMUNICATION INFORMATION:
THE FERENCE/DOCKET NUMBER: ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY ATTORNEY AT
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Sequence 457, Application US/08637759B

Settle No. 5876931

GENERAL INFORMATION:

APPLICANT: David William Holden

TITLE OF INVENTION: Identification of Genes

NUMBER OF SEQUENCES: 501

CORRESPONDENCE ADDRESS:

ADDRESSER: Patree L. Pabst

STREET: 2800 One Atlantic Center

STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                            ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (404) 873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 230 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                     NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24998
LENGTH: 228
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.(
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 DYSWL 6
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67 DYSWL 71
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PRIOR FILING DATE:
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RESULT 6

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'^. 1.5e+02; Indels
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                                                                                                                Sequence 457, Application US/09201945
Patent No. 6342215
GENERAL INFORMATION:
APPLICANT: David William Holden
ITILE OF INVENTION: Identification of Genee
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
Sequence 457, Application US/08871355A
Patent No. 6015669
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                      ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: COLDS COMPUTER: USA ZIP: 30309-3450 COMPUTER READABLE FORM: MEDIUM TYPE: Eloppy disk COMPUTER: IBM PC COMPAtible
                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 230 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 DYSWL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 DYSWL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-871-355A-457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
US-09-201-945-457
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GENERAL INFORMATION:
APPLICANT: Brzezinski, Ryszard
APPLICANT: Dery, Claude V
APPLICANT: Beaulieu, Carole
TITLE OF INVENTION: Thermostable Kylanase DNA, Protein and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.9%; Score 32; DB 2; Length 404;
                                                                                                                                                                                                                                                                                                                                                                                                                                            88.9%; Score 32; DB 3; Length 375; 100.0%; Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                      NUMBER OF SEQUENCES: 13
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
APPLICATION NUMBER: US/08/591,685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Ave., NW CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATUR SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 29-JUL-1994
CLASSIFICATION: 435-
                                     APPLICANT: Thermostable xylanases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 62, Application US/08282197C
; Patent No. 5871730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A
REGISTRATION NUMBER: 33,851
REFRENCE/DOCKET NUMBER: 1050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                         CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 62: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                         LENGTH: 375 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 404 amino acids
amino acid
3Y: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
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                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-591-685-11
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                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 DYSWL 332
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                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: DC
COUNTRY: US
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-08-282-197C-62
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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1.5e+02;
hes 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 13
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,685
                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/201,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
TITLE OF INVENTION: Thermostable xylanases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Prec. ...
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                                                                    PILING DATE:
CLASSIFICATION:
PILING APPLICATION:
PRIOR APPLICATION
PRIOR APPLICATION
PILING DATE:
CLASSIFICATION:
CLASSIFICATION:
ATTORNER: Paber, Patrea L.
REGISTRATION NUMBER: 31.284
REFERENCE/DOCKET NUMBER: RPMS 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEPHONE: (404) 873-8794
INFORMATION FOR SEQ ID NO: 457:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                             RPMS 101
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-08-591-685-11
; Sequence 11, Application US/08591685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08591685
Patent No. 6083733
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                    230 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 351 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 DYSWL 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: pr
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 DYSWL 71
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Gaps

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Sequence 3, Application US/08887518
Patent No. 5843721
GENERAL INFORMATION:
APPLICANT: Wu, Lin
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
                       CORRESPONDENCE ADDRESS:
ADDRESSE: Howeon and Howeon
STREET: Spring House Corporate Center, P.O. Box 457
CITY: Spring House
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                   COMPUTER: 1BM COMPACTALDE
COMPUTER: 1BM COMPACTALDE
OPERATING SYSTEM: DOS
CURRENT APPLICATION NAMER: US/09/136,574A
FILING DATE: 19-Aug-1998
CLASSIFICATION: VURKNOWN:
PRICASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NAMER: US 08/932,571
ATTOREY/ACENT INFORMATION:
NAME: BAK, Mary E.
REGISTRATION NUMBER: 31,215
REPERRICE/DOCKET NUMBER: 1997US001/CIP
TELECOMMUNICATION INFORMATION:
TELEFRAK: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPES Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32; DB 3; Le Pred. No. 9.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: NO. 6294366e

SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-136-574A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEB: SCIENCE & TECHNOLOGY LAW STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.9%; Scc. 100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1426 amino acida
                                                                                                                                                                                    MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: <UNKNOWN>
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSITCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
                                                                                                                                            ZIP: 19477
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 88.9
Best Local Similarity 100.
Matches 5; Conservative
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                           Gaps
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                                                                                                                                                                                                                                                           APPLICANT: Brzezinski, Ryszard
APPLICANT: Berzezinski, Ryszard
APPLICANT: Beaulieu, Carole
TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREE: 1100 New York Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATENTIN BATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/282,197C
FILING DATE: 29-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.9%; Score 32; DB 2; Length 438; 100.0%; Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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Patent No. 6294366
GENERAL INFORMATION:
GENERAL INFORMATION:
Anderson, Graham K.
Anderson, Paige
Glbbs, Moreland
Bergquist, Peter
Daniels, Roy
Morgan, Hugh W.
Williams, Diane P.
TITLE OF INVENTION: Compositions and Methods for .
Treating Cellulose Containing Fa
      Pred. No. 2.6e+02;
                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                   Sequence 59, Application US/08282197C
Patent No. 5871730
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 29-UL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A
REGISTRATION NUMBER: 33,851
REFRENCE/DOCKET NUMBER: 1050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 438 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 5; Conservative
                       5; Conservative
Best Local Similarity
Matches 5; Conserv
                                                                                      328 DYSWL 332
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                                                            2 DYSWL 6
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US-08-890-853-4
                                                           RESULT 15
US-08-890-853-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09023321
Patent No. 5844073
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                               Score 31; DB 2; Length 745;
Pred. No. 7.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 745;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 31; DB 2; I
Pred. No. 7.2e+02;
1; Mismatches 0;
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REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
INFORMATION POS SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
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NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4341
INFORMATION FOR SEQ ID NO: 3:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
                                                                                                                                                                                                                                                                 86.1%;
83.3%;
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Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                  LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: peptide

US-08-887-518-3
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738 LDWSWL 743
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conserv
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STRANDEDNESS: Si
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1 LDYSWL 6

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Gaps
                                   GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Goeddel, David V.

APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK-
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STRIEE: CALIFORNIA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 2;
Pred. No. 7.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: February 18, 2004, 14:41:49 Job time: 7.06579 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                          ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
; Sequence 4, Application US/08890853
; Patent No. 5851812
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TELEFAX: (415) 343-434
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 745 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 86.1
Best Local Similarity 83.3
Matches 5; Conservative
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MOLECULE TYPE: peptide
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ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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Appl
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Sequence 9, Appli
Sequence 11, Appl
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                                                                                                                                    February 18, 2004, 14:16:39; Search time 7.06579 Seconds (without alignments) 35.929 Million cell updates/sec
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Sequence 23,
Sequence 23,
Sequence 29,
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Sequence 2
Sequence 2
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-798-897-13
US-08-978-523-13
US-08-978-523-13
US-08-977-326-23
US-08-927-326-29
US-08-927-326-29
US-09-911-640-3
US-09-111-640-3
US-09-111-640-3
US-08-408-095-17
US-08-408-095-17
US-08-408-095-18
US-08-408-095-18
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US-08-607-269-21
US-08-607-269-21
US-08-607-269-21
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US-08-607-269-21
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US-08-607-269-21
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                                                                                                                                                                                                                                                                                                                                                                                                                  328717 segs, 42310858 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                           - protein search, using sw model
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Maximum DB seq length: 200000000
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35
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Match Length
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                                                                                                                                                                                                                                                                      Perfect score:
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                                                                                                                                                                                                                                                                                          Sequence:
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Sequence 31360, Application US/09252991A

Pacent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVERTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVERTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31360
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; Sequence 13, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
APPLICANT: GUASTELLA, John
TITLE OF INVENTION: Genes Coding For BCl-y, a BCl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32; DB 4; Length 452
Pred. No. 3.3e+02;
1; Mismatches 0; Indels
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US-08-248-819A-10
US-08-607-269-20
US-08-407-269-20
US-08-407-058-12
US-08-407-058-12
US-08-465-485A-12
US-08-65-485A-11
US-08-65-486A-15
US-08-365-486A-15
US-08-365-486A-10
US-08-37-646A-10
US-08-37-646A-10
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US-08-856-531-10
US-08-871-057-12
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ORGANISM: Pseudomonas aeruginosa
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nilarity 83.3%;
Conservative
    410 LDFAWL 415
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Best Local Similarity
Matches 5; Conserv
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    US-09-252-991A-31360
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US-08-798-897-13
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USA

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; MOLECULE TYPE: peptide US-08-978-523-13
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GENERAL INFORMATION:
TITLE OF INVENTION:
CORRESPONDENCE 53
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1100 New York Avenue, N.W., Suite 600
CITY:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: E-bruary 11, 1997
CLASSIFICATION: 424
ATTONEY/AGENT INFORMATION:
NAME: ESSINGL/POCKET NUMBER: 32,893
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 32,240
TELEFRANCE/DOCKET NUMBER: 1483.0140002
TELEFRANCE/DOCKET NUMBER: 32,240
TELEFRANCE/DOCKET NUMBER: 32,240
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TELEFRANCE/DOCKET NUMBER: 1483.0140002
TELEFRANCE/DOCKET NUMBER: 32,240
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TELEFRANCE/DOCKET NUMBER: 1483.0140002
TELEFRANCE/DOCKET NUMBER: 1483.0140002
TELEFRANCE/DOCKET NUMBER: 1483.0140002
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: Pebruary 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 1483.0140001
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2540
INPORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
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88.6%; Score 31; DB
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: not relevant
TOPOLOGY: linear
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STRANDEDNESS: not relevant
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US-08-978-523-13
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                 88.6%; Score 31; DB 2; Length 21; 100.0%; Pred. No. 24; 0; Indels tive 0; Mismatches 0; Indels
                                                                                                                                            ; Sequence 23, Application US/08337646A; Sequence 23, Application US/08337646A; Patent No. 5856171
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; STRESPONDENCE ADDRESS:
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; CITY: Palo Alto
; ZID:
ZID:
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ZID:
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.6%; Score 31; DB 2; Length 23; 100.0%; Pred. No. 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,646A
FLING DATE: 10-NOV-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/317,646A
FLING APPLICATION DATA:
APPLICATION NUMBER: US/08/317,646A
FLING APPLICATION DATA:
APPLICATION NUMBER: US/08/112,208
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: US/08/112,208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INPOMMATION:
NAME: SMICH, WAIlliam M
REGISTRATION NUMBER: 15726A-000620
TELERHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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US-08-927-326-23
US-08-927-326-23
; Sequence 23, Application US/08927326
; Patent No. 6184202
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
Query Match
Best Local Similarity 100.
المالية S; Conservative 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 23 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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Matches 5; Conserv
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DB 2; Length 25;
29;
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Patent No. 6184202
GENERAL INFORMATION:
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRAIT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,326
                                   CLASSIPCATION: 435
PRIOR APPLICATION 435
PRIOR APPLICATION NUMBER: US 08/248,819
FILING DATE: 25-MAX-1994
PRIOR APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993
ATPORNEY/AGENT INFORMATION:
NAME: Smith, William M REGISTRATION NUMBER: 15,726A-000620
TELEPRANCE/DOCKET WUMBER:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,646
FILING DATE: 10-NOV-1994
APPLICATION NUMBER: US 08/248,819
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REFERENCE/DOCKET NUMBER: 15726A-0006
TELECOMUNICATION INFORMATION:
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TELECOMUNICATION INFORM
             10-NOV-1994
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 100.
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US-08-927-326-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,646A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,326
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US 08/337,646
PILING DATE: 10-NOV-1994
APPLICATION NUMBER: US 08/248,819
FILING DATE: 25-NAX-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-NG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERRINCE/DOCKET NUMBER: 15726A-000620
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415) 326-2400
TELEFPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
TITLE OF INVENTION: CELL DEATH REGULATORS
                                                                                                                                                                                                                                                                                                                                    ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Flappy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                      STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 88.6
Best Local Similarity 100.
Matches 5; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
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16 DFSWL 20
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Sequence 3, Application US/09211640
Patent No. 6020466
GENERAL INFORMATION:
APPLICANT: Craig, Ruth W.
TITLE OF INVENTION: ANTHRODIES WHICH SPECIFICALLY BIND mcl-1
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09378536
Patent No. 6200763
GENERAL INFORMATION:
TAPLICANT: Craig, Ruth W.
TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
CHEBERSEE: Spensley Horn Jubas & Lubitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31; DB 3; Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                      SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

88.6%; Score 31; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                 ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/441,375
FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: Haile, Ph.D., Liga A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: PD-2845
                                                                                                                                                                                                                                                                                         ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Paint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 154 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
CLONE: bcl-2alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Protein
LOCATION: 1..154
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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0
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Patent No. 5470955
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 88.6%; Score 31; DB 1; Length 154; Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                DB 3; Length 25; 29;
                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,848A
FILING DATE: 16-JUN-1993
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: PB-2845
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
                                                                                                                                                                                88.6%; Score 31; DB 100.0%; Pred. No. 29; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 455-5110 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                   LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: aingle
TOPOLLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 154 amino acids
TYPE: amino acid
                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 5; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: bcl-2alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: Protein
; LOCATION: 1..154
US-08-077-848A-3
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16 DFSWL 20
                                                                                                                                                                                                                                                                          2 DFSWL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
                                                                                                                                   US-08-927-326-29
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-08-077-848A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31; DB 4; Length 154; Pred. No. 1.7e+02; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/08408055; Patent No. 5858678
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: APOPTOPSIS-REGULATING PROTEINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONTEST 2003.

CONTEST 2003.

MEDIUM TYPE: Floppy disk COMPUTER: Eloppy disk COMPUTER: Eloppy disk COMPUTER: Eloppy disk COMPUTER: Elem PC COMPOTER: Elem PC COMPUTER: Elem PC COMPUTER: PAPLICATION DATA:

APPLICATION NUMBER: US/08/408,095

FILING DATE: 21-MAR-1995

CLASSIFICATION: 435

ATTONNEY/AGENT INPOMPATION:
NAME: MACK, SUBBA J.

REGISTRATION NUMBER: 30,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 88.6%; Score 31; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..154
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                 (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                   88.6%; SCUL
100.0%; Pre
                       TELECOMMUNICATION INFORMATION
                                                               TELEFAX: (619) 455-5110
INFORMATION FOR SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION TELEPHONE: (202)293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 229 amino acide TYPE: amino acid
                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein
                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                        CLONE: bcl-2alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 DFSWL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 DFSWL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 DFSWL
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                                                                                                                                                                                                                                                                                                FEATURE
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US-08-408-095-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09687260
Patent No. 6528263
GENERAL INFORMATION:
APPLICANT: Craig, Ruth W.
TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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MEDIUM TYPER: FLOPPY disk

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/687,260
FILING DATE: 12-Oct-2000
CLASSIFICATION: VUNROWN->
PRIOR APPLICATION NUMBER: 09/378,536
FILING DATE: cUnknown->
APPLICATION NUMBER: 09/378,536
FILING DATE: CURROWN->
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

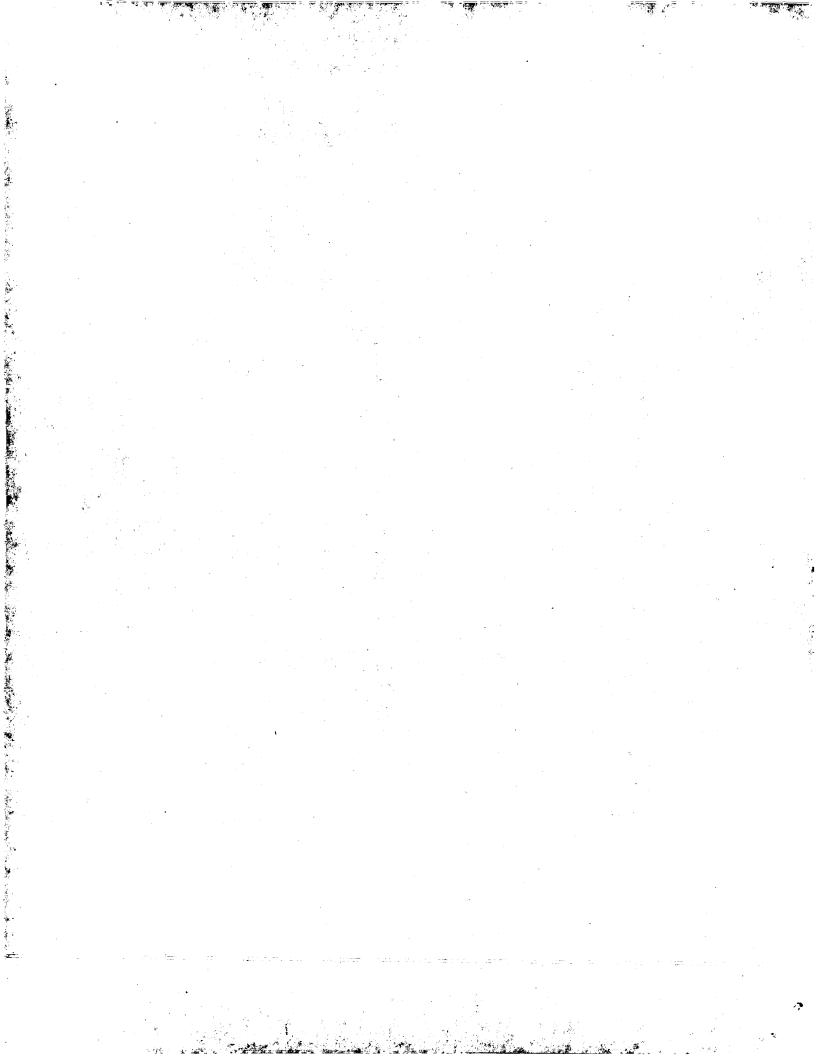
88.6%; Score 31; DB 3; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
                                 COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,536
FILING DATE:
                                                                                                                                                         PILLING DAILS:
CLASSIPICATION:
CLASSIPICATION DATA:
PRIOR APPLICATION NUMBER: US/08/077,848
FILLING DATE: 16-UNN-1993
ATTORNEY AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REPERNEK/DOCKET NUMBER: 9D-2845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
COUNTY. 154 Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 154 amino acide
TYPE: amino acid
STRANDEDNESS: Bingle
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
COMPUTER READABLE FORM:
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CLONE: bcl-2alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: 1.154
US-09-378-536-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 DFSWL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto CITY: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppa disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SUGTYARE: Patentin Release #1.0, Version #1.25
SUGTYARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/112,208C
FLING DATE: 26-AUG-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/POCKET NUMBER: 15726A-000610
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                         Score 31; DB 2; Le
Pred. No. 2.5e+02;
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Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KORSMEYER, Stanley J.
TITLE OF INTENTION: CELL DEATH REGULATORS
UNUBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/08112208C Patent No. 5691179 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.6%; Sc.
100.0%; Pred
0; F
                                   ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (202)293-7060
                                                                                                                             TELEFAX: (202)293-7060
INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS: LENGTH: 232 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (415) 326-2400
  21-MAR-1995
                                                                                                                                                                                                     : 232 amino acids
amino acid
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-408-095-18
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,095
FILING DATE: 21-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J. 30,951
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFARE: (202)293-7060
INFORMATION FOR SEQ ID NO: 17:
                                                                                            Sequence 17, Application US/08408095
Patent No. 5858678
GENERAL INFORTION:
GENERAL INFORTION:
APPLICANT: Chinnadurai, Govindaswamy
TITLE OF INVENTION: APOPTOPSIS-REGULATING PROTEINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/08408095
Patent No. 5888678
GENERAL INFORTION:
GENERAL INFORTION:
TITLE OF INVENTION: APOPTOPSIS-REGULATING PROTEINS
NUMBER OF SEQUENCES: 35
CORRESPONDENC ADDRESS:
ADDRESSEE: 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                          ADDRESSE: SUGHRUE, MON, ZINN, MACPEAK & SEAS STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,095
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                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 232 amino acids
TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity 100.
Matches 5; Conservative
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COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                   ZIP: 20037
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
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  201 DFSWL 205
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                                                         RESULT 13
US-08-408-095-17
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Search completed: February 18, 2004, 14:41:49 Job time : 8.06579 secs



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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions also as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The crystal structure of the L1 metallo-beta-lactamase from Stenotrophomonas malcophila at 1.7 A resolution.";
J. Mol. Biol. 284:125-136(1998).
-!- FUNCTION: HAS A HIGH ACTIVITY AGAINST IMIPENEM. UNSTABLE BELOW B, UNLESS ZINC IS PRESENT.
-!- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- COFACTOR: BINDS TWO ZINC IONS PER MOLECULE.
-!- ENZYME REGULATION: Inhibited by Hg(2+) or Cu(2+). Reduced
enzymatic activity in presence of Co(2+), N1(2+), Cd(2+), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBUNTT: Homotetramer.
-1- SUBURLILULAR LOCATION: Periplasmic (Potential).
-1- SIMILARITY: Belongs to the class-B beta-lactamase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P52700 xanthomonas
Q14699 homo sapien
P12880 corruebacte
Q93mh3 corruebacte
P29899 paracoccus
P25899 paracoccus
P25906 escherichia
P25324 gallus gall
P25324 gallus gall
P25324 gallus gall
P25325 homo sapien
P97532 rattus norv
Q8ypl9 anabaena sp
P5535 homo sapien
P97532 rattus norv
Q8ypl9 anabaena sp
P6555 homo sapien
P76656 homo sapien
P76656 mus musculus
Q16762 homo sapien
P52196 mus musculu
P52196 mus musculu
P53197 salmonella
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caenorhabdi
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                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                     February 18, 2004, 13:39:39; Search time 3.55263 Seconds (without alignments) 79.423 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
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O26914
O32140
P032110
P043911
P24255
P06223
P26223
P063100
P09098
P04053
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O60832
P06526
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                             127863 segs, 47026705 residues
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CRIGR
HUMAN
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Listing first 45 summaries
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SHEON
CAEEL
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Maximum DB seq length: 200000000
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33
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Match
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Q9nris homo sapien O52847 bacillus me Q9imm4 nodamura vi P2742 emericalla P00885 pseudomonas Q8K9n1 buchnera ap P10914 homo sapien P74592 synechocyst Q9ng67 homo sapien Q9muq6 mesostigma P36195 gallus gall O44081 drosophila	·	update) on update) (Beta-lactamase, type II) s maltophilia) (Stenotrophomonas	-d). Proteobacteria, Gammaproteobacteria, Xanthomonadales, daceae, Stenotrophomonas. D=40324;	Nichols W.W., Cartwright S.J., o-beta-lactamase from Xanthomonas	y S.G.; f the zinc beta-lactamase	D.C., Verma C.S., sta-lactamase from
1 DISI_HUMAN 1 BGAL_BACME 1 RRPO_NODAV 1 ACVS EMENI 1 ALKD PSEPU 1 GPMA_BUCAP 1 IRF1_HUMAN 1 IRF1_HUMAN 1 DPOM_HUMAN 1 NU2C_MESVI 1 TDT_CHICK 1 NO60_DROME	ALIGNMENTS PRT; 290 AA	Created) Last sequence update) Last annotation update) Li precursor (Beta-lactama inase) a (Pseudomonas maltophilis)	cteria; Gammaproteobacte: Stenotrophomonas.	FROM N.A. 19 1275; 94289479; PubMed=8018721; R., Hall L., Assinder S.J., Nichols W.W., Cs A.P., Bennett P.M.; analysis of the Ll metallo-beta-lactamase	3931629; , Gagnon J., Waley ular properties of a IID 1275."; 985).	LOGRAPHY (1.7 ANGSTROMS). 1465; PubMed=9811546; Alsh T.R., Taylor I.A., Emery D.C., Verma (Spencer J.; the L1 metallo-beta-lactamase
87.9 854 87.9 1034 87.9 1043 87.9 3770 84.8 230 84.8 325 84.8 401 84.8 601 84.8 601 84.8 601	STANDARD;	P52700; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence 15-SEP-2003 (Rel. 42, Last annotation Metallo-bectalactemase Li precursor (EC 3 5.2.6) (Penicillinase). Xanthomonas maltophilia (Pseudomona	oteobacteria; ceae; Stenotr 0324;	SEQUENCE FROM N.A. STRAIN=IID 1275; MEDLINE=94289479; PubMed=8018721; Walsh T.R., Hall L., Assinder S.J., Macgowan A.P., Bennett P.M.; "Sequence analysis of the L1 metallc mallcophila.";	SEQUENCE OF 34-65. STRAIN=IID 1275; Bicknell R., Emanuel E.L., Gagnon J., "The production and molecular propert: Of Pseudomonas maltophilia IID 1275." Biochem. J. 229:791-797(1985).	[3] XE-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) MEDLINE-99030465; PubMed-9811546; Ullah J.H., Walsh T.R., Taylor I.A., Gamblin S.J., Spencer J.; "The cryetal structure of the L1 meta
3334 334 337 337 337 338 338 447 447 447 447 447 447 447 447 447 44	3 1	P5270; 01-0CT-1996 (Rel. 34, C: 01-0CT-1996 (Rel. 34, Li 15-SEP-2003 (Rel. 42, Li Metallo-beta-lactamase) Rel 3.5.2.6) (Pendicillia Xanthomonas maltophilia	marcophilia). Bacteria; Proteob Xanthomonadaceae; NCBI_TaxID=40324;	SEQUENCE FROM N.A. STRAIN-IID 1275; MEDLINE-94289479; Publ Walsh T.R., Hall L., Macgowan A.P., Bennet, "Sequence analysis of maltophila.";	SEQUENCE OF STRAIN=IID 1 MEDLINE=8602 Bicknell R., "The product of Pseudomon Biochem. J.	[3] X-RAY CRYSTALLOGRA MEDLINE=99030465; Ullah J.H., Walsh Gamblin S.J., Spen "The crystal struc
	RESULT BLA1_X ID_B	AC DOD DOD DOD DOD DOD DOD DOD DOD DOD DO	8008	RA RA RA RA RA RA RA RA RA RA RA RA RA R	R R R R R R R R R R R R R R R R R R R	RR RR RR RR R

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Bone marrow;
MEDLINE=59308125; Pubmed=7788527;
Nagase T., Miyajima N., Tanaka A., Sazuka T., Seki N., Sato S.,
Tabata S., Ishikawa K.-I., Kawarabayasi Y., Kotani H., Nomura N.;
"Prediction of the coding sequences of unidentified human genes. III.
The coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by analysis of cDNA clones from human cell line KG-1.";
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-007-1989 (Rel. 12, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase) (PEPC).
PPC OR CGI1585.
Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria, Actinobacteria, Actinobacteriaes, Corynebacterium.
                                                  Score 30; DB 1; Length 290; Pred. No. 73; 1; Mismatches 0; Indels
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   267 287
290 AA; 30801 MW; 0B34CAB54518BCIE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        648 AA; 70463 MW; 88F68A62D6C1CDA1 CRC64;
                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein KIAA0084 (HA2022) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30; DB 1; 1
Pred. No. 1.6e+02;
1; Mismatches 0;
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                                                                                                                                                                                                                                               648 AA
                                                    90.9%;
83.3%;
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                                                                  Local Similarity 83.3
                                                                                                                                                                                                                                               STANDARD;
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NON TER
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PROSITE; PS00743; BETA LACTAWASE B 1; 1.
PROSITE; PS00744; BETA LACTAWASE B 2; FALSE NEG.
Hydrolase; Zinc; Antibiotic resistance; Periplasmic; Signal;
                                                                                                                                                                                                                                                                                          ZINC 1.
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or send an email to license@isb-sib.ch)
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                                             EMBL, X75074, CAA52968.1, -...
PIR, S45349, S45349.
PDB, 120.28P-99.
InterPro, IPR001018; Beta lactamase B.
InterPro, IPR001279; Blactmase-like.
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                                                                                                                                                                                                                                               Liu Y., Ding J., Wang Y.; "Cloning and expression of phosphoenolpyruvate carboxylase-coding gene
                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase) (PEPC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paracoccus denitrificans.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Pd 1222;
MEDLINE=92041581; PubMed=1657871;
van Spanning R.J.M., Wansell C.W., de Boer T., Hazelaar M.J.,
                                                                                                                    Corynebacterium crenatum.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.9%; Score 30; DB 1; Length 919; 83.3%; Pred. No. 2.3e+02; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dioxide fixation; Tricarboxylic acid cycle.
38 138 BY SIMILARITY.
79 579 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          919 AA; 103331 MW; 10AF3F464AFFE604 CRC64;
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28-FEB-2003 (Rel. 41, Last annotation update)
Cytochrome c-L precursor (Cytochrome C5511) (C552).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 AA
919 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00781; PEPCASE 1; 1. PROSITE; PS00393; PEPCASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF406314; AAK92540.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last seq
28-PEB-2003 (Rel. 41, Last ann
                                   28-FEB-2003 (Rel. 41, Created)
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PRINTS; PR00150; PEPCARBXLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF 00595; -; 1.
InterPro; IPR001449; PEPcase.
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                MEDLINE-89384466; PubMed=2779518;
Eikmanns B.J., Follettie M.T., Griot M.U., Sinskey A.J.;
"The phosphonolpyruvate carboxylase gene of Corynebacterium
glutamicum: molecular cloning, nucleotide sequence, and expression.";
Mol. Gen. Genet. 218:330-339(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.
STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
MEDLINE-89326141; PubMed=2666264;
O'Regan M., Thierbach G., Bachmann B., Villeval D., Lepage P.,
Viret J.F., Lemoine Y.;
Cloring and nucleotide sequence of the phosphoenolpyruvate
carboxylase-coding gene of Corynebacterium glutamicum ATCC13032.";
Gene 77:237-251(1989).
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PROSITE; PS00393; PEPCASE_2; 1.
PROSITE; PS00781; PEPCASE_1; 1.
PAGSS: Carbon dioxide fixation; Tricarboxylic acid cycle;
Complete proteome.

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ACT_SITE 137 137 BY SIMILARITY.
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KL -> NV (IN REF. 1).

FT -> LP (IN REF. 1).

L -> V (IN REF. 1).
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
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EMBL; MX5819; AAA8337.1; -.
EMBL; AO9073; CAA00827.1; -.
EMBL; AP005279; BAB99978.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; SO5512; OYFKG.
HASAP; PO0864; IFIY.
HAMAP; MP 00595; -; 1.
InterPro; IPR001449; PEPcase.
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918 AA;
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                                                                                                                                                                                                                                                                                                           Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos B.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Debaran M., Brinkac L., Daugherty S., Deboy R.T., Taspin A., Scott J., Bearan M., Brinkac L., Daugherty S., Deboy R.T., Dodson R.J., Umayam L.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Muller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nat. Biotechnol. 20:1118-1123(2002).
-1-CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) methylideneamino] imidazole-4-carboxamide [(5-phosphorl-deoxyribulos-1-ylamino)methylideneamino] -1-(5-
                15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-(5-phosphoribosyl)-5-(6-phosphoribosylamino)methylideneamino)
imidazole-4-carboxamide isomerase (EC 5.3.1.16)
(Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide
                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
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15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative thiosulfate sulfurtransferase F11G11.9 (EC 2.8.1.1).
Caenorhabditis elegans.
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HAMAP; MP_01014; -; 1.
HAMAP; MP_01014; -; 1.
HAMAP; MP_01014; -; 1.
HAMAP; MP_01014; -; 1.
HIGHENPRO; IPRO0602; Hisb biosynth.
Pfam; PF00977; His biosynth; 1.
TIGHRAMB; TIGHR00007; TIGHR00007; 1.
ISOMERABE; Histidine biosynthesis; Complete proteome.
RROHENCE 245 AA; 26017 MW; 6040B1B3604527DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 29; DB 1;
Pred. No. 96;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277 AA.
                                                                                                                                                                                                                                                                          STRAIN=MR-1;
MEDLINE=22297686; PubMed=12368813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.55,
100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE015648; AAN55116.1; -.
    Created)
                                                                                                                                                                                           Alteromonadaceae; Shewanella.
NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
(Rel. 42, (Rel. 42, 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shewanella oneidensis.
                                                                                                                                      HISA OR SO2069.
Shewanella oneidensis.
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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P91247;
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ID THT1_CAEEL

ID THT1_CAEEL

DT 15-UUL.

DT 28-FEB-

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OC CAENON

OC CAENON
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                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (COVALENT) (BY SIMILARITY).
(COVALENT) (BY SIMILARITY).
(HEME AXIAL LIGAND) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                         dehydrogenase, amicyanin, and cytochrome c5511."; Science 264:86-90(1994).
-!- FUNCTION: ELECTRON ACCEPTOR FOR MDH. ACTS IN METHANOL OXIDATION.
THIS CYTOCHROME HAS A REDOX POTENTIAL OF ABOUT +190 MV.
-!- SUBCELLULAR LOCATION: Periplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000345; CytC heme bind.
PROSITE; PS00190; CYTOCHRÖME C; 1.
Electron transport; Heme; Signal; Methanol utilization; Periplasmic;
Anazawa H., Harms N., Oltmann L.F., Stouthamer A.H.; "Isolation and characterization of the moxJ, moxJ, moxI, and moxR genes of Paracoccus denitrificans: inactivation of moxJ, moxG, and moxR and the resultant effect on methylotrophic growth."; J. Bacteriol. 173:6948-6961(1991).
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                                                                                                                                  MEDLINE=94188715; PubMed=8140419;
Chen L., Durley R., Mathews F.S., Davidson V.L.;
"Structure of an electron transfer complex: methylamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19396 MW; 6949FBDC8B2C056E CRC64;
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69;
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HEME (COVALENT) (
HEME (COVALENT) (
IRON (HEME AXIAL
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M57684; AAA25583.1; -.
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122
129
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151
155
162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; B41377; B41377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5; Conserv
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HIS4_SHEON
ID HIS4_SHEON
AC Q8EFB5;
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Length 245; Indels

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Science 277:1453-1474(1997)
                                            SEQUENCE FROM N.A.
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NCBI_TaxID=9031;
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SEQUENCE.
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                                                                                                    Latreille P., Deadman R.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.
-!- SIMILARITY: Contains 2 rhodanese domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=S7426617; PubMed=9278503;
MEDLINE=S7426617; PubMedt G III. Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moszer I., Glaser P., Danchin A.; "Multiple IS insertion sequences near the replication terminus in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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InterPro; IPR001763; Rhodanese-like.

InterPro; IPR001307; Rhodanese.

InterPro; IPR001307; Rhodanese.

Pfam; PF00581; Rhodanese.

R PR0STTE; PS00683; RHODANESE 2; FALSE_NEG.

R PROSTTE; PS006083; RHODANESE 2; FALSE_NEG.

HYPOCHECIAI PROCESI; TANBECE 2; RHODANESE 1; DOMAIN 155 243 RHODANESE 1.

T DOMAIN 155 243 RHODANESE 1.

T ACT SITE 258 258 BY SIMILARITY.

SEQÜENCE 277 AA; 30699 MW; 25EDF666CE12824C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.9%; Score 29; DB 1; Length 277; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
19pochetical oxidoreductase ydbC (EC 1.-.-.)
YDBC OR B1406.
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Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-K12;
MEDLINE-92190338; Pubmed=1665988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochimie 73:1361-1374(1991).
                                                                                                                                                                                                                                                                                                                                                                                EMBL; U80451; AAB37840.1; -.
PIR; T29979; T29979.
HSSP; P00586; 1RHS.
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                  STRAIN=Bristol N2;
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                      NCBI_TaxID=6239;
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P25906;
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J. Biol. Chem. 273:25974-25986(1998).
--- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapa
                                                                                                       Alba H., Baba T., Fullita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Yamamoto Y., Horiuchi T., Takeuchi Y., Wada C., Yamanoto Y., Horiuchi T., Sivasundaram S., Mananoto Y., Horiuchi T., Mana S., Mananoto Y., Horiuchi T., Mada C., Mananoto Y., Mada C., Mananoto Y., Mada C., Mananoto Y., Mananoto Y., Mada C., Mananoto Y., Mananoto Y., Mada C., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Mananoto Y., Manano
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R EMBL; AE000238; AAC74488.1; -.
R EMBL; D90779; BAA15021.1; -.
R EMBL; A937452; CAA66103.1; -.
R PIR; A48399; A48399.
R HSSP; P06632; 1HW6.
R ECOGENE; EQ11309; YdbC.
R INTERPRO; IPR001395; Aldo/ket_red; I.
R PRINTS; R000068; ALDKETRDTASE.
R PYDODM; PD000288; Aldo/ket_red; I.
R PYDODM; PD000288; Aldo/ket_red; I.
R PYDODM; PD000288; Aldo/ket_red; I.
R PYDODM; PD000288; Aldo/ket_red; I.
R PYDOTHETCAI protein; Oxidoreductase; Complete proteome.
SEQUENCE 286 AA; 30706 MW; 82B587AEA9115EF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.9%; Score 29; DB 1; Length 286; 100.0%; Pred. No. 1.18+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=W / ATCC 11105;
MEDLINE=98421522; PubMed=9748275;
STRAIN=12;
MEDLINE=97251357; PubMed=9097039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-69 FROM N.A. STRAIN=W / ATCC 11105;
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Best Local Similarity 100.0
Matches 5; Conservative
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171
185
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Q8YPL9;
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DOMAIN
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                                                              -:- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.
-:- SUBUNIT: Monomer.
-:- SUBCELLULAR LOCATION: Mitochondrial matrix.
-:- TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.
-:- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER, THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
-:- SIMILARITY: Contains 2 rhodanese domains.
PIR; A37209; A37209.
                                                                                                                                                                                                                                                         RHODANESE 2.
MAY PLAY A ROLE IN SUBSTRATE BINDING (BY
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weiland K.L., Dooley T.P.;
"Molecular cloning, sequencing and characterization of cDNA to rat liver rhodanese, a thiosulphate sulphurtransferase.";
Biochem. J. 275:227-231(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Liver;
MEDLINE=95332330; PubMed=7608189;
Nagahara N., Okazaki T., Nishino T.;
"Cytosolic mercaptopyruvate sulfurtransferase is evolutionarily
                                                                                                                                                                                                                                                                                                                                                                        ;
                Kohanski R.A., Heinrikson R.L.,
"Primary structure of avian hepatic rhodanese.";
J. Protein Chem. 9:369-377(1990).
-!- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES AND CYANIDE DETOXIFICATION.
                                                                                                                                                                                                                                                                                                       (BY SIMILARITY).
SUBSTRATE (THIOSULFATE) BINDING
                                                                                                                                                                                                                                                                                    BY SIMILARITY.
SUBSTRATE (THIOSULFATE) BINDING
                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 289;
                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                  BBFCF671DE0B2BA4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                              1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 AA.
                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                       RHODANESE 1.
HINGE.
                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                     87.9%; Score 29;
                                                                                                                                                         InterPro; IPR001763; Rhodanese-like.
InterPro; IPR001307; Rhodanese.
Pfam; PF00581; Rhodanese; 2.
SMART; SM00450; RHOD; 2.
PROSITE; PS00380; RHODANESE 1; 1.
PROSITE; PS00683; RHODANESE 2; 1.
PROSITE; PS50266; RHODANESE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Sprague-Dawley, TISSUE-Liver;
MEDLINE-91207296; Pubmed-2018478;
                                                                                                                                                                                                                               Transferase; Mitochondrion; Repeat
         MEDLINE=91113289; PubMed=2275748;
                                                                                                                                                                                                                                                                                                                                   32286 MW;
                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                   186
                                                                                                                                                                                                                                                                                                                                   289 AA;
                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 5; Conserv
                                                                                                                                                     HSSP; P00586; 1RHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            31 LDASW 35
                                                                                                                                                                                                                                                                                                                                                                                           1 LDASW 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                               245
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                                                                                                                                                                                                                                               DOMAIN
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                                                                            mutagenesis.";
J. Biol. Chem. 270:16230-16235(1995).
-!- FUNCTION: INVOLVED IN THE FORMATION OF IRON-SULFUR-COMPLEXES,
CYANIDE DETOXIFICATION OR MODIFICATION OF SULFUR-CONTAINING
ENZYMES. OTHER THIOL COMPOUNDS, BESIDES CYANIDE, CAN ACT AS SULFUR
ION ACCEPTORS. ALSO HAS WEAK MERCAPTOPYRUVATE SULFURTRANSFERASE
related to mitochondrial rhodanese. Striking similarity in active site amino acid sequence and the increase in the mercaptopyruvate sulfurtransferase activity of rhodanese by site-directed
                                                                                                                                                                                                                                     (MST) ACTIVITY. CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAY PLAY A ROLE IN SUBSTRATE BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
SUBSTRATE (THIOSULFATE) BINDING.
SUBSTRATE (THIOSULFATE) BINDING.
R->G: UNALTERED RHODANESE ACTIVITY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                        INCREASED MST ACTIVITY.
K->S: DECREASED RHODANESE ACTIVITY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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24C55B35690934E1 CRC64;
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Pred. No. 1.2e+02;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P00586; IRHS.
InterPro; IPR001763; Rhodanese-like.
InterPro; IPR001307; Rhodanese.
Pfam; PF00581; Rhodanese; 2.
SMART; SM00450; RHOD; 2.
PROSITE; PS00681; RHODANESE 1; 1.
PROSITE; PS00681; RHODANESE 2; 1.
PROSITE; PS50206; RHODANESE 3; 2.
Transferase; Mitochondrion; Repeat.
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100.0%; Pic
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                                   MEDLINE=21555285; PubMed=11759840; Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguothi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Pomplete genomic sequence of the filamentous nitrogen-fixing Cyanobacterium Anabaena sp. strain PCC 7120."; DNA Res. 8:205-213(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20057165; PubMed=10591208; Bruskiewich R., Beare D.M., Clunham I., Hunt A.R., Collins J.E., Bruskiewich R., Babbage A.K., Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K., Bagguley C., Bailey J., Barlow K.F., Bates K.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J., Burrill W.D., Burtcon J., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M., Cobley V.E., Coll C.G., Collier R.E., Connor R., Conroy D., Corby M.R., Coville G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pallini R., Guazzi G.C., Cannella C., Cacace M.G.; "Cloning and sequence analysis of the human liver rhodanese: comparison with the borne and chicken enzymes."; Biochem. Biophys. Res. Commun. 180:887-893 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                       87.9%; Score 29; DB 1; Length 296; 100.0%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P25375; 076750;
01-MAY-1992 (Rel. 22, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
3-mercaptopyruvate sulfurtransferase (EC 2.8.1.2) (MST).
MPST OR TST2.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                 DNA repair; DNA recombination; Complete proteome.
SEQUENCE 296 AA; 32728 MW; ASB3DS40F162BE72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. ....
                                                                                                                                                                       (By similarity).
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                                                                                                                                                                                                                                                                                                                  EMBL; AP003595; BAB75874.1; -.
                                                                                                                                                                                                                                                                                                                                            HAMAP; MF 00201; -; 1.
InterPro; IPR003717; RecO.
Pfam; PF02565; RecO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                              AH2327; AH2327.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 DASWL 260
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NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 DASWL 6
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THTM_HUMAN
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Cilibers (Y., Fer, J. M., Fenders, R., French L., Garner A.A.,

R. Marin R. E., Hall-Tranging G., Ferdersche M. H., Hologa A.,

R. Hunt S.E., Hall-Tranging G., Fer, Levershe M.A., Libord C.,

R. Hunt S.E., Hall-Tranging G., Fer, Levershe M.A., Libord C.,

R. Hunt S.E., Hall-Tranging G., Levershe M.A., Libord C., Libord D.T.,

R. Harry I.D., Mashreshi-Hohamadi M., Matthewa L.H., Mcchann O.T.,

R. Harry I.D., Mashreshi-Hohamadi M., Matthewa L.H., Mcchann O.T.,

R. Harry I.D., Mashreshi-Hohamadi M., Matthewa L.H., Mcchann O.T.,

R. Harry I.D., Mashreshi-Hohamadi M., Matthewa L.H., Mcchann O.T.,

R. Harry I.D., Mashreshi-Hohamadi M., Matthewa L.H., Mcchann O.T.,

R. Soderlund C., Spragon L., Steward C.A., Sulten J.E., Minning L.,

R. Millama S., Manasa M., Mallaman H., Millam M., Millam B.,

R. Millama S., Shawasa M., Young S.A., Williaman H., Millam B.,

R. Minnen S., Shawasa M., Young S.A., Millaman H., Mallam B.,

R. Minnen S., Shawasa M., Wang Z., M., Matthewa S., Manasa S., Don T.,

R. Minnen S., Shawasa M., Wang S., Lin S.-P., Loh P., Mahaj E., Salan D., Song L.,

R. Minnen S., Shawasa M., Wang S., Lin S.-P., Loh P., Mahaj E., Mallam S., Shawasa M.,

R. Man M., Zhang G., Changone S., Lin S.-P., Loh P., Mahaj E., Salan D., Song L.,

R. Man M., Shang G., Mang S., Lin S.-P., Loh P., Mahaj E., Shawasa M.,

R. Man M., Shang G., Mang S., Lin S.-P., Loh P., Mahaj E., Shawasa M.,

R. Man M., Shang G., Mang S., Lin S.-P., Loh P., Mahaj E., Shawasa M.,

R. Man M., Shang G., Mang S., Lin S.-P., Loh P., Mahaj E., Shawasa M.,

R. Man M., Shang G., Mang S., Lin S.-P., Loh P., Mahaj E., Shawasa M.,

R. Man M., Shang G., Mang S., Lin S.-P., Loh P., Mahaj E., Shawasa M.,

R. Man M., Shang G., Mang S., Lin S.-P., Loh P., Mahaj E., Shawasa M.,

R. Man M., Shang G., Mang S., Lin S.-P., Loh P., Mahaj E., Shawasa M.,

R. Man M., Shang G., Mang S

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MEDLINE=95332330; PubMed=7608189;
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Matches
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nagahara N., Nishino T., "Rolles in the active site of rat liver "Rolle of amino acid residues in the active site of rat liver mercaptopyruvate sulfurtransferase. CDNA cloning, overexpression, and site-directed mutagenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                    GO; GO:000440; P:cyanate catabolism; TAS.
GO; GO:0009440; P:cyanate catabolism; TAS.
GO; GO:0009563; P:response to toxin; TAS.
GO; GO:0009655; P:response to toxin; TAS.
InterPro; IPR001763; Rhodanese...
InterPro; IPR001307; Rhodanese...
R Ffam; PR00581; Rhodanese; 2.
SMART; SM00450; RHODANESE 1; 1.
PROSITE; PS00683; RHODANESE 1; 1.
R PROSITE; PS00683; RHODANESE 2; 1.
R PROSITE; PS00683; RHODANESE 2; 1.
R PROSITE; PS00683; RHODANESE 2; 1.
R PROSITE; PS00683; RHODANESE 2; 1.
R Transferase; Repeat. 0 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                         RHODANESE 2.
SUBSTRATE (MERCAPTOPYRUVATE) BINDING
                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY).
SUBSTRATE (MERCAPTOPYRUVATE) BINDING
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Pred. No. 1.2e+02;
0: Mismatches 0; Indels
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15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
3-mercaptopyruvate sulfurtransferase (EC 2.8.1.2) (MST).
                                                                                                                                                                                                                                                                                                                                                                                                                   247 247 BY SIMILARITY.
45 47 RRE -> TQ (IN REF. 1).
296 AA; 33047 MW; 1991F0PICAE8C8E1 CRC64;
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STRAIN=Wistar; TISSUE=Liver;
MEDLINE=97066916; PubMed=8910318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE OF 8-76 AND 146-284, AND CHARACTERIZATION.
STRAIN=Wistar; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                        EMBL; BC003508; AAH03508.1; -. EMBL; BC016737; AAH16737.1; -. EMBL; BC018717; AAH18717.1; -.
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100.0%;
                                                                                  EMBL; X59434; CAA42060.1; -. EMBL; Z73420; CAA97763.1; -.
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                                                                                                                                                                  Genew; HGNC:7223; MPST.
MIM; 602496; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat)
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159
287
187
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Best Local Similarity
Matches 5; Conserv
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HSSP; P00586; 1RHS
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Nagahara N., Okazaki T., Nishino T.; "Cytosolic mercaptopyruvate sulfurtransferase is evolutionarily related to mitochondrial rhodanese. Striking similarity in active site amino acid sequence and the increase in the mercaptopyruvate sulfurtransferase activity of rhodanese by site-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R->G: LARGE DECREASE IN MST ACTIVITY;
SOME DECREASE IN RHODANESE ACTIVITY.
R->G: DECREASED MST ACTIVITY; INCREASED
RHODANESE ACTIVITY.
C->S: LOSS OF BOTH MST AND RHODANESE
ACTIVITIES.
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S->K: SLIGHT DECREASE IN MST ACTIVITY;
                                                                                                                                           J. Biol. Chem. 270:16230-16235(1995).
-!- FUNCTION: TRANSFERS A SULFUR ION TO CYANIDE OR TO OTHER THIOL COMPOUNDS. ALSO HAS WEAK RHODANESE ACTIVITY. MAY HAVE A ROLE IN CYANIDE DECRADATION OR IN THIOSULFATE BIOSYNTHESIS.
-!- CATALYTIC ACTIVITY: 3-mercaptopyruvate + cyanide = pyruvate +
                                                                                                                                                                                                                                                                                     -i- SUBUNIT: MONOMER OR DISULFIDE-LINKED HOMODIMER.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC (MOSTLY) AND MITOCHONDRIAL.
-i- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR
CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOMEVER,
THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
-i- PTM: THE N-TERMINAL IS BLOCKED.
-i- SIMILARITY: Contains 2 rhodanese domains.
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S->A: SLIGHT DECREASE IN MST ACTIVITY.
0BCC176AC14C717C CRC64;
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Pred. No. 1.2e+02;
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InterPro; IPR001307; Rhodanese.
Pfam; PF00581; Rhodanese; 2.
SMART; SM00450; RHOD, 2.
PROSITE; PS00380; RHODANESE 1; 1.
PROSITE; PS00683; RHODANESE 2; 1.
PROSITE; PS00683; RHODANESE 2; 1.
PROSITE; PS50206; RHODANESE 3; 2.
Transferase; Mitochondrion; Repeat.
INIT MET 0 0 0
DOMAIN 24 143 RHODANESE
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296 AA; 32809 MW;
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                                                                                                                       mutagenesis.";
J. Biol. Chem.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUTAGENESIS OF ARG-186 AND LYS-249.

MEDLINE=94179198; PubMed=8132546;
Luo G.-X., Horowitz P.M.;

"The sulfurtransferase activity and structure of rhodanese are affected by site-directed replacement of Arg-186 or Lys-249.";
J. Biol. Chem. 269:8220-8225(1994).
-!- FUNCTION: FORWATION OF IRON-SULFUR COMPLEXES AND CYANIDE DETOXIFICATION. BINDS MOLECULAR OXYGEN AND SULFUR.
-!- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.
-!- SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-19007483; PubMed-691057;
Ploegman J.H., Drent G., Kalk K.H., Hol W.G.J.;
"Structure of bovine liver rhodanese. I. Structure determination at 2.5-A resolution and a comparison of the conformation and sequence of its two domains.";
                                                                                                                                                                                                                         MEDLINE=91161544; Pubmed=2002017;
Miller D.M., Delgado R., Chirgwin J.M., Hardies S.C., Horowitz P.M.;
Expression of cloned bovine adrenal rhodanese.";
J. Biol. Chem. 266:4686-4691(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
-1- TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.
-1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER, THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
-1- SIMILARITY: Contains 2 rhodanese domains.
                                                                                             Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=79948424; PubMed=711737;
Russell J., Weng L., Keim P.S., Heinrikson R.L.;
"The covalent structure of bovine liver rhodanese. Isolation and
partial structural analysis of cyanogen bromide fragements and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98437562; PubMed=9761843; Galbulich F., Berna L., Zanotti G.; Structure of sulfur-substituted rhodanese at 1.36-A resolution."; Acta Crystallogr. D 54:481-486(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=79048425; PubMed=711738; Weng L., Heinrikson R.L., Westley J.; Wacrive site cysteinyl and arginyl residues of rhodanese. A novel formation of disulfide bonds in the active site promoted by
01-AUG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete sequence of the enzyme."; J. Biol. Chem. 253:8102-8108(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 253:8109-8119(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Mol. Biol. 123:557-594(1978).
                                                                                taurus (Bovine).
                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-294.
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                       NCBI_TaxID=9913;
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EMBL; M58561; AAA30753.1; -.

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(BY SIMILARITY).
SUBSTRATE (THIOSULFATE) BINDING
(BY SIMILARITY).
MISSING (IN SOME PREPARATIONS, BUT THESE
STILL EXHIBIT COMPLETE ENZYME ACTIVITY).
K->L: REDUCED RHODANESE ACTIVITY.
K->A: NO RHODANESE ACTIVITY.
                                                                                                         RHODANESE 2.
MAY PLAY A ROLE IN SUBSTRATE BINDING.
                                                                                                                           SUBSTRATE (THIOSULFATE) BINDING
                                          Interer; IPR001763; Rhodanese-like.
InterPro; IPR001307; Rhodanese.
InterPro; IPR001307; Rhodanese.
Pfam; Pr00581; Rhodanese; 2.
SMART; SM00450; RHOD; 2.
PROSITE; PS00080; RHODANESE 1; 1.
PROSITE; PS00080; RHODANESE 2; 1.
PROSITE; PS00063; RHODANESE 3; 2.
Transferase; Mitochondrion; 3D-structure; Repeat.
                                                                                                                                                                       D -> N (IN REF. 2).
N -> D (IN REF. 2).
D -> N (IN REF. 2).
                                                                                              RHODANESE 1.
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    1RHD; 27-JAN-84.

1RHS; 21-JAN-98.

20RA; 01-40G-96.

10RB; 15-0CT-95.

1BOH; 27-APR-99.

1BOI; 27-APR-99.
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Search completed: February 18, 2004, 14:28:08 Job time : 4.55263 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB_COVATY,

X MEDLINE=96.06946, PubMed=8535164;

A Trevino R.J., Hunt J., Horowitz P.M., Chirgwin J.M.;

A Trevino R.J., Hunt J., Horowitz P.M., Chirgwin J.M.;

Trevino R.J., Hunt J., Horowitz P.M., Chirgwin J.M.;

Trevino R.J., Hunt J., Horowitz P.M., Chirgwin J.M.;

Trevino R.J., Hunt J., Horowitz P.M., Chirgwin J.M.;

Thinself R. Chirach R. Chirach R. Complexes AND Cyanible Protein Exp. Purif. 6:693-699(1995).

C -1 FUNCTION: FORMATION OF IRON-STILFUR COMPLEXES AND CYANIDE DETOXIFICATION. BINDS MOLECULAR OXYGEN AND SULFUR.

C -1 CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.

C -1 SUBCELULAR LOCATION: Mitochondrial matrix.

C -1 SUBCELULAR LOCATION: Mitochondrial matrix.

C -1 SUBCELULAR LOCATION: Mitochondrial matrix.

C -1 SUBLINIT: MORDOMER CONSISTS OF 2 DOMAINS OF UNIGIN. HOWEVER,

THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.

THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                     .
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1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Thiosulface sulfurtransferase (EC 2.8.1.1) (Rhodanese).
                                                                                                                                                                                                                                                                      33164 MW; C8769696FA6AC111 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 AA.
                                                                                                                                                                                                                                                                                                                                             100.0%; Preu. ...
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PROSITE; PS00683; RHODANESE 2; 1.
PROSITE; PS50206; RHODANESE 3; 2.
Transferase; Mitochondrion; Repeat.
INIT MET 0 BY SIMILARI:
DOMAIN 24 142 RHODANESE 1.
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100.0%; Pred. No.
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InterPro; IRP001307; Rhodanese.
Pfam; PF00581; Rhodanese; 2.
SMART; SM00450; RHOD; 2.
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                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
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                                                                                                                                                                                                                                                                      296 AA;
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Matches 5
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RHODANESE 2.
RHODANESE 2.
MAY PLAY A ROLE IN SUBSTRATE BINDING (BY SIMILARITY).
BY SIMILARITY.
SUBSTRATE (THIOSULFATE) BINDING (BY SIMILARITY).
SUBSTRATE (THIOSULFATE) BINDING (BY SIMILARITY).
(BY SIMILARITY).
WM; 8811022BF9BAD666 CRC64;
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                                                                                                                                     Length 296;
                                                                                                                                   87.9%; Score 29; DB 1; Length 296
100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                              296 AA; 33205 MW;
                                                                                                                                                              5; Conservative
   158
287
186
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Best Local Similarity
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                                                                                                                                                                                    1 LDASW 5
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ACT_SITE
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                          ACT_SITE
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Query Match
Best Local Similarity 83.34;
S; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Appli
Sequence 124, App
Sequence 123, App
Sequence 22578, A
Sequence 26048, A
Sequence 16758, A
Sequence 16758, A
Sequence 1825, A
Sequence 254, App
Sequence 254, App
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Sequence 25, Appl
Sequence 2619, A
Sequence 27306, A
Sequence 17, Appl
Sequence 17, Appl
Sequence 244, Appl
Sequence 244, Appl
Sequence 354, Appl
Sequence 354, Appl
Sequence 395, Appl
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Sequence 27758, A
Sequence 4, Appli
Sequence 5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                           (without alignments)
35.929 Million cell updates/sec
                                                                             February 18, 2004, 14:16:39 ; Search time 7.06579 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                           1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-370-818-123
US-09-252-991A-12578
US-09-252-991A-16758
US-09-252-991A-16758
US-09-252-991A-17616
US-09-252-991A-17616
US-09-252-991A-17616
US-09-205-291A-17616
US-09-205-291A-17616
US-09-2138-52
US-09-223-991A-27306
US-09-252-991A-27306
US-09-252-991A-27306
US-09-252-991A-18661
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US-09-252-991A-27758
US-08-790-137-4
US-08-824-874-5
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US-09-732-210-395
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                                                                                                                                                                                                                              328717 segs, 42310858 residues
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                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                 Issued Patents AA:*
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Maximum DB seq length: 200000000
                                                                                                                                US-09-643-260-10
33
1 LDASWL 6
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Match Length
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Sequence 16, Application US/08985916
Sequence 16, Application US/08985916
Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence Sequence Applicant: APPLICANT: ATSUSHI HAYAKAWA, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: OBLON, SPIYAK, MCCLELLAND, MAIER & NEUSTADT, P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
COUNTRY: VA
                                                             Sequence 22260, A Sequence 22260, A Sequence 22260, A Sequence 2, Appli Sequence 7, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 30, Appli Sequence 30, Appli Sequence 30, Appli Sequence 23, Appli Sequence 23, Appli
                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUNTRY ARLINGTON
CULTIFICATION
CULTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,916
FILING DATE: 05-DEC-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: UP 8-325658
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION TOPPAGE 2220
US-08-807-151-5
US-09-210-084-5
US-09-210-084-5
US-09-764-762-5
US-09-252-991A-22260
US-08-58-991A-18153
US-08-694-915-2
US-08-694-915-4
US-08-694-915-4
US-08-694-915-4
US-09-614-328-285
US-09-614-328-285
US-09-634-295-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 919 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
 , MOLECULE TYPE: protein US-08-985-916-16
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Gaps

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Score 30; DB 3; Length 919; Pred. No. 1.2e+03; 1; Mismatches 0; Indels

90.9%;

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                                                                                                                                                                                                                                                                                               APPLICANT: Christenson, Anna C.
APPLICANT: Christenson, Anna C.
APPLICANT: O'Toole, Paul W.
APPLICANT: No'Toole, Paul W.
APPLICANT: Reid, Julian R.
APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: 1000.1043 U.
CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6444425

GENERAL INPORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roadoh
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
FILE REPERENCE: 210121-475C1
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09
EARLIER FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
NUMBER OF SEQ ID NOS: 289
SOSTWARE: FRASEDE FOR WINDOWS VERSION 3.0
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Pred. No. 2.9e+02;
0; Mismatches 0; Indels
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100.0%; Pred. No. 2.5e+02;
iive 0; Mismatches 0;
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US-09-634-238-354
; Sequence 354, Application US/09634238
; Patent No. 6544772
; RENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Lactobacillus rhamnosus US-09-634-238-354
                                                                                                                                 Glenn, Matthew
Havukkala, Ilkka J.
Bloksberg, Leonard, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.98;
                                                                                                                                                                                                                                     Lubbers, Mark W.
Dekker, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 87.9
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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; ORGANISM: Homo sapien
US-09-370-838-123
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LENGTH: 136
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APPLICANT:
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                                                                                     APPLICANT: IZUI, Hiroshi
APPLICANT: ONO, Eiji
APPLICANT: ONO, Eiji
APPLICANT: MATSUI, Kazuhiko
APPLICANT: MATSUI, Kazuhiko
APPLICANT: HTO, Hisao
APPLICANT: HTO, Hisao
APPLICANT: HTO, Hisao
TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GI
TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GI
TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GI
TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GI
CURRENT PRILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1998-10-19
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 3
LENGTH: 935
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APPLICANT: IZUI, HITCSHI
APPLICANT: IZUI, HITCSHI
APPLICANT: MATSUI, Kazuhiko
APPLICANT: MATSUI, Kazuhiko
TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GL
TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GL
TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GL
TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GL
TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GL
TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GL
TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GL
TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GL
TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GL
TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GL
TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GL
TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GL
TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GLUTAMIC APPLICATION NUMBER: US99-03-18
PRIOR FILING DATE: 1998-10-19
PRIOR FILING DATE: 1998-10-19
PRIOR FILING DATE: 1998-10-19
PRIOR FILING BACTERIUM AND METHOD FOR PRODUCING L-GLUTAMIC APPLICATION NUMBER: JP90-03-18
PRIOR FILING BACTERIUM ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GLUTAMIC APPLICATION NUMBER: JP90-03-18
PRIOR FILING BACTERIUM ACID-PRODUCING BACTERIUM ACID-PRODUCING BACTERIUM ACID-PRODUCING BACTERIUM ACID-PRODUCING BACTERIUM ACID-PRODUCING BACTERIUM ACID-PRODUCING BACTERIUM ACID-PRODUCING BACTERIUM ACID-PRODUCING BACTERIUM ACID-PRODUCING BACTERIUM ACID-PRODUCING BACTERIUM ACID-PRODUCING BACTERIUM ACID-PRODUCING BACTERIUM ACID-PRODUCING BACTERIUM ACID-PRODUCING BACTERIUM ACID-PRODUCING BACTERIUM ACID-PRODUCING BACTERIUM ACID-PRODUCING BACTERIUM ACID-PRODUCING BA
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   Sequence 3, Application US/09271438A
Patent No. 6331419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Enterobacter agglomerans
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Patent No. 6331419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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                                                                    GENERAL INFORMATION:
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US-09-252-991A-17616

Sequence 17616, Application US/09252991A

Sequence 17616, Application US/09252991A

Sequence 17616, Application US/09252991A

Patent No. 6551798

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARGUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ASRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ASRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18225, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18225
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                                                                                                                                                                                       Score 29; DB 4; Length 438; Pred. No. 9e+02;
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                                                                                                                                                                                                                                             0; Mismatches
                                                                                           ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16758
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US-09-252-991A-17616
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83.3%;
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                    NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16758
LENGTH: 438
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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PRIOR FILING DATE:
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US-09-252-991A-18225
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APPLICANT: Warc J. Rubenfield et al.

APPLICANT: Warc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERCIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

REIOR PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26048
                                   APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AUCIENCA ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PEPLICATION NUMBER: US 60/09/25.991A
CURRENT FILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 194
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Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TURNENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: US 60/094,190
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Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Matches 5; Conservative
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US-09-252-991A-16758
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APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007Pl
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EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
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CURRENT FILING DATE: 1998-12-04
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048, 971
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048, 964
APPLICATION NUMBER: 60/048, 964
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,375
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PLICATION NUMBER: 60/048,876
LING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,915
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PPLICATION NUMBER: 60/049,019
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PPLICATION NUMBER: 60/048,970
ILING DATE: 1997-06-06
ILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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NG DATE: 1997-06-06
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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LING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,900
FILING DATE: 1997-06-06
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ILING DATE: 1997-06-06
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MILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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                                                                                                             US-09-205-258-254
; Sequence 254, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
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LOCATION: (4)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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NAME/KEY: SITE
LOCATION: (12)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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APPLICANT: MONTERNINI, LAURA
APPLICANT: MOLTO, MARIA D
APPLICANT: Koenig, Michael
APPLICANT: Campuzano, Victoria
APPLICANT: Campuzano, Victoria
APPLICANT: Cossee, Mirchile
ITULE OF INVENTION: Direct Diagnosis of Friedreich Ataxia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 128;
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4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (128)
; OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-254
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Pred. No. 4e+02
0; Mismatches
                                                                                                         EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
                                                                                                                                                                                                                                                                                                                  EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SEQ ID NO 254
LENGTH: 128
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,883
                                             FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08611587; Patent No. 6150091; GENERAL INFORMATION:
                                                                                             FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.8%;
83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 LDISWL 19
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NAME/KEY: SITE
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NAME/KEY: SITE
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APPLICANT: CHRISTIAN, Peter D.
TITLE OF INVENTION: RECOMBINANT HELICOVERPA BACULOVIRUSES
TITLE OF INVENTION: EXPRESSING HETEROLOGOUS DNA
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                 SITELIA OUT ISLIED, NA CITY: Washington STATE: District of Columbia COWTRY: USA CONTRY: USA COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Floppy disk COMPUTER: PatentIn Release #1.0, Version #1.30 CURRANT APPLICATION DATA: APPLICATION NUMBER: US/09/029,213B FILING DATE: 31-AUG-1998 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION: NUMBER: 41,455 REGISTRATION: WINDER: 41,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28; DB 3; 3
Pred. No. 9.9e+02;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50179-048
                                                                                                                                                  ADDRESSEE: McDermott, Will & Emery
STREET: 600 13th Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-756-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-756-8087
INFORMATION FOR SEQ ID NO: 25:
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LENGTH: 323 amino acids
TYPE: amino acid
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Best Local Similarity 83.3
Matches 5; Conservative
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MOLECULE TYPE: protein
US-09-029-2138-25
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191 LDSSWI 196
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LENGTH: 342
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Sequence 52, Application US/09247373B
Patent No. 6168954
GENERAL INFORMATION
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
FRIOR APPLICATION NUMBER: 08/924,747
NUMBER OF SEQ ID NOS: 56
NUMBER OF SEQ ID NOS: 56
SOFTWARE: MICROSOft Office 97
LENGTH: 219
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Best Local Similarity 66.7%; Pred. No. 6.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,587
FILING DATE: 03-MAR-1996
CLASSIFICATION: 436
ATTORNEY/ACTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                      CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Brashears-Macatee, Sarah J.
RECISTRATION NUMBER: 38,087
REPERENCE/DOCKET NUMBER: D-5901
TELEPOMNINICATION INFORMATION:
TELEFAX: 713-651-5620
TELEFAX: 713-651-5620
TELEFAX: 76-2829
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acide
TYPE: amino acid
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: Innear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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; Setten No. 6180098; GENERAL INFORMATION:
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Best Local Similarity 83.3%;
Matches 5; Conservative
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POSITION IN GENOME:
UNITS: bp
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102 LDAAWI 107
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; ORGANISM: SOYBEAN
US-09-247-373B-52
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US-09-247-373B-52
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Length 323;

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GENERAL INFORMATION:

APPLICATION BOTH TO US/09328352

GENERAL INFORMATION:

APPLICAN: GARY L. Breton et al.

ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

ITILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION VUBBER: US/09/328,352

CURRENT APPLICATION VUBBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252
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83.3%; Pred. No. 1e+03;
ive 0; Mismatches 1; Indels
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: February 18, 2004, 14:41:48 Job time : 7.06579 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Acinetobacter baumannii
US-09-328-352-5861
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February 18, 2004, 14:09:39; Search time 17.3684 Seconds (without alignments) 89.145 Million cell updates/sec
                                                                                                                                                                                                                                                                                                          830525
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                       830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fungi:*
sp_human:*
sp_nwertebrate:*
sp_mamma1:*
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sp_vertebrate:*
sp_unclassified:*
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sp_phage:*
sp_plant:*
sp_rodent:*
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Maximum DB seq length: 200000000
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40
1 LNWSWL 6
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                                                                                                                                                          Title:
Perfect score:
Sequence:
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                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		Q9b964 ceratosolen	Q9gv77 lytechinus	O9ker2 bacillus ha	Q92mu7 rhizobium m	OBub44 agrobacteri		Q8fle3 leptospira	Q9epg8 rattus norv	Q9lby3 shewanella	Q8xya4 ralstonia s	047545 chlamydomon	Q9fed7 oryza sativ	Q8hlg1 parazen pac	Q8hl32 aptocyclus	08zl24 salmonella	Q8z2j8 salmonella
SUMMARIES		Q9B964	Q9GV77		Q92MU7	Q8UB44	Q9WRS0	Q8F1E3			Q8XYA4	_		QBHLG1	Q8HL32	. Q8ZL24	082238
* Query Match Length DB		526 8	03		11 16	37 16	64 12				330 16		42 10	8 09	8 09	60 16	60 16
Leng	1		31	~													
* Query Match	-	95.0	95.0	92.5	92.5	92.5	92.5	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0
Score		38	38	37	37	37	37	36	36	36	36	36	36	36	36	36	36
Result No.		7	8	m	4	ហ	9	7	80	σ	10	11	12	13	14	15	16

	Q8fp18 corynebacte	anto	300 800	Q99k28 mus musculu	œ	Q9i496 pseudomonas		Q8g651 bifidobacte	073637 fugu rubrip	ч			Q8d964 vibrio vuln	Q22375 caenorhabdi	Q94515 drosophila	Q98134 rhizobium l	O47815 geomys pers	Q95kvl bos taurus	Q8bci2 gremmeniell	m			O59898 ampelomyces	O9p8j3 coniothyriu	O87032 vibrio chol	Q8clu5 mus musculu	Q9k4k4 streptomyce	Q96eq6 homo sapien	
		O	ОЭЛН1	Q99K28						068039	005744	OBIOTO	Q8D964	022375	094515	Q98134	047815	Q95KV1	QBBCI2	QBCBT3	Q95KV0	Q9P491	059898	Q9P8J3	087032	QBC1US	Q9K4K4	903960	
	-					90 16					35 2			80 5			8 66	40 6	741 12			70 3				٦	51 16		
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36	36	36	36	36	36	36	36	36	36	32	35	35	35	35	35	35	35	35	35	35	35	35					34	34	
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

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PRELIMINARY; PRT; 526 AA. (Tremblrel. 17, Created) (Tremblrel. 17, Last sequence update) (Tremblrel. 17, Last sequence update) xidase subunit I (EC 1.9.3.1) (COI) (Cytochron Industry and Industry	RESULT 1 OBBS64 DE GOBS64 OBBS65 OL-JUN-2001 (TrEMBLrel. 17, Last sequence update) OL-JUN-2001 (TrEMBLrel. 17, Last sequence update) OL-JUN-2001 (TrEMBLrel. 17, Last sequence update) OL-OCT-2002 (TrEMBLrel. 22, Last annotation update) OL-OCT-2002 (TrEMBLrel. 22, Last annotation update) OL-OCT-2002 (TrEMBLrel. 22, Last annotation update) OL-OCT-2002 (TrEMBLrel. 22, Last annotation update) OC Statcosolen nanus. OC Gratcosolen nanus. OC Gukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Noblera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Noblera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Noblera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Noblera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Noblera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Noblera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Noblera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Metalial Daya sequences and morphology; C GTALIATION; CTYOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY C CATALITIC SUBMIT OF THE BINETALLIC CENTER PORMED BY HEME AS AND COPERR B (BY SIMILARITY). C CATALITIC SHOUTY OF THE BINETALLIC CENTER PORMED BY HEME AS AND COPERR B (BY SIMILARITY). C C CATALITIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME C C A 2 H(2) O. C A 2 H(2) O.
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Gaps

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RESULT 2 Q9GV77

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STRAIN=101;

MEDLINE=21396507; PubMed=11481430;

Kapala D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

A Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

A Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,

Rodrie T., Fortetelle D., Puehler A., Purnelle B., Ramsperger U.,

Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;

"Analysis of the chromosome sequence of the legume symbiont

Sinorhizobium meliloti strain 1021.";

FMBL; AL591790; CAC47091.1;

RMBL; AL591790; CAC47091.1;

RMBL; PRO0528; BPD transp; 1.

RPROSITE; PSO0402; BPD transp; 1.

RPROSITE; PSO04001; BPD TRANSP_INN_MEMBR; 1.

COMPLEE PORCEOME.

SEQUENCE 311 AA; 34300 MW; 48F3487341A2C198 CRC64;
                                                                                                                                                     "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                           Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 22, Last annotation update)
Putative sugar transport system permease ABC transporter protein.
R02512 OR SMC01978.
Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 16; Length 204;
Pred. No. 1.5e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.5%; Score 37; DB 16; Length 311;
83.3%; Pred. No. 2.3e+02;
.ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                      EMBL; AP001509; BAB04506.1; -.
InterPro; IPR006938; DUF624.
Pfam; PF04884; DUF624.
Hypothetical protein; Complete proteome.
SEQUENCE 204 AA; 23786 MW; 7C476B67E71015E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
ABC transporter, membrane spanning protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    337 AA.
                                               MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                            92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
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  SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 LNWAWL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNWAWL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LINWSWL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LNWSWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8UB44;
01-JUN-2002 (
01-JUN-2002 (
01-OCT-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q92MU7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8UB44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8UB44
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                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lytechinus variegatus (Sea urchin).
Bukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Temnopleuroida, Toxopneustidae,
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Embryonic blastocoelar extracellular matrix protein precursor.
                         PROSITE; PS00077; COX1; 1.
Copper; Electron transport; Heme; Inner membrane; Membrane;
Oxidoreductase; Respiratory chain; Transmembrane; Transport;
                                                                                                                                                                                                             Score 38; DB 8; Length 526;
Pred. No. 2.6e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 38; DB 5; Length 3103; 83.3%; Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
WW; 79D7EBEDE1C54393 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=86665;
                                                                                                                              NON TER 1 1 SEQUENCE 526 AA; 59586 MW; 587FE82D8C4F2B62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
BH0787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 3103 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=20340282; PubMed=10885756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 3103 AA; 343770 MW;
PR01165; CYCOXIDASEI.
                                                                                                                                                                                                             Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1724 LNWSWI 1729
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                               10 INWSWL 15
                                                                                                                                                                                                                                                                                                                           1 LNWSWL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7654;
                                                                                                          Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lytechinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9KER2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9GV77
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Desrosiers R.C.;

"The primary sequence of rhesus monkey rhadinovirus isolate 26-95:
"The primary sequence of kaposi's sarcoma-associated herpesvirus and rhesus monkey rhadinovirus isolate 17577.";

J. Virol. 74:3388-3398(2000).

EMBL, AP0210726; AAP001138.1;

Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                         Alexander L., Denekamp L., Knapp A., Auerbach M.R., Damania B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.5%; Score 37; DB 12; Length 464; 83.3%; Pred. No. 3.38+02; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
Michaelis M.L., Hadwiger G.H., Islam S.I., Kumar K.N.;
Submitred (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U53512, AAG38872.1; -.
InterPro; IPR000456; Ribosomal_L17.
Pfam; PF01196; Ribosomal_L17.
                                                                                                                                                                                                                                                                                                                                                                                                                                         464 AA; 51993 MW; ADB519AE96F511E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 AA; 23460 MW; 14775910CB7BB668 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAR-2003 (TrEMBLrel. 23, Created)
1-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Fruiting body developmental protein S-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Brain Na++/Ca++ exchanger-associated protein.
                                     SPECIES-Macaca mulatta rhadinovirus 26-95;
STRAIN-MACACA MULATTA RHADINOVIRUS ISOLATE 26-95;
MEDLINE-20173730; PubMed=10708456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.0%; Score 36; DB 16; L
100.0%; Pred. No. 2.2e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE011481; AANS0391.1; -. Complete proteome. SEQUENCE 207 AA; 23460 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 83.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100 es 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leptospira interrogans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397 VNWSWL 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 NWSWL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LINWSWL 6
             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LA3193.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ren S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9EPG8;
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Q8F1E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
Q9EPG8
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Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Goodner B., Hinkle G., Gattung S., Miller N., Halling C., Mullin L.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.,
"Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
Science 294:2223-2228(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                    MEDLINE=2160856; PubMed=11743193;
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Kaymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Nester E.W.,
Mester E.W.,
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SPECIES=Macaca mulatta rhadinovirus 17577;
MEDLINE=99174001; PubMed=10074154;
MEDLINE=99174001; PubMed=10074154;
Searles R.P., Berguence and genomic analysis of a Rhesus macaque rhadinovirus with similarity to Kaposi's sarcoma-associated herpesvirus/human herpesvirus 8.";
J. Virol. 73:3040-3053(1999).
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ATU3173 OR AGR L_3272.
grobacterium tumefaciene (strain C58 / ATCC 33970).
Bacteria, Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizoblaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.5%; Score 37; DB 16; Length 337; 83.3%; Pred. No. 2.4e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE009247; AA443989.1; -.
EMBL; AE008366; AAK90213.1; -.
InterPro; IPR000515; BPD transp.
Pfam; PF00529; BPD transp; 1.
PROSITE; PS00402; BPD TRANSP_INN_MEMBR; 1.
Complete proteome.
SEQUENCE 337 AA; 37313 MW; 0F35E9A6E0D34813 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Hypotherical 52.0 kDa protein (ORF32).
Macaca mulatta rhadinovirus 17577, and
Macaca mulatta rhadinovirus 26-95.
Viruses; GBDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
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Best Local Similarity 83.3<sup>3</sup>
Matches 5, Conservative
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                                                                                                                              MCBI_TaxID=176299;
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InterPro; IPR005798; Cytb_b6_C.
InterPro; IPR005797; Cytb_b6_N.
Pfam; PF000032; cytochrome_D_C; 1.
Pfam; PF000133; cytochrome_D N; 1.
PROSITE; PS00193; CYTOCHROME_B_Q0; 1.
Electron transport; Heme; Respiratory chain; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
NCBI_TaxID=3053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=89145414; PubMed=948440;
Denovan-Wright B.M., Nedelou A.M., Lee R.W.;
Complete sequence of the mitochondrial DNA of Chlamydomonas eugametos.";
                                                                                                                                                                                                                             Score 36; DB 16; Length 330; Pred. No. 3.4e+02;
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100.0%; Pred. No. 3.9e+02;
ive 0; Mismatches 0; Indels
                                                                                        Probom; PD000131; Copper GuA; 1.
TIGREMAS; TIGRO1433; CyOA; 1.
Oxidoreductase; Complete proteome.
SEQUENCE 330 AA; 36117 MW; B82DF114452359E8 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Mol. Biol. 36:285-295(1998)
        EMBL, AL646067; CAD15560.1; -.
InterPro; IPR001505; Copper CuA.
InterPro; IPR006333; CyoA_II.
                                                                                                                                                                                                                             90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydomonas eugametos.
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                                                                                                                                                                                                                                                    Best Local Similarity
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"Pressure-regulation of a membrane-bound quinol oxidase in a deep-sea
piezophilic bacterium, Shewanella violacea.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB033827; BAA94864.1;
                                                                                                                          Gaps
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Probable transmembrane cytochrome O ubiquinol oxidase (Subunit II)
oxidoreductase protein (EC 1.10.3.-).
CYOA2 OR RSC1858 OR RS03418.
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Alteromonadaceae; Shewanella.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                           Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 90.0%; Score 36; DB 2; Length 254; Best Local Similarity 83.3%; Pred. No. 2.6e+02; Matches 5; Conservative 0; Mismatches 1; Indels
                                                                                                                    Indels
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InterPro; IPR006333; CyoA II.
ProDom; PD000131; Copper_Cua; 1.
TIGRPAMS; TIGR01431; CyoA; 1.
SEQUENCE 254 AA; 28657 MW; F1870460580AACED CRC64;
24405 MW; 3C9170304235B02D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Quinol oxidase subunit III.
                                                           Score 36; DB 11; I
; Pred. No. 2.2e+02;
0; Mismatches 0;
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                                                              90.0%; Score 36; 100.0%; Pred. No.
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MEDLINE=21681879; PubMed=11823852;
                                             Query Match
Best Local Similarity 100.0%;
Marches 5; Conservative 0
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                                                                                                                                                                                                                             126 LNWSW 130
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                                                                                                                                                                          1 LNWSW 5
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           SEQUENCE
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Q8XYA4; Q8XYA4

RESULT 10

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Gaps

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SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534949; PubMed=11677609;
MCDLINE=21534949; PubMed=11677609;
MCDLINE-21534949; PubMed=11677609;
MCDLIAND M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
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                                                                 Gape
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Miya M., Takeshima H., Endo H., Ishiguro N.B., Inoue J.G., Mukai T.,
Satoh T.P., Yamaguchi M., Kawaguchi A., Mabuchi K., Shirai S.M.,
Nishida M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Major Patterns of higher teleostean phylogenies: A new perspective based on 100 complete mitochondrial DNA sequences."; Mol. Phylogenet. Evol. 26:121-138(2002).
EMBL AP004443; BAC23666.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
Cottoidei; Cyclopteridae; Aptocyclus.
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Enterobacteriaceae, Salmonella.
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90.0%; Score 36; DB 8; Length 460; 100.0%; Pred. No. 4.7e+02; ive 0; Mismatches 0; Indels
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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Last annotation update)
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Matches 5; Conservative
                                                           5; Conservative
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Ouery Match
Best Local Similarity
Matches 5; Conserv
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Q8ZL24;
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Q8HL32
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Miya M., Takeshima H., Endo H., Ishiguro N.B., Inoue J.G., Mukai T.,
Satoh T.P., Yamaguchi M., Kawaguchi A., Mabuchi K., Shirai S.M.,
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MO1. Phylogenet. Evol. 26:121-138(2002).
EMBL, AP004433; BAC23537.1; -...
                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Zelformes; Parazenidae; Parazen.
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                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Nipponbare;
Saeaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0671811.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
P0001B06.11 protein (P0671B11.33 protein).
P0001B06.11 OR P0671B11.33.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Best Local Similarity 100.
Matches 5; Conservative
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Q8HLG1
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90.0%; Score 36; DB 16; Length 460;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
                  Maruré 413:852-856(2001).

EMBL; AE008876; AAL22633.1; -.

InterPro; IPPO1360; Glyco.hydro_1.

Pfam; PF00232; Glyco.hydro_1; 1.

PRINTS; PR00131; GLHYDRLASE1.

PROSITE; PR00550; Glyco.hydro_1; 1.

PROSITE; PR00572; GLYCOSYL_HYDROL; 1.

PROSITE; PR0572; GLYCOSYL_HYDROL; 1.

Hydrolase; Hypothetical protein; Complete proteome.

SEQUENCE 460 AA; 53173 MW; 1FCSF45D6E996709 CRC64;
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418 NWSWL 422
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Search completed: February 18, 2004, 14:35:46 Job time : 19.3684 secs

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96 NWSWL 100
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2 NWSWL 6
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METE BIFLO
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010919;
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                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                            (without alignments)
79.423 Million cell updates/sec
                                                                               February 18, 2004, 13:39:39; Search time 3.55263 Seconds
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           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compuc
                                                                                                                                                                                                                                     rotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                127863 seqs, 47026705 residues
                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METE BIFLO
RIRZ MYCLE
IKKA HUWAN
IKKA HUWAN
IKKB HUWAN
IKKB WOUSE
IKKB RAT
Y451 SYNY3
NOON PARDE
NUON RHOCA
TISD ECOLI
YAWD SCHPO
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BOVIN
HUMAN
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EMB_MOUSE
CYB_RHOSH
PHR_STRGR
NRAM_IAKIE
NRAM_IALEN
NRAM_IALEN
NRAM_IALEN
LAMB_BACSU
13RH_HAEIN
YQP4_CAEEL
                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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YEAST
TRYCR
SCHPO
                                                        - protein search, using sw model
                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                         Perfect score:
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                                                                 anopheles g
anopheles q
artemia san
cochliomyia
                                                                                                                                                                                    strongyloce
homo sapien
                        schizosacch
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vibrio chol
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
(EC 2.1.1.14) (Methionine synthase, vitamin.Bl2 independent isozyme)
(Cobalamin-independent methionine synthase).
METE OR BLO798
Bifidobacterium longum.
Bifidobacterium actionbacteria, Actinobacteridae, Bifidobacteriales;
Bifidobacteriaceae, Bifidobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                               P34836
P33506
Q37707
Q9mfp7
P12697
P15997
Q9br46
P81329
                     Q9p7m8
P27920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 90.0%; Score 36; DB 1; Length 204; Best Local Similarity 100.0%; Pred. No. 32; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Du Z., Waterston R.; Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hypothetical 23.6 kDa protein B0252.6 in chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U23453; AAC46760.1; -.
PIR, T15295; T15295.
Wormhep; B0252.c; CE02422.
Hypothetical protein.
SEQUENCE 204 AA; 23610 WW; 59FB15536CD22P43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 AA
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                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                              VGF1_IBVB
ATPB_ANOGA
ATPB_ANOGA
ATPB_ANOQU
ATPB_COLHO
ATPB_PARLI
ATPB_STRPU
CT78_HWAN
YE6A_METJA
ISPZ_VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last seq
01-0CT-1996 (Rel. 34, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
1053
1564
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thioredoxin.
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SEQUENCE
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METAL
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                                                                                                           HAMAP; MP 00172; -; 1.
InterPro; IPR005629; Methionine synt.
InterPro; IPR006576; Met syn Bl2ind.
Pfam; PF01717; Methionine synt; 1.
ProDom; PD004692; Methionine synt; 2.
TIGRFAMS; TIGR01371; met syn Bl2ind; 1.
Transferase; Methyltransferase; Methionine biosynthesis; Zinc; Repeat;
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Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
                                                         STRAIN=NCC 2705;
MEDLINE=22294977; PubMed=12381787;
Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Ribonucleoside-diphosphate reductase beta chain (EC 1.17.4.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corymebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1769,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 767;
1.2e+02;
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SIMILARITY).
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ZINC (BY SIMILARITY)
ZINC (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Ribonucleotide reductase small subunit). NRDF OR ML1731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.0%; Score 36; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE014702; AAN24613.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85358 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 90.0
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYCLE STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                  synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          767 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome.
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Q9CBQ2;
NAME OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                            FOR DNA SYNTHESIS (BY SIMILARITY).

CATALYTIC ACTIVITY: 2'-deoxyribonucleoside diphosphate + oxidized thioredoxin + H(2)0 = ribonucleoside diphosphate + reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IKKA HUMAN STANDARD; PRT; 745 AA.

O1511; O14666; O13132; O92467;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-Kappa-B kinase alpha (KKPA) (IKK-alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha) (IKK-Alpha)
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE RIBONUCLEOSIDE DIPHOSPHATE REDUCTASE SMALL CHAIN FAMILY. MORE SIMILAR TO ENTEROBACTERIAL NRDF THAN TO
                                                                                                                                                                                                               "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-i- FUNCTION: CATALYZES THE BLOSYNTHESIS OF DEOXYRIBONUCLEOTIDES FRO
THE CORRESPONDING RIBONUCLEOTIDES, PRECURSORS THAT ARE NECESSARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó,
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IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
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Pred. No. 71;
); Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- COFACTOR: BINDS 2 IRON IONS (BY SIMILARITY).
-!- PATHWAY: DNA replication pathway; first step.
-!- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
A80D29751183358B CRC64;
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PROSITE; PS00368; RIBORED SMALL; 1.
Oxidoreductase; DNA replication; Iron; METAL 73 73 IRON 1 (B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, P17424, 2R2F.
Leproma, ML1731, -.
InterPro, IPR000358, Ribonucl_redctse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL583923; CAC30684.1; -. PIR; E87125; E87125.
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107
164
198
201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 1
325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY)
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15 INWNWL 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LNWSWL 6
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ikk PHOSPHORYLATION.
MEDLINES-99038238; PubMed-9819420;
MEDLINES-99038238; PubMed-9819420;
MEDLINES-90138238; PubMed-9819420;
"Coordinate regulation of ItappaB kinases by mitogen-activated protein (Coordinate regulation of ItappaB kinases by mitogen-activated protein kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
Mol. Cell. Biol. 18:7336-7343(1998).
                                                                                           MEDLINE-97394468; PubMed-9252186;
DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
"A cytokine-responsive IkappaB Kinase that activates the transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delhase M., Hayakawa M., Chen Y., Karin M.;
"Positive and negative regulation of IkappaB kinase activity through
                                                                                                                                                                                                                                                                                                                                                                                                                                                 interacting proteins, contains a serine-threonine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ling L., Cao Z., Goeddel D.V., "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
                                                                                                                                                                   SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179
                                                                                                                                                                                        TISSUE=Cervical carcinoma;
MEDLINE=98008813; PubMed=9346484;
Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
Maran J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
"IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for NF-kappaB activation.";
                                                                                                                                                                                                                                                                                                   TISSUB=Heart;
MEDLINE=29032998; PubMed=9813230;
Hu M.C.-T., Wang Y.-P.;
"IkappaB kinase-alpha and -beta genes are coexpressed in adult and embryonic tissues but localized to different human chromosomes.";
                                    Σ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "NF-kappaB activation by tumour necrosis factor requires the Akt serine-threonine kinase."; Nature 401:82-85(1999).
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 32-745 FROM N.A.
TISSUE-Cervical carcinoma;
MEDLINE-96258477; Pubmed-8777433;
Connally M.A., Marcu K.B.;
"CHUK, a new member of the helix-loop-helix and leucine zipper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M.,
                                    Z., Rothe
kinase.";
           TISSUE=T.cell;
MEDLINE=97386461; PubMed=9244310;
MEGILINE=97386461; Song H.Y., Gao X., Goeddel D.V., Cao "Identification and characterization of an IkappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
 SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44
                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                families of interacting proteins, contactatalytic domain.", Cell. Mol. Biol. Res. 41:537-549(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99212141; PubMed=10195894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKKbeta subunit phosphorylation.";
Science 284:309-313(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99413720; PubMed=10485710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20178139; PubMed=10712233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND SER-180.
MEDLINE=98188283; PubMed=9520446;
                                                                                                                                                                                                                                                                Science 278:860-866(1997).
                                                                                                                                            Nature 388:548-554(1997).
                                                         Cell 90:373-383(1997).
                                                                                                                                                                                                                                                                                                                                                                Gene 222:31-40(1998).
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKKA-IKKB BINDING.
                                                                                                                                  factor NF-kappaB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Donner D.B.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           also as an homodimer. Directly interacts with IKK-GAMMA/NEWO.

Heterotdimers form the active complex. The tripartite complex can also bind to MAPSIA/NIK, MEKKI, IKAP and IKB-1Pha-P65-P50 complex. A weak interaction with TRAF2 cannot be excluded. Part of a complex composed of NCOA2, NCOA3, IKKB, IKBKG and CREBBP.

-!-SUBCELLULAR LOCATION: Cytoplasmic.
-!-TISSUB SPECIFICITY: Widely expressed.
-!-PIM: Phosphorylated by MAPSK14/NIK, AKT and to a lesser extent by MEKKI, and dephosphorylated by PP2A. Autophosphorylated.
-!-SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                               MEDLINE=21968797; PubMed=11971985; WCDA2; NCDA3; IKKB AND IKBKG. MEDLINE=21968797; PubMed=11971985; Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J., Malley B.W.; Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator activity by I kappa B kinase."; Mol. Cell. Biol. 22:3549-3561(2002).

-!- FUNCTION: Phosphorylates inhibitors of NP-kappa-B thus leading to the dissociation of the inhibitor/NP-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENZYME REGULATION: Activated when phosphorylated and inactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         when dephosphorylated.
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BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SEMPLYATION (BY PKB/AKT1).

PHOSPHORYLATION (BY MAP3K14).

T->A: LOSS OF PHOSPHORYLATION AND

DECREASE OF KINASE ACTIVITY.
"The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF012890; AAC51662.1; -...
EMBL; AF009225; AAC51671.1; -...
EMBL; AF009225; AAC50713.1; -...
EMBL; AF009225; AAC50713.1; -...
EMBL; U22512; AAC50713.1; -...
HSSP; Q63450; LA06.
Genew; HGMC:1974; CHUK.
MIM; 600664; -...
GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0003884; F:lkappaB kinase activity; TAS.
GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.
GO; GO:000725; P:lkappaB phosphorylation; TAS.
GO; GO:000755; P:lmmune response; TAS.
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InterPro; IPR00290; Ser thr pkinase.
InterPro; IPR00145; Tyr pkinase.
InterPro; IPR00145; Tyr pkinase.
Pfam; Pr00069; Prinase; I.
ProDom; PR001001; Prot kinase; I.
SMART; SM0020; S TKC; I.
SMART; SM00107; PROTEIN KINASE ATP; I.
PROSITE; PS00109; PROTEIN KINASE ATP; I.
PROSITE; PS001109; PROTEIN KINASE DOM; I.
PROSITE; PS00111; PROTEIN KINASE DOM; I.
Transferase; Serine/threonine-protein kinase; ATP-binding;
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LEUCINE-ZIPPER (POTENTIAL)
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                            Am. J. Physiol. 278:C451-C462(2000).
[11]
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                      G606B0; Q9D2X3;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1nhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
(I kappa-B kinase alpha) (IKBKA) (IKK-alpha) (IKK-A) (IkappaB kinase)
(I-kappa-B kinase 1) (IKM1) (Conserved helix-loop-helix ubiquitous kinase) (Nuclear factor NPkappaB inhibitor kinase alpha) (NPKBIKA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96044444; PubMed=7558004;
MocK B.A., Connelly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
MocK B.A., Connelly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
"CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human
chromosome 10 and mouse chromosome 19.";
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interacting proteins, contains a serine-threonine kinase
                                                                S->E: FULL ACTIVATION.
T->A: NO CHANGE IN PHOSPHORYLATION.
S->A: NO CHANGE IN PHOSPHORYLATION.
E -> G (IN REF. 2).
L -> R (IN REF. 5).
TS -> AY (IN REF. 5).
P -> A (IN REF. 5).
TS -> D (IN REF. 5).
TS -> D (IN REF. 5).
                 AUTOPHOSPHORYLATION.
PHOSPHORYLATION AND OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Connelly M.A., Marcu K.B., "CHUK, a new member of the helix-loop-helix and leucine zipper
KINASE ACTIVITY
                                                                                                                                                                                                                                     Score 35; DB 1; Length 745; Pred. No. 1.6e+02; 1; Mismatches 0; Indels
                                                                                                                                            AY (IN REF. 5).

A (IN REF. 3 AND 5).

DL (IN REF. 5).
                                                                                                                                                                                                      7A90B59BC98A56C2 CRC64;
LOSS OF P
LOSS OF P
                                                                                                                                                                                                                                                                                                                                                                                                                           745 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     catalytic domain.";
Cell. Mol. Biol. Res. 41:537-549(1996).
                                   S->A: LOS
ACTIVITY.
                 K->M:
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MEDLINE=96258427; PubMed=8777433;
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179
180
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604
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686
745 AA;
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738 LDWSWL 743
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                         1 LAWSWL 6
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 44
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176
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CHUK OR IKKA.
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Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynghaw-Boris A., Yoshida K., Haßegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nemoto S., Dibonato J.A., Lin A.; "Coordinate regulation of Ikappas kinases by mitogen-activated protein kinase kinase kinase kinase kinase kinase (1 MP-kappas inducing kinase."; Mol. Cell. Biol. 18:7336-7343 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBBUNITY Preferentially found as a heterodimer with IKK-beta but also as an homodimer. Directly interacts with IKK-gamma/NEMO. Heterodimers form the active complex. The tripartite complex can also bind to MAD3K14/NIK, MEKKI, IKAP and IKB-alpha-P65-P50 complex. A weak interaction with TRRP2 cannot be excluded. Part of a complex composed of NCOA2, NCOA3, IKKB, IKBKG and CREBBP (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jobin C., Sartor R.B.;
"The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";
Am. J. Physiol, 278:C451-C462(2000).
-!-FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor.
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                                                                                                                                                                                          MEDLINE=20198447; PubMed=10733566;
McKenzie F.R., Connelly M.A., Balzarano D., Mueller J.R.,
Gelaziunas R., Marcu K.B.;
"Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking
leucine zipper and helix-loop-helix domains reveal that IKKalpha and
IKKbeta have different activation requirements.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCOA3. ENSYME REGULATION: Activated when phosphorylated and inactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delhase M., Hayakawa M., Chen Y., Karin M.;
"Positive and negative regulation of IkappaB kinase activity through
                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION BY MAP3K14/NIK.
MEDLINE=98188238; PubMed=9520401;
Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=2; Synonyms=Delta LH;
Isolia=Q60680-1; Sequence=VSP_004866, VSP_004867;
Isolia=Q60680-2; Sequence=VSP_004866, VSP_004867;
Name=3; Synonyms=Delta H;
Isolia=Q60680-3; Sequence=VSP_004868, VSP_004869;
TISSUE SPECIFICITY: Ubiquitous only for isoform 1, isoforms 2 as are expressed predominantly in brain and T-lymphocytes.
DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by B11, B15 and B17 days. In the limb development, its expression predominates in the limb buds at E12.5 day.
                                                                                                                                                                                                                                                                                                                                                                                                                                            "Differential regulation of IkappaB kinase alpha and beta by two upstream kinases, NF-kappaB-inducing kinase and mitogen-activated protein kinase/ERK kinase kinase-1.";
                                                                                                               "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
SUBCELIOLAR LOCATION: Cytoplasmic.
SUBCELIOLAR PRODUCTS:
Event-Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99212141; PubMed=10195894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKKbeta subunit phosphorylation.";
Science 284:309-313(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99038238; PubMed=9819420;
                                                                                                                                    Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          when dephosphorylated
                                                                                                                                                                             ALTERNATIVE SPLICING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKA-IKKB BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                               Okumura K.;
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REVIEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
PHOSPHORYLATION (BY MAPSK14)
(BY SIMILARITY).
MASLLRXNANLTKORKOTLIS -> IFRKNVKSMERNGRKGH
SLF (in 180form 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JAND BOUND STANDARD; FRI; 756 AA.

10-071-2001 (Rel. 40, Created)
116-077-2001 (Rel. 40, Last sequence update)
115-087-2003 (Rel. 42, Last sequence update)
115-088-2003 (Rel. 42, Last annotation update)
116-088-2003 M: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VSP_004867.
DHLYSDST -> GKTLQSQY (in isoform 3).
                 MEKKI, and dephosphorylated by PP2A. Autophosphorylated.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
IKAPPAB KINASE SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY
PHOSPHORYLATION (BY PKB/AKT1)
                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0109; TYRKINASE.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
TRANSFERSE; SESO011; PROTEIN KINASE DOM; 1.
Transferase; Sexine/threonine-protein kinase; ATP-binding; Phosphorylation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE.
LEUCINE-ZIPPER (POTENTIAL).
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K -> E (IN REF. 3).

S -> Y (IN REF. 3).

3FEF5582AFF92233 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VSP 004866.
Missing (In isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VSP 004868.
Missing (in isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 1; I
Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                             PIR; 149101; 149101.
HSSP; Q63450; 1A06.
MGD; MGI:99464; Chuk.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
PEam; PP00069; pkinase.
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Best Local Similarity
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400 4
745 AA;
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CONFLICT
SEQUENCE
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MOD_RES
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MEDLINE=2238257; PubMed=12477932;

MEDLINE=2238257; PubMed=12477932;

MEDLINE=2238257; PubMed=12477932;

MARIANE=2238257; PubMed=12477932;

MARIANE=2238257; PubMed=12477932;

MARIANE R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MARCHAIN R.F., Jordan H., Moore T., Wax S.I., Wang J., Haidh F.,

MARCHAIN M., Wadren M., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

MARCHAIN S., World M., Noderran K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

MARCHAIN S., Wardy D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Malkealey R.W., Tuckhman J.W., Green E.D., Dickson M.C.,

Matting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Matting M., Karywinski M.I., Skalska U., Smailus D.E.,

Matterffield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Matterffield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Matterffield Y.S.N., Warywinski M.I., Warkwinski M.I., Skalska U., Smailus D.E.,

Matterffield Y.S.N., Warkwinski M.I., Warkwinski M.I.,

Matterffield Y.S.N., Warkwinski M.I., Warkwinski M.I.,

Matterffield Y.S.N., Warkwinski M.I., Warkwinski M.
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Nemoto S., DiDonato J.A., Lin A.;
"Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase land MP-kappaB-inducing kinase.";
Mol. Cell. Biol. 18:7336-7343(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
MEDLINE=98008814; PubMed=9246485;
Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;
Watopas kinase-beta: NF-kappas activation and complex formation with Ikappas kinase-alpha and NIK.";
Science 278:866-869(1997).
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MEDLINE=98438415; PubMed=9763654;
Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
Hasignment of Ikappab kinase beta (IKBKB) to human chromosome band
8p12--p11 by in situ hybridization..;
Cytogenet. Cell Genet. 82:32-33(1998).
                                                                                                                                                                                                                                                                                        TISSUE-Cervical carcinoma;
MEDLINE-98008813; PubMed-9346484;
Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
Mi J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
"IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for NF-kappaB activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hu M.C.-T., Wang Y.-P.; "IkappaB kinase-alpha and -beta genes are coexpressed in adult and embryonic tissues but localized to different human chromosomes.";
                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Jobin C., Sartor R.B.;
"The I kappa B/NF-kappa B system: a key determinant of mucosal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99032998; PubMed=9813230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 278:860+866(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION.
K-AR: LOSS OF KINASE ACTIVITY AND NO
EFFECT ON BINDING TO NIK.
S-AR: DECREASE OF ACTIVITY.
S-AR: DECREASE OF ACTIVITY.
S-AR: DECREASE OF ACTIVITY.
S-AR: PULL ACTIVATION.
WHSKVRQKSEVDIVVSEDLNGTVKF -> CVRMWPGTVAHS
                                                                 "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator activity by I kappa B kinase.";
Mol. Cell. Biol. 22:3549-3561(2002).

Mol. Cell. Biol. 22:3549-3561(2002).

-I-FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates NCOA3 (By similarity).

-I-SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but also as a homodimer. Directly interacts with IKK-gamma/NEMO. Heterodimers form the active complex. The tripartic complex can also bind to MEKKI, MAPSHL4/NIK, IKAP and IKB-alpha-P65-P50 complex. Phosphorylated IKB-alpha is further released from the complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKBKG
IDENTIFICATION IN A COMPLEX WITH CREBBP; NCOA2; NCOA3; IKKA AND IKBKG.
                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal
             MEDLINE-21968797; PubMed=11971985; Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J., O'Malley B.W.;
                                                                                                                                                                                                                                                                                                                                                              muscle, kidney, pancreas, spleen, thymus, prostate, testis and
                                                                                                                                                                                                                                                                                                                                                                              peripheral blood.
PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
                                                                                                                                                                                                                                                                                                                                                                                                            Weakly autophosphorylated.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
IKAPPAB KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM, 602258; —.
GO; GO:0005737; C:cytoplasm; NAS.
GO; GO:0005524; P:ATP binding activity; NAS.
GO; GO:0004674; F:Protein serine/threonine kinase activity; NAS.
GO; GO:0004664; F:Protein amino acid phosphorylation; NAS.
GO; GO:0006466; P:Protein amino acid phosphorylation; NAS.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser Lhr pkinase.
Pfam; PP00069; pkinase; I.
Pfam; PP00069; pkinase; I.
Pfam; PP00140; Protein amino acid phosphorylation; NAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase; Serine/threonine-protein kinase; ATP-binding;
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ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
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PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
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EMBL; AF080158; AAD08997.1; -.
EMBL; AF031416; AAC64675.1; -.
EMBL; BC006231; AAH06231.1; -.
HSSP; Q63450; 1A06.
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DOMAIN 15
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MOD RES
MOD RES
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NP BIND
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MUTAGEN
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CONFLICT

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IKK PHOSPHORYLATION.
MEDLINE-99038238; PubMed=9819420;
Nemoto S., DiDonato J.A., Lin A.;
"Coordinate regulation of IkappaB kinases by mitogen-activated protein
kinase kinase l and NF-kappaB-inducing kinase.";
Mol. Cell. Biol. 18:7336-7343(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
"Murine IKB kinase-B, a developmentally regulated protein kinase that
constitutively phosphorylates serine residues of IkB.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
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"The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";
Am. J. Physiol. 278:C451-C462(2000).
-!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates
                                                                                                                                                                                                                                                                               IKKB_MOUSE STANDARD; PRT; 757 AA.
088351; 09R106;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last annotation update)
18-FEB-2003 (Rel. 41, Last annotation update)
1nhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
(1-kappa-B-kinase beta) (IKR-BKB) (IKK-B) (1-kappa-B kinase
2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIKB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but also as a homodimer. Directly interacts with IKK-gamma/NEMO. Heterodimers form the active complex. The tripartite complex can
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99455228; PubMed=10523828; Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.; "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling pathway activates IkappaB kinases (IKK-alpha/beta) and IKK-beta is a developmentally regulated protein kinase."; Oncogene 18:5514-5524(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEKKI.
STRAIN-ESTRIL/6, TISSUE-SPIDen,
MEDLINE-98188238; PubMed-9550401;
Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Differential regulation of IkappaB kinase alpha and beta by two upstream kinases. NF-kappaB-inducing kinase and mitogen-activated protein kinases/ERK kinase-1."; proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                              .;
0
                                                                        Length 756;
                                                                                                            0; Indels
CNPSTLGGRGRWI (IN REF. 5).
               425 Q -> H (IN REF. 1).
86563 MW; F9CADF671AE9E14E CRC64;
                                                                        Score 35; DB 1; Pred. No. 1.6e+02;
                                                                                                            1; Mismatches
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MEDLINE=20178139; PubMed=10712233;
                                                                      87.5%;
                                                                                                                5; Conservative
               425 4
756 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
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DEVELOPMENTAL STAGE.
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                                                                        Query Match
Best Local Similarity
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               CONFLICT
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ACT_SITE
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                                        -I- SUBCELLULAR LOCATION: Cytoplasmic.
-I- SUBCELLULAR LOCATION: Cytoplasmic.
-I- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
-I- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout the mouse embryo, at E9.5 day its expression begins to be localized to the brain, neural ganglia, neural tube, and in liver at E12.5 day. At E15.5 day, the expression is further restricted to specific tissues of the embryo.
-I- TPM: Phosphorylated by MEKKI and probably also by MAP3KI4/NIK.
-- Weakly autophosphorylated.
-- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
          complex. Phosphorylated IKB-alpha is further released from the complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKBKG and CREBBP (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REF
also bind to MEKK1, MAP3K14/NIK, IKAP and IKB-ALPHA-P65-P50
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                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase; Serine/threonine-procein kinase; ATP-binding;
Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.6e+02;
1; Mismatches 0; Indels
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NEMO-BINDING.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000001; Prot_Kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
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N -> D (IN REF. 2
L -> F (IN REF. 2
P -> Q (IN REF. 2
F -> R (IN REF. 2
K -> R (IN REF. 2
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                                                                                                                                                                                                                                                                                                HSSP; Q63450; IA06.
MGD; MGI:1338071; Ikbkb.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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PRINTS; PR00109; TYRKINASE.
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nes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99038238; PubMed=9819420;
Nemoto S., Dibonato J.A., Lin A.;
"Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase a 1 and MP-kappaB-inducing kinase.";
MOI. Cell. Biol. 18:7336-7343(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but also as a homodimer. Directly interacts with IKK-gamma/NEWO.

Also as a homodimer. Directly interacts with IKK-gamma/NEWO.

Also bind to MEKKI, MAPSKI4/NIK, IKAP and IKB-alpha-P65-P50

complex. Phosphorylated IKB-alpha is further released from the complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKBKG and CREBBP (By similarity).

PTM: Phosphorylated by MEKKI and probably also by. MAP3KI4/NIK.

Weakly autophosphorylated.

SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

IKAAPAB KINASE SUBFAMILY.
28-FEB-2003 (Rel. 41, Last annotation update)
Inhibitor of nuclear factor Kappa B kinase beta subunit (EC 2.7.1.-)
(T-kappa-B-kinase beta) (IKK-beta) (IKK-B) (I-kappa-B kinase)
(Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIKB)
                                                                                                                                               Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinse; Rattus.
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PHOSPHORYLATION (BY SIMILARITY).
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PRINTS; PR00109; TYRKINASE.
PRODOM; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Zhang Y., Sun S., Ravid K.;
"IKK beta in megakaryocyte differentiation.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE.
LEUCINE-ZIPPER (POTENTIAL)
NEMO-BINDING.
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InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR0012845; Tyr pkinase.
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HSSP; Q63450; 1A06.
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                      Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
                                                                                                                                     STRAIN=ATCC 13543;
MEDLINE=93136200; PubMed=8422400;
                                                 Rhodobacteraceae; Paracoccus
                                                                                                              SEOUENCE FROM N.A
                                                                      NCBI_TaxID=266;
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NUOH_RHOCA
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01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
NADH-quinone oxidoreductase chain 8 (EC 1.6.99.5) (NADH dehydrogenase
1, chain 8) (NDH-1, chain 8).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Manager T., Sato S., Koteni H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
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177 PHOSPHORYLATION (BY SIMILARITY).
181 PHOSPHORYLATION (BY SIMILARITY).
86866 MM; 3AFFE46A7DF91F9C CRC64;
                                                                                     87.5%; Score 35; DB 1; Length 757;
83.3%; Pred. No. 1.6e+02;
iive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.0%; Score 34; DB 1; Length 154; 80.0%; Pred. No. 49;
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Pfam, PF00583; Acetyltransf; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 154 AA; 17612 MW; C84777660627F9C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                          U1-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein sll0451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=97061201; PubMed=8905231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D90917; BAA18794.1; -.
                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                      181
757 AA;
                                                                                                                                                                                                                      737 LDWSWL 742
                                                                                                            Best Local Similarity
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Best Local Similarity
                                                                                                                                                                              1 LNWSWL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1148;
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P74676;
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P29920;
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SEQUENCE
                                                                                     Query Match
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NOOS PARDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P42032;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
NADH-quinone oxidoreductase chain H (EC 1.6.99.5) (NADH dehydrogenase
1, chain H) (NDH-1, chain H).
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB 1; Length 345;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                345 AA; 38751 MW; E33B667E569506B4 CRC64;
                                                                                                                                                                                       345 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                         or send an email to license@isb-sib.ch).
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                                                                                                                                                                                 PIR; C45456; C45456.
InterPro; IPR001694; Resp_NADH_dh1.
                                                                                                                                                                EMBL; L02354; AAA25592.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.04;
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                                                                                                                                              Gaps
                                                                                                Dupuis A.; "Identification of two genes of Rhodobacter capsulatus coding for proteins homologous to the ND1 and 23 kDa subunits of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Type I restriction enzyme EcoDI specificity protein (S protein)
(S.EODD).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase; NAD; Quinone; Ūpiquinone; Transmembrane. TRANSMEM 14 34 POTENTIAL. TRANSMEM 84 104 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001694; Resp_NADH_dhl.
Pfam; PF00146; NADHdh; 1.
                                    SEQUENCE FROM N.A.
STRAIN=ATCC 33303 / B10;
MEDLINE=92233948; Pubmed=1568483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF029365; AAC24997.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z11611; CAA77684.1; -. PIR; S22368; S22368.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                345 AA;
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NCBI_TaxID=1061;
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P06991;
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TEAGGE IN DNA molecules.";

U. Mol. Biol. 166:11-19(1981).

I. Mol. Biol. 166:11-19(1981).

I. Mol. Biol. 166:11-19(1981).

I. FUNCTION: THE MAND S SUBUNITS TOGETHER FORM A METHYLTRANSFERASE (MTASE) THAT METHYLATES TWO ADENINE RESIDUES IN COMPLEMENTARY STRANDS OF BIPARTITE DNA RECOGNITION SEQUENCE. IN THE PRESENCE OF THE RANDONUCLEASE, BINDING TO THE SAME TARGET SEQUENCE. WHEN THE DNA SOME DISTANCE FROM THIS SITE, WHETHER THE DNA IS CUT OR MODIFIED DEPENDS ON THE METHYLATION STATE OF THE TARGET SEQUENCE. WHEN THE TARGET SITE IS UNMODIFIED, THE DNA IS CUT OR MODIFIED DEPENDS ON THE HEMIMETHYLATED, THE COMPLEX ACTS AS A MAINTENANCE WTASE MODIFYING THE DNA SO THAT BOTH STRANDS BECOME METHYLATED. SUBUNIT S DICTATES ON THE BOAD SECONE METHYLATED. SUBUNIT S DICTATES TARKIN) GGCY-3.

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Gough J.A., Murray N.E.; "Sequence diversity among related genes for recognition of specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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Pfam; PF01420; Methylase S; 2.
Restriction system; DNA-binding.
SEQUENCE 444 AA; 49893 MM; 14BE17B5325294F0 CRC64;
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Schizosaccharomycetales; Schizosaccharomycetaceae;
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(Rel. 34, Last seq
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215 NWSWM 219
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SEQUENCE FROM N.A., AND TISSUE SPECIFICITY. STRAIN=Canton-S; TISSUE=Larval brain;
     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transmembrane receptor Ror precursor
                                                                                                                                                                                                                                                                                                                                                                    85.0%; Score 34; DB 1; Length 612;
80.0%; Pred. No. 1.9e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                     68720 MW; 3FBFDF3808F554CD CRC64;
                                                                                                                                                                                                                                                                                                                                       (GLCNAC. . .)
                                                                                                                                                                                                                                            Geneba Sponbe; SPAC3F10.13; -.
InterPro; IPR000449; UBA_domain.
Fran, PF00627; UBA; 1.
SWART; SW00165; UBA; 1.
PROSITE; PS50030; UBA; 1.
Hypothetical protein; Glycoprotein; Transmembrane.
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N-LINKED (GLCNAC...
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128
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296
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ROR OR CG4926.
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REC STRAIN—Serkeley.

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REC Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

Record R.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazef K.G., Change M., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Beeson K.Y., Bence P.V., Baxendall J., Baytzkataroglu L., Beasley E.M.,

RA Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Dahle C., Davemport L.B., Davies P., Act Pablos B., Delchan M.R., Boule C., Perrac C., Perriac C., Perrac S., Dunkov B.C., Dun P.,

RA Burtis R.C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Ballon K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P.,

RA Harris N.L., Ravageliste C.C., Perrac C., Perriac S., Dunkov B.C.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

Alalla M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A.,

RA Harris N.L., Matush F., Karpen G.H., Re Z., Kennison J.A., Matter S.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshefi A.,

Rollon D.R., Nellon K.A., Nixon K., Nusskern D.R., Peacleb J.M.,

Raboo D.R., Pittenan G.S., Pan S., Pollard J., Puri V., Santh H.,

Spier E., Spadling A.C., Staplecon M., Strong R., Sunt R.,

Reinert K., Remington K., Saunders R., Wenter E., Wang X.,

Wallsher R., Tector C., Turner R., Wenter E., Wang A.,

Wallsher S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhu X., Smith H.O.,

Rabon R., Pittenan G. S., Zhan M., Zhang G., Zhan S., Zhu X., Zhu K., Zhu S., Zhu X., Zhu S., Zhu K., Zhu S., Zhu K., Zhu S., Zhu K., Zhu S., Zhu K., Zhu S., Zhu K., Zhu S., Zhu K., Zhu S., Zhu K., Zhu S., Zhu K., Zhu S., Zhu K., Zhu S., Zhu K
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-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- TISSUB SPECIFICITY: Expressed in neurons of the developing nervous
MEDLINE-9334822; PubMed=8394009;
Wilson C., Goberdhan D.C.I., Steller H.;
"Dror, a potential neuroricophic receptor gene, encodes a Drosophila
homolog of the vertebrate Ror family of Trk-related receptor tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98401146; PubMed=9731193;
Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;
Cates A.C., Wollberg P., Achen M.G., Wilks A.F.;
Sampling the genomic pool of protein tyrosine kinase genes using the polymerase chain reaction with genomic DNA.";
Biochem. Biophys. Res. Commun. 249:660-667(1998).
-!- FUNCTION: Tyrosine-protein kinase receptor that functions during early stages of neuronal development.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -! - SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. ROR
                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 90:7109-7113(1993).
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-!- SIMILARITY: Contains 1 kringle domain.
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SEQUENCE OF 545-597 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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STANDARD;

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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).
MTATP8 OR ATP8.
                                                                                                                                                                                                   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
NCBI_TaxID=7594;
                                                                                                                                                        Asterina pectinifera (Starfish). Mitochondrion.
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       loved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R PRINTS; PROUGUS; KINGGE.

R PRINTS; PROUGUS; KINGGE.

R PRINTS; PROUGUS; TYRKINASE.

R PRODOM; PD000001; Prot_Kinase; 1.

R PROSOM; P000001; Prot_Kinase; 1.

R SMART; SM00130; KR; 1.

R RAST; SM00130; KR; 1.

R PROSITE; PS50019; FZ; 1.

R PROSITE; PS50010; KRINGLE 1; 1.

R PROSITE; PS50010; KRINGLE 1; 1.

R PROSITE; PS00109; PROTEIN_KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN_KINASE TYP; 1.

R PROSITE; PS00109; PROTEIN_KINASE TYP; 1.

R PROSITE; PS00109; PROTEIN_KINASE TYP; 1.

R PROSITE; PS00109; PROTEIN_KINASE TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE TYR; 1.

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R PROSITE; PS00109; PROTEIN_KINASE TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE TYR; 1.
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                      FlyBase; FBgn001007; Ror.

GO; GO: 0016621; C: integral to membrane; NAS.

GO; GO: 0016621; C: integral to membrane; NAS.

GO; GO: 0004713; F: protein tyrosine kinase activity; NAS.

GO; GO: 0006468; P: central nervous system development; IEP.

GO; GO: 0006468; P: protein amino acid phosphorylation; NAS.

InterPro; IPR000201; Fz domain.

InterPro; IPR000019; Prot kinase.

InterPro; IPR002011; RTKinaseII.

InterPro; IPR002011; RTKinaseII.

InterPro; IPR002011; Tyr pkinase.

Pfam; PF00051; kringle; I.

Pfam; PF00069; pkinase; I.
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PHOSPHORYLATION (AUTO-) (BY
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CYTOPLASMIC (POTENTIAL)
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modified and this statement is not remo-
entities requires a license agreement (
or send an email to license@isb-sib.ch)
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                                                                                         EMBL; L20297; AAA28860.1; -.
EMBL; AE003628; AAF52885.1; -.
EMBL; AJ0029098; CAA05743.1; -.
PIK; A48289; A48289.
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Matches 5; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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                     Agakawa S., Himeno H., Miura K.-I., Watanabe K.;
"Nucleotide sequence and gene organization of the starfish Asterina
pectinifera mitochondrial genome.";
Genetics 140:1047-1060(1995).
-!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
(CP(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pfam; PF00895; ATP-8ynt 8; 1.
Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
TRANSMEM 8 28 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 1; Length 54;
Pred. No. 25;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                      H(+) (Out).
-!- SUBCELLULAR LOCATION: Membrane-bound.
-!- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM 8 28 POTENTIAL.
SEQUENCE 54 AA; 6241 MW; 9EABDACEB9CDF5F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: February 18, 2004, 14:28:07
MEDLINE=95402698; PubMed=7672576;
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80.0%;
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Matches 4; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 18, 2004, 14:12:09; Search time 6.5921 Seconds Run on:

(without alignments) 87.531 Million cell updates/sec

US-09-643-260-9 40 1 LINWSWL 6 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	hypothetical prote	_	probable integral	hypothetical prote	ubiquinol-cytochro	probable glycosyl	hypothetical prote	hypothetical prote	Ω	hypothetical prote	ribonucleotide red	conserved helix-lo	glucan 1,3-beta-gl	hypothetical prote	NADH2 dehydrogenas	NADH2 dehydrogenas	probable serine pr	hypothetical prote	neurotrophic recep	protein T01H3.2 [i	probable transcrip	hypothetical prote		hypothetical prote	끕	hypothetical prote	a	benzodiazepine rec	peripheral-type be
	Ω	C83748	AG2946	C98336	T15295	T11041	AG0965	C83491	T10035	T03472	T24773	E87125	I49101	T09056	S76882	C45456	S22368	F70983	T38714	A48289	E88221	T37062	T24336	T35781	D90532	870600	AD2464	138724	JC1393	157953
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*	당섭	92.5	95.5	92.5	0.06	90.0	90.0	90.0	ö	87.5	7	ζ.	87.5	87.5	S	£	S	85.0	85.0	S	85.0	S	S	S	ä	ď.	ς.	82.5	'n	82.5
	Score	37		37					36	32	35			32	34	34	34	34	34	34	34		34	34				33	33	33
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peripheral-type be	benzodiazepine rec	peripheral-type be	peripheral benzoda	ABC transporter su	cation-efflux syst	ATP synthase A cha	hypothetical prote	44	transposase of 1S9	transposase of IS9	transposase of 189	transposase of IS9	transposase of 1S9	transposase of IS9	transposase of IS9
A53405	S14257	A39473	JE0149	AB2466	AF2161	A82953	C84701	A86710	G86712	D86741	G86787	G86794	C86814	B86837	E86860
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ALIGNMENTS

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		Bacillus halodurans	
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		BH0787 [imported]	9
		BH0787	halodura
		protein	, סוון (ייטר
7 177	48	othetical protein	peries. Barillus halodurans

hypothetical protein BH0787 [imported] - Bacillus halodurans (strain C-125)
Cypecies Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: C83748
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, P.; Hir.
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83550; MUID:20512582; PMID:11058132
A;Reference number: C8374
A;Accession: C8374
A;Accession: C8374
A;Rosidues: 1-204 <5TO>
A;Cross.references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB04506.1; GSPDB:GNO0
C;Genetics
A;Genetics
A;Genetics
C;Genetics
C;Superfamily: Bacillus subtilis conserved hypothetical protein yesL

ö Gaps ö Query Match 92.5%; Score 37; DB 2; Length 204; Best Local Similarity 83.3%; Pred. No. 49; Matches 5; Conservative 1; Mismatches 0; Indels

22 LNWAWL 27 1 LINWSWL 6 ò 셤

hypothetical protein Atu3173 [imported] - Agrobacterium tumefaciens (atrain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Accession: AG2946
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I krapo, D.; Rimber, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W. A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; MUID:21608550; PMID:11743193

A; Accession: AG2946

A; Status: preliminary

A, Molecule type: DNA

A;Residues: 1.537 *KUR.>
A;Residues: 1.537 *KUR.>
A;Cross-references: GB:AE008689; PIDN:AAL43989.1; PID:g17741546; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics: A;Gene Atu3173
A;Map position: linear chromosome

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ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b - Chlamydomonas eugametos maces especies: mitochondrion Chlamydomonas eugametos
C.Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinol (*Keywords : electron transfer; heme; iron; metalloprotein; mitochondrion; oxidative phosi F;10-340/Domain: cytochrome b homology <CMB>
F:10-210/Domain: cytochrome b6 homology <CB6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;222-340/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>F;82,183/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted F;96,197/Binding site: heme iron (His) (axial ligands) (high potential) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable glycosyl hydrolase STY4009 [imported] - Salmonella enterica subsp. enterica ser c; Species: Salmonella enterica subsp. enterica serovar Typhi shote: this species has also been called Salmonella typhi c;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AG0965 K;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, D. A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov. A;Accession: AG0965
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C;Species: Pseudomonas aeruginosa
C;Date: 15.Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: (83491
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
                                                                                                                                    Ribenovan-Wright, E.M.; Nedelcu, A.M.; Lee, R.W.
Plant Mol. Biol. 36, 285-295, 1998
A;Title: Complete sequence of the mitochondrial DNA of Chlamydomonas eugametos.
A;Reference number: Z17244; MUID:98145434; PMID:9484440
                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-380 <DEN>
A;Cross-references: EMBL:AF008237; NID:g2865253; PID:g2865267; PIDN:AAC39350.1
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100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0;
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A;Molecule type: DNA
A;Residues: 1-460 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome: mitochondrion
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                                                                                                         C; Accession: T11041
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A; Description: The sequence of C. elegans cosmid B0252.
A; Reference number: S55415
A; Reference number: S55415
A; Reference number: S55415
A; Accession: T15295
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-204 < DUZ>
A; Cross-references: EMBL: U23453; NID: 9733572; PID: 9733579; PIDN: AAC46760.1; CESP: B0252.6
A; Experimental source: strain Bristol N2
A; Genetics:
A; Genetics:
A; Genetics:
A; Construction: 149/3; 182/2
C; Superfamily: Caenorhabditis elegans hypothetical protein B0252.6
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R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Goience 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:2160851; PMID:11743194
A;Reference number: A97359; MUID:2160851; PMID:11743194
A;Reference number: A97359; MUID:2160851; PMID:11743194
A;Reference number: A97359; MUID:2160851; PMID:11743194
A;Reference number: A97359; MUID:2160851; PMID:11743194
A;Cross-references: GB:AB007870; PIDN:AAK90213.1; PID:g15160224; GSPDB:GN00170
                                                                                                                                                                                                                                                                                                                                                                                                          probable integral membrane transport protein (141665) [imported] - Agrobacterium tumefad
رنگاهونایه: Agrobacterium باستهایگیات
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C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
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C.Species Caenorhabditis elegans
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 23-Mar-2001
C.Accession: T15295
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                                                                    Match 92.5%; Score 37; DB Local Similarity 83.3%; Pred. No. 81; es 5; Conservative 1; Mismatches
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A;Map position: linear chromosome
C;Superfamily: inner membrane protein ugpA
          C;Superfamily: inner membrane protein ugpA
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164 LNWAWL 169
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164 LNWAWL 169
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Matches 5; Conservative
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Matches 4; Conservative
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15 INWNWL 20
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                           June 1977, S.; Olson, M.V.
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C;Species: Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C;Accession: T03472
R;Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003
A;Reference number: Z14955; MUID:9740444; PMID:9256491
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C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
C;Caccession: T10035
R;Eiglameier, K.; Honore, N.; Woods, S.A.; Caudron, B.; Cole, S.T.
Mol. Microbiol. 7, 197-206, 1993
A;Title: Use of an ordered cosmid library to deduce the genomic organization of Mycobact A;Reference number: 216917; MUID:93188700; PMID:8446027
A;Accession: T10035
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
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C;Genetics:
A;Note: MLCB628.16c
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90.0%; Score 36; DB 2; Length 744;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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A;Molecule type: DNA
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Best Local Similarity 83...
Best Local Si Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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265 NWSWL 269
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ribonucleotide reductase small subunit [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: E87125
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hr.; Davies, R.M.; Devlin, K.M.
N.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; SALtitle: Massive gene decay in the leprosy bacillus.
A;Accession: E87125
A;Accession: E87125
A;Accession: E87125
A;Accession: Draiminary
A;Molecule type: DNA
A;Esterence DNA
A;Esterence DNA
A;Esterence SG:AL450380; NID:g13093483; PIDN:CAC30684.1; GSPDB:GN00147
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C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: 149101
R;Mock, B.A.; Connelly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.
Genomics 27, 348-351, 1995
A;Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome
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hypothetical protein T10B10.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
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C;Superfamily: ribonucleoside-diphosphate reductase beta
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A;Gene: CESP:T10B10.8
A;Map position: X
A;Introns: 40/3; 54/2; 64/3; 123/3; 229/2; 262/3
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Search completed: February 18, 2004, 14:38:43 Job time: 7.5921 secs
C; Superfamily: hypothetical protein b2267
                                                                                                                                                                              4; Conservative
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A; Residues: 1-345 <XU1>
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3 INWSW 7
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                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-745 <RES>
A;Cross-references: EMBL:U12473; NID:g1079492; PIDN:AAC52589.1; PID:g1079493
C;Genetics:
A;Gene: CHUK
C;Genetics: CHUK
C;Genetics: CHUK
C;Genetics: CHUK
C;Genetics: CHUK
C;Keywords: ATP; phosphotransferase
C;Keywords: ATP; phosphotransferase
F;13-283/Domain: protein kinase homology <KIN>
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A;Accession: S76882
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-154 <KAN>
A;Residues: 1-154 <KAN>
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R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA, Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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C;Function:
A;Description: catalyzes the hydrolysis of beta-D-glucose units from the non-reducing C;Keywords: glycosidase; hydrolase
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C,Species: Ampelomyces quisqualis
C,Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
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C;Species: Synechocystis sp. A;Variety: PCC 6803
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000 C;Accession: S76882
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A;Experimental source: strain AQ10
C;Genetics:
A;Reference number: I49101; MUID:9604444; PMID:7558004
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R; Rotem, Y.; Yarden, O.; Sztejnberg, A.
submitted to the EMBL Data Library, October 1997
A; Reference number: Z16541
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A;Status: translated from GB/EMBL/DDBJ
A;Moolecule type: mRNA
A;Residues: 1-777 <ROT>
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Best Local Similarity 83.3.
Pest Local Si Conservative
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266 MNWNWL 271
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C;Accession: C45456
R;Xu, X.; Matsuno-Yagi, A.; Yagi, T.
Biochemistry 32, 968-981, 1993
A;Title: DNA sequencing of the seven remaining structural genes of the gene cluster encc A;Reference number: A45456; MUID:93136200; PMID:8422400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: NADH dehydrogenase (ubiquinone) chain 1
C;Keywords: membrane-associated complex; NAD; oxidative phosphorylation; oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                    NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - Paracoccus denitrificans N.Alternate names: NADH-quinone oxidoreductase chain I
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Date: 24-Feb-1994 #sequence_revision 15-Oct-1994 #text_change 03-Jun-2002
                                                                              Gaps
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A;Note: sequence extracted from NCBI backbone (NCBIN:123409, NCBIP:123413)
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Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels
85.0%; Score 34; DB 2;
80.0%; Pred. No. 1.1e+02;
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US-09-149-476-360
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                                                                        February 18, 2004, 14:16:39; Search time 7.06579 Seconds (without alignments) 35.929 Million cell updates/sec
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/cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-880-853-4
US-09-032-321-3
US-09-032-475-3
US-09-099-125A-4
US-09-099-125A-4
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US-09-168-64-4
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US-09-023-324-2
US-09-168-629-15
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Maximum Match 100%
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Perfect score:
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28 35 87.5 756 4 US-08-910-820-9 Sequence 9, Appli 30 35 87.5 756 4 US-09-109-986-2 Sequence 2, Appli 31 35 87.5 756 4 US-09-868-9 Sequence 2, Appli 32 87.5 756 4 US-09-868-9 Sequence 2, Appli 32 87.5 996 4 US-09-817-197-121 Sequence 121, Appli 33 87.5 997 4 US-09-417-197-121 Sequence 121, Appli 34 85.0 144 4 US-09-417-197-121 Sequence 121, Appli 34 85.0 144 4 US-09-252-991A-1138 Sequence 2113, Appli 34 85.0 355 4 US-08-818-112-79 Sequence 79, Appli 34 85.0 355 4 US-09-818-1112-79 Sequence 79, Appli 36 34 85.0 355 4 US-09-072-596-80 Sequence 80, Appli 39 82.5 151 4 US-09-072-991A-28780 Sequence 80, Appli 39 82.5 303 4 US-09-252-991A-28780 Sequence 28780, Appli 39 82.5 396 4 US-09-252-991A-28780 Sequence 19160, Appli 39 82.5 396 4 US-09-252-991A-19160 Sequence 19160, Appli 39 82.5 396 4 US-09-252-991A-19160 Sequence 19160, Appli 43 82.5 396 4 US-09-252-991A-19160 Sequence 19160, Appli 43 82.5 5 PCT-US95-0865-14 Sequence 14, Appli 44 33 82.5 5 PCT-US95-0865-14 Sequence 168, Appli 45 33 82.5 471 4 US-08-311-731A-168 Sequence 168, Appli 45 33 82.5 471 4 US-08-311-731A-168 Sequence 168, Appli 45 33 82.5 471 4 US-08-311-731A-168
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ALIGNMENTS

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SCHOOLOGY AND STATE OF THING DATE: 1997-03-73

SCHORAL INFORMATION: ADDITION: APPLICANT: ROSEN et al. TITLE OF INVENTION: 186 Human Secreted proteins FILE REFERENCE: PZ002P1

CURRENT FILING DATE: 1998-09-08

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EARLIER FILING DATE: 1998-03-06

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R FILING DATE: 1997-05-23
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R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,612
R APPLICATION NUMBER: 60/047,632
R PILING DATE: 1997-05-23
R PELLING DATE: 1997-05-23
R PELLING DATE: 1997-05-23
R PELLING DATE: 1997-05-23
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,601 R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,312

R FILING DATE: 1997-04-11

R PILING DATE: 1997-04-11

R PILING DATE: 1997-04-11

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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/056,910 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,864 APPLICATION NUMBER: 60/056,875 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,862 PLICATION NUMBER: 60/056,894 LING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,636 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,874 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,845 APPLICATION NUMBER: 60/047,595 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,599 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,578 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,576 APPLICATION NUMBER: 60/056,911 APPLICATION NUMBER: 60/056,892 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/057,761 60/047,588 APPLICATION NUMBER: 60/047,585 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,586 APPLICATION NUMBER: 60/047,590 APPLICATION NUMBER: 60/047,594 APPLICATION NUMBER: 60/047,589 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,614 APPLICATION NUMBER: 60/047,501 APPLICATION NUMBER: 60/043,670 APPLICATION NUMBER: 60/056,632 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,664 APPLICATION NUMBER: 60/056,876 APPLICATION NUMBER: 60/056,881 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,909 APPLICATION NUMBER: 60/056,887 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,908 APPLICATION NUMBER: 60/057,650 FILING DATE: 1997-09-05 APPLICATION NUMBER: 60/056,884 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,631 APPLICATION NUMBER: 60/047,593 APPLICATION NUMBER: 60'9 FILING DATE: 1997-08-22 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 1997-05-23 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 FILING DATE: 1997-04-11 1997-08-22 FILING DATE: 1997-06-06 FILING DATE: 1997-08-22 1997-08-22 1997-08-22 FILING DATE: 1997-08-23 FILING DATE: 1997-04-11 FILING DATE: 1997-08-2 1997-05-FILING DATE: FILING DATE: LING DATE: FILING DATE: FILING DATE: FILING DATE: EARLIER EARLIER

Gaps

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GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                        Score 35; DB 2; Length 745;
Pred. No. 7.3e+02;
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Pred. No. 7.3e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/023,321
                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                 REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEPAX: (415) 343-4342
INFORMATION POR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRICA PRELICATION DATA:
APPLICATION NUMBER: US/08/887,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09023321
Patent No. 5844073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: T9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                          87.5%;
83.3%;
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Best Local Similarity 83.3%;
Matches 5; Conservative
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INFORMATION FOR SEQ ID NO: 3:
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amino acid
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Matches 5; Conservative
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MOLECULE TYPE: peptide
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US-09-023-321-3
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Sequence 20134, Application US/09252991A

Sequence 20134, Application US/09252991A

Sequence 20134, Application US/09252991A

Sequence 20134, Application US/09252991A

Sequence 20134, Application US/09252991A

Sequence 20134, Application US/09252991A

Sequence 20134, Application US/09252, 991A

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT PILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 609
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                                                                                                                                                 DB 4; Length 117; 91;
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                                                                                                                                                                                             0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATR:
APPLICATION NUMBER: US/08/887,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Le
4.4e+02;
                                                                                                                                                                     Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                 90.0%; Score 36; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36;
Pred. No.
                      EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
EARLIER APPLICATION NUMBER: 60/057,669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.08;
100.08;
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 100.
Matches 5; Conservative
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US-09-252-991A-20134
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Gaps

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(415) 343-4341
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 87.5
Best Local Similarity 83.3
Matches 5; Conservative
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MOLECULE TYPE: peptide
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                                                                                                              FILING DATE:
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                                                                                                                                             Sequence 4, Application US/08890853
; Sequence 4, Application US/08890853
; Patent No. 5851812
; GENERAL INFORMATION:
    APPLICANT: Goeddel, David V.
    APPLICANT: Woronicz, John
    TITLE OF INVENTION: IK-
    NUMBER OF SEQUENCES: 4
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
    STREET: 268 BUSH STREET, SUITE 3200
    CITY: SAN FRANCISCO
    STATE: CALLFORNIA
    COUNTRY: USA
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Patent No. 5854003
Fatent Rothe, Mike
Fatent Rothe, Mike
Fatent Rothe, Mike
Fatent Rothe, Mike
Fatent Rothe, Mike
Fatent Number OF Sequences:
Fatent Rother Address:
Fatent Rother Address:
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Fatent Satent Rother Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Satent Saten
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Pred. No. 7.36+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/890,853
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83.3%; Pred
1;
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ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFRENCE/DOCKET NUMBER: 197-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 83.3
Matches 5; Conservative
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738 LDWSWL 743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                     US-08-890-853-4
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Sequence 4, Application US/09099125A

Patent No. 5916760

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Woronicz, John

TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,475
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Pred. No. 7.3e+02;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: USA
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CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,125A
                                                                                                                    FILING TABLES

CIASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,518

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 797-008

TELEPONENICATION INFORMATION:
TELEPHONE: (415) 343-4341

TELEPAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: single
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US-08-990-854-4

Sequence 4, Application US/08890854

Facent No. 6235512

APPLICANT: Rothe, Mike

APPLICANT: Cao, Zhaodan

TITLE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 5

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ACIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALLFORNIA
                APPLICANT: R gnier, Catherine
TITLE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods
INUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSES: SCLENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.5%; Score 35; DB 3; Length 745;
83.3%; Pred. No. 7.3e+02;
iive 1; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,854
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/032,476
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSNAN, RICHARD A
REGISTRATION NUMBER: 36,627
REPERROK/POCKET NUMBER: T97-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acids
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Best Local Similarity 83.3
Matches 5; Conservative
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ZIP: 94104
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          APPLICANT:
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Patent No. 5939302
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ACIGNESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 258 BUSH STREET, SUITE 3200
                                                                                                                                                                  Score 35; DB 2; Length 745; Pred. No. 7.3e+02; 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,124A
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
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Patent No. 6235492
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
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NAME: OSMAN, RICHARD A
REGISTATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                  87.5%;
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                              Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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STRANDEDNESS: single
                                        ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-099-125A-4
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738 LDWSWL 743
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STRANDEDNESS: si
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-099-124A-4
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GENERAL INFORMATION:

APPLICANT: Karin, Michael
APPLICANT: Rothwarf, David M.
APPLICANT: DiDonato, Joseph A.
APPLICANT: Bolowarf, David M.
APPLICANT: Applicant: Rothwarf, David M.
APPLICANT: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins Applicant: Brins 
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Patent No. 6258579
GENERAL INFORMATION:
APPLICANT: Mercurio, Frank
APPLICANT: Barbosa, Miguel
APPLICANT: Liu, Hengyi
APPLICANT: Li, Gian
APPLICANT: Li, Gian
APPLICANT: STIMULUS-INDUCIBLE PROTEIN KINASE
TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,820
FILING DATE: 12-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 3; Pred. No. 7.3e+02;
         Mismatches
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.413C1
                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09168629
Patent No. 6242253
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
         5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-168-629-2
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STATE: Washington
                                                                                                                                738 LDWSWL 743
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                                                                1 LAWSWL 6
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         Matches
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APPLICANT: Cao, Zhaodan
APPLICANT: Cao, Zhaodan
APPLICANT: R gnier, Catherine
ATILE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.5%; Score 35; DB 3; Length 745; 83.3%; Pred. No. 7.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 3; Lengtn 7.3 Pred. No. 7.3 8+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REPRENCE/DOCKET NUMBER: 197-006-1
TELECOMMUNICATION INFORMATION:
TELEFRY: (415) 343-4341
TELEFRY: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94104
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09023324
Patent No. 6235513
GENERAL INFORMATION:
                                                            NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T9-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                            TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 83.3.
                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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COUNTRY:
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Patent No. 6268194
GENERAL INFORMATION:
APPLICANT: Karin, Michael
APPLICANT: Rothwarf, David M.
APPLICANT: Hayakawa, Makio
APPLICANT: Zandi, Ebrahim
TITLE OF INVENTION: I kappa-B Kinase and Methods of Using
                                                                                                                                                                                                                          87.5%; Score 35; DB 3; Length 745; 83.3%; Pred. No. 7.3e+02; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.5%; Score 35; DB 3; Length 745; 83.3%; Pred. No. 7.3e+02; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UNITED STATES

ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,131A
FILING DATE: 25-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2408
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-9001
TELEPAX: GROUD NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores Lip
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                   TELEPHONE: (206) 622-4900
TELEPAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acids
STRANDEDNESS:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 745 amino acids
amino acid
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Best Local Similarity 83.3
Matches 5; Conservative
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Matches 5; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                ; TOPOLOGY: linear
US-08-910-820-10
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738 LDWSWL 743
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Sequence 4, Application US/09109986

Patent No. 6479266

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

APPLICANT: Cao, Zhaodan

TITLE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods

CORRESPONDENCE: 5

CORRESPONDENCE ADDRESS: ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,986
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 4; 1 Pred. No. 7.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: February 18, 2004, 14:41:48 Job time : 8.06579 Becs
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSNAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-00f
TELECOMMULICATION INFORMATION:
TELEPAX: (415) 343-4341
TELEPAX: (415) 343-4341
TELEPAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
                                                                                                                                                                                                                                                                                    ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                           CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      738 LDWSWL 743
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Q8erjo oceanobacil Q91060 streptomyce Q91060 streptomyce Q91061 coturnix co Q91ffwl ashbya goss Q92713 caenorhabdi O68039 rhodobacteri Q81010 drosophila Q8w205 homo sapien Q94515 drosophila Q97416 sulfolobus P74568 synechocyst Q97710 sulfolobus P74568 synechocyst Q8P011 xanthomonas Q8p912 xanthomonas

QBKPQ4
QBYPT8
QBYCV5
QBSX313
QBLAH9
QBH175
QBY475
QG9Y475
QG9Y175
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QG9Y175

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Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poacese;
Ehrhartoldeae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
Supmitred (FRB-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (FRB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003367; BAC03279-1; -.
Gramene; QBLJE0; AR, 41273 MW; C3D070BB5980BACB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.3%; Score 36; DB 10; Length 387; 83.3%; Pred. No. 4.1e+02; ive 1; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9VQ45 PRELIMINARY; PRT;
Q9VQ45;
01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                          01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23, P0496H05.7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.3%;
Best Local Similarity 63.3%;
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242 VEWSWL 247
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Q8LJE0
Q8LJE0;
01-OCT-2002
01-OCT-2002
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RESULT 2
Q9VQ45
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Q9'q45 drosophila
Q9feel oryza sativ
Q63620 balanogloss
Q95kv1 bos taurus
Q8cbt3 mus musculu
Q95kv0 bos taurus
Q8vkb2 mycobacteri
Q8vkb2 mycobacteri
Q9'hig7 halobacteri
Q9'hig7 halobacteri
Q9'hig7 erreptococc
Q9'hig7 erreptococc
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Q9'hig7 erreptococc
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Q9'fw8 brucella me
Q85331 leishmania
Q8'fw8 brucella me
Q8g12 brucella su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8lje0 oryza sativ
                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                       February 18, 2004, 14:09:39; Search time 17.3684 Seconds (without alignments) 89.145 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                   830525 seqs, 258052604 residues
                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                        OM protein - protein search, using sw model
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Q9VQ45
Q9FEE1
O63620
Q95KV1
Q8CBT3
Q95KV0
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Q9HHP7
Q9YH31
Q47020
Q94380
Q25333
Q8YFW8
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                        sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
sp_phage:*
sp_plant:*
sp_plant:*
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sp_vertebrate:*
sp_unclassified:*
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sp_bacteriap:*
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sp_bacteria:*
sp_fungi:*
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Maximum DB seq length: 200000000
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39
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Last sequence update) Last annotation update)

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SEQUENCE FROM N.A.
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RX STALAN-BETKEL FROM N.A.

RX Adams M.D. (Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Sabburner M., Henderson S.N.,

Sutton G.G., Wortman J.E., Yandell M.D., Zhang O., Chen L.X.,

RA Brandon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pétiffer B.D.,

RA Bardon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pétiffer B.D.,

RA BAIL M.F., Adpayani A., An H.-J., Andrews Pfemnkoch C., Baldwin D.,

RA Ballew R.M., Bason A., Berman B.P., Bhandari D., Bolshakov S.,

RA Ballew R.M., Cawley S., Daller H., Cadieu E., Center A., Chandre I.

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandre I.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandre I.,

RA Ballew R.M., Cawley S., Dalnike C., Davrapendor L.B., Davise P.,

RA Grerry J.M., Cawley S., Dalnike C., Davrapendor J., Diet Z. S.M.,

RA Ballew R.D., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Adlali M., Kalush F., Karpen G.H., Ke Z., Ganbart W.M., Glasser K.,

Alli M., Mattel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Liu X., Mattel B. M. Chrosh T.C., Mocleod M.D., Morberson D.,

RA Merkulov G., Milshina N.V., Mochery C., Morris J., Month S., Mattel S.,

Roller K., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

Ras Reinert K., Remington K., Stapleton M., Stupski M.P., Smith T.,

Ras R., Peter C., Turner R., Venter E., Wang S., Yao Q.A.,

RA Mang Z.-Y., Wassarman D.A., Weinster B., Wang S., Yao Q.A.,

RA Mang Z.-Y., Wassarman D.A., Weinster B., Wang S., Yao Q.A.,

RA Mang Z.-Y., Wassarman D.A., Weinster B., Sun S.,

RA Shirskas R., Teccer C., Turner R., Venter E., Staple D.,

RA Mang S., Peter R., Remington K., Stapleton M., Staple S., Sholp S.,

RA Shirskas R., Teccer C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
A Bvans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
Pacleb J., Paragas V., Park S., Patel S., Ffeiffer B., Scheeler F.,
A Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
L. Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
                                 CG31664 protein.
CG31933 OR CG16522.
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TAXID=7227;
01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                     FROM N.A.
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Gaps
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P0688A04.9 OR P0006C01.24.

Oryza sativa (Rice).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of Drosophia melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                   SEQUENCE FROM N.A. Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.3%; Score 36; DB 10; Length 544; 83.3%; Pred. No. 5.7e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 5; Length 482;
Pred. No. 5e+02;
1; Mismatches 0; Indels
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02995; DUF229; 1.
SEQUENCE 482 AA; 55495 MW; A91F2F2D2FDFBC5D CRC64;
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SEQUENCE 544 AA; 60867 MW; 273EAF5968D1A024 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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PROSITE; PS00086; CYTOCHROME_P450; 1.
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InterPro, IPR001128, Cytochrome_P450.
Pfam; PF00067; P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE003585; AAF51336.2; -...
FlyBase; FBgn0051664; CG31664.
FlyBase; FBgn0051933; CG31933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004245; DUF229.
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nes 5; Conservative
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01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2003 (TrEMBLrel. 23,
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738 LDWSWL 743
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Matches 5; Conserv
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SEQUENCE FROM N.A.
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BIKKBETA.
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Q8CBT3
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                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=99016090; PubMed=9799263;
Castressana J., Feldmaier-Fuchs G., Yokobori S., Satoh N., Paabo S.;
"The mitochondrial genome of the hemichordate Balanoglossus carnosus and the evolution of deuterostome mitochondria.";
Genetics 150:1115-1123(1998).
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Hemichordata; Enteropneusta; Ptychoderidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=98188267; PubMed=9520430;
Castresana J., Feldmaier-Fuchs G., Paabo S.;
"Codon reassignment and amino acid composition in hemichordate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.3%; Score 36; DB 8; Length 645; 83.3%; Pred. No. 6.7e+02; tive 1; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Castreagna J., Feldmater-Fuchs G., Paabo S.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF0S1097; AAD11945.1; -.
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                                                                                                                                                                                      01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
NADH dehydrogenase subunit 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003916; NADHub oxreds.
InterPro; IPR001750; Oxidored_q1.
InterPro; IPR001516; Oxidored_q1.
InterPro; IPR001516; Oxidored_q1.
Pfam; PF00162; Oxidored_q1, 1.
Pfam; PF00662; Oxidored_q1 N; 1.
PRINTS; PR01434; NADHDHGNASES.
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                                                                                                                                                 PRT;
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
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Matches 5; Conserv
                                       LEWAWL 53
1 LEWSWL 6
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NCBI_TaxID=35080;
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BIKKALPHA.
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The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 clul-length CDNAs."; Nature 420:563-573 (2002).

EMBL; AK035326; BAC29034.1; -. SEQUENCE 745 AA; 84770 MW; 48C9E01C17A61184 CRC64;
alpha, beta and gamma.";

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

RMBL; AJ41455; CAC93686.1; -.

RMBL; AJ41455; CAC93686.1; -.

RICEPTO: IPRO00219; Prot kinase.

InterPro; IPRO00219; Ser_thr_pkinase.

R probom; PRO00601; Prot kinase; 1.

R PRODOM; PROTEIN KINASE ATP; 1.

R PROSITE; PSO010; PROTEIN KINASE DOM; 1.

R PROSITE; PSO0109; PROTEIN KINASE DOM; 1.

R PROSITE; PSO0109; PROTEIN KINASE ST; 1.

R PROSITE; PSO0109; PROTEIN KINASE ST; 1.

R PROSITE; PSO0109; PROTEIN KINASE ST; 1.

R PROSITE; PSO0109; PROTEIN KINASE ST; 1.

R PROSITE; PSO0109; PROTEIN KINASE ST; 1.

R PROSITE; PSO0109; PROTEIN KINASE ST; 1.

R PROSITE; PSO0109; PROTEIN KINASE ST; 1.

R PROSITE; PSO0109; PROTEIN KINASE ST; 1.

R PROSITE; PSO0109; PROTEIN KINASE ST; 1.

R PROSITE; PSO0109; PROTEIN KINASE ST; 1.

R PROSITE; PSO0109; PROTEIN KINASE ST; 1.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.3%; Score 36; DB 6; Length 740;
83.3%; Pred. No. 7.6e+02;
ive 1; Mismatches 0; Indels
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Conserved helix-loop-helix ubiquitous kinase.
Mus musculus (Mouse).
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Last annotation update)
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STRAIN=C57BL/6J; TISSUE=Urinary bladder;
MEDLINE=22354683; PubMed=12466851;
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MEDLINE-20504483; PubMed=11016950;
MEDLINE-20504483; PubMed=11016950;
MEDLINE-20504483; PubMed=11016950;
MA GW.V., Kennedy, S.P., Mahairas G.G., Berquist B., Pan M.,
A Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
A Swartzell S., Weir D., Hall J., Dahl T.A., Welti, R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
A haddocks D.G., Jablonski P.B., Krebs M.P., Angevine C.M., Dale H.,
A lam M., Freitas T., Hou S., Danisla C.J., Dennis P.P., Omer A.D.,
A bhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
P. Genome sequence of Halobacterium species NRC-1.",
P. Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
BRBL, AE005159; AAG20299:1; -.
REMBL, AE005159; AAG20299:1; -.
REMBL, AE005159; ABG200299:1; -.
                                                                                                      SECUENCE FROM N.A.
SETAAIR=2603 V/R / Serctype V;
MEDLINE=2222988; PubMed=1220547;
Tettelin H., Masignani V., Cleslewicz M.J., Eisen J.A., Peterson S., Messells M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence and comparative genomic analysis of ar emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.7%; Score 35; DB 16; Length 11
100.0%; Pred. No. 1.7e+02;
.ive 0; Mismatches 0; Indels
        Streptococcus agalactiae (serotype V).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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110 AA; 12689 MW; 243D6BE9029709A4 CRC64;
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Halobacteriaceae; Halobacterium.
NCBI_TaxID=64091;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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100.0%; Pred. No. 2.6e+02;
ive 0; Mismatches 0;
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Best Local Similarity
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Best Local Similarity
Matches 5; Conserv
                                                                    NCBI_TaxID=216466;
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SEQUENCE 11
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01-JUN-2001
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SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                      Length 756;
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83.3%; Pred. No. 7.8e+02;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE006980; AAK45193.1; -.
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Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
Hypothetical protein.
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Best Local Similarity 83.3
Matches 5; Conservative
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Matches 5; Conservative
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Q8DYI4;
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Q8VKB2

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coli dapD gene.";
J. Biol. Chem. 259:14824-14828(1984).
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"Transcription control of the arop
Analysis of operator mutants.";
J. Bacteriol. 169:386-393(1987).
                                                                                                                        Eur. J. Biochem. 133:481-489(1983)
                                                                                                                                                                                                                                                                                 Eur. J. Biochem. 135:519-527(1983)
                                                                                                                                                                                                                                                                                                                                           STRAIN=K-12;
MEDLINE=85054973; PubMed=6094577;
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                        MEDLINE=83234434; PubMed=6345153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     structure.";
J. Bacteriol. 169:751-757(1987)
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"The pyruvate dehydrogenase complex of Escherichia coli K12.
Nucleotide sequence encoding the pyruvate dehydrogenase component.";
Bur. J. Blochem. 133:155-162(1983).
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2003 (TrEMBLrel. 13, Last annotation update)
Putative fibroblast growth factor-4.
Notophthalmus viridescens (Bastern newt) (Triturus viridescens).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Amphibia, Betrachia, Caudata; Salamandroidea; Salamandridae;
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Enterobacteriaceae, Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                          "Putative Newt Fibroblast Growth Factor-4.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, 976999; AAC98812.1;
HSSP, P09039; 1BFP.
InterPro; IPR001064; Crystallin.
InterPro; IPR002348; ILI_HBGF.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
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ches 0;
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PROSITE; PS00247; HBGF FGF; 1.
SEQUENCE 196 AA; 22033 MW; AC4688CD9890
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ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; I.
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Best Local Similarity
Matches 5; Conserv
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  EWSWL 46
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MEDLINE=86085668; PubMed=1079747; Coulton J.W., Mason P., Cameron D.R., Carmel G., Jean R., Rode H.N.; "Protein fusions of beta-galactosidase to ferrichrome-iron receptor of Escherichia coli K-12."; MEDLINE-87109068; PubMed=3027045; Ben-Bassat A., Bauer K., Chang S.; Ben-Bassat A., Bauer K., Chang S.?, "Processing of the initiation methionine from proteins: Properties of the Escherichia coli methionine aminopeptidase and its gene Richaud C., Richaud F., Martin C., Haziza C., Patte J.C.; "Regulation of expression and nucleotide sequence of the Escherichia coli dapD gene."; STRAIN=K-12;
MEDLINE=86278132; PubMed=3015933;
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Breton R., Sanfacon H., Papayannopoulos I., Biemann K., Lapointe J.;
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FROM N.A.
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gene involved in plasmid copy number control.";
J. Bacteriol. 171:1254-126(1988).
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J. Biol. Chem. 262:16037-16040(1987).
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"Secular Sequence and organization of copper resistance genes from
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Roncero M.I., Jepsen L.P., Stroman P., van Heeswijck R.;
"Characterization of a leuA gene and an ARS element from Mucor
circinelloides.";
                                           Coulton J.W., Mason P., Allatt D.D.;
"fhuc and fhub genes for Iron(III)-ferrichrome transport into Escherichia coli K-12.";
J. Bacteriol. 169:3844-3849(1987).
                                                                                                                              MEDLINE=88058963; PubMed=3316212;
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MEDLINE=89155419; PubMed=2537812;
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MEDLINE=89057448; PubMed=3057437;
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MEDLINE=87279948; PubMed=3301821;
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Rhabditidae; Peloderinae; Caenorhabditis.
STRAIN=K-12;
MEDLINE=88327165; PubMed=2666401;
Xie Q.W., Tabor C.W., Tabor H.;
"Spermidine blosyntheais in Bscherichia coli the promoter and the termination regions of the speED operon.";
J. Bacteriol. 171:4457-4465(1989).
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                                                                                                                                                                                    STRAIN=K-12;
MEDLINE=90113890; PubMed=2691840;
Lindquist S., Galleni M., Lindberg F., Normark S.;
"Signalling_proteins in enterobacterial ampC beta-lactamase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998). BEL; 281141; CAB03488.2; -. WormPep; ZC47.13; CE25668. InterPro; IPR001900; DUF38.
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100.0%; Pred. No. 4.1e+02;
/ative 0; Mismatches 0; Indels
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 AA; 36603 MW; 928464208868C48B CRC64;
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Mol. Microbiol. 3:1091-1102(1989)
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MEDLINE=99069613; PubMed=9851916;
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Pfam; PF01827; FTH; 1.
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Matches 5; Conserv
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

C STRAIN=16M / ATCC 23456 / Biotype 1;

NEDLINE=20020109; PubMed=11756688;

NEDLINE=20020109; PubMed=11756688;

DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,

La DelVecchio V.G., Kapatral V., Bernal A., Mazur M., Goltsman E.,

Aslbonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

Aslbor R., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

Haselkorn R., Kyrpides N., Overbeek R.;

Haselkorn R., Kyrpides N., Overbeek R.;

The genome sequence of the facultative intracellular pathogen

RT Brucella melitensis.";

L Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).

REMBL, Abc09577; AALS2575.1; --

RISOMERASE, CROMPlete proteome.
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                                                                                                                                         Leishmania major.
Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
NCBI _TaxID=5664;
                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=V12.;
MEDLINE=92105105, PubMed=1761547;
Muxray P.J., Spithill T.W.;
"Variants of a Leishmania Surface Antigen Derived from a Multigenic
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89.7%; Score 35; DB 16; Length 387;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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Brucellaceae; Brucella.
NCBI_TaxID=29459;
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89.7%; Score 35; DB 5; Length 371;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Surface antigen P2 (Fragment).
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Mannose-6-phosphate isomerase (EC 5.3.1.8).
                                      PRT; 371 AA.
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                                                                                                                                                                                                                                                                                              Family.",
J. Biol. Chem. 266:24477-24484(1991).
EMBL; X57134; CAA40413.1; -.
InterPro; IPR001611; LRR.
InterPro; IPR002965; LRR.
InterPro; IPR002965; P. Ich_extensn.
Ffam; PF00560; LRR; 2.
PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS50502; LRR. PS; 1.
                                      PRELIMINARY;
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Brucella melitensis.
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RESULT 14
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Search completed: February 18, 2004, 14:35:44 Job time : 18.3684 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 18, 2004, 13:39:39; Search time 3.55263 Seconds (without alignments) 79.423 Million cell updates/sec Run on:

US-09-643-260-8 39

1 LEWSWL 6 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

127863 segs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	015111 h inhibitor	E	O14920 homo sapien	-		P36646 escherichia	P58354 bos taurus	Q9ny64 homo sapien	Q9jif3 mus musculu		_		Q9bxt4 homo sapien	Q99mv1 mus musculu		Q05252 mycobacteri	_	P57544 buchnera ap	-	Q9wwrl pseudomonas		-	P29954 rhizobium m	P28327 bos taurus		Q9wv14 mus musculu	Q63651 rattus norv	P43250 homo sapien	O70293 mus musculu	P97711 rattus norv	P32298 homo sapien	P43249 bos taurus	P34947 homo sapien
SUMMARIES	ID	IKKA HUMAN	IKKA MOUSE	IKKB HUMAN	IKKB MOUSE	IKKB RAT	HOFC_ECOLI	GTR8 BOVIN	GTR8_HUMAN	GTR8_MOUSE	GTR8_RAT	ROR1_DROME	VG29_BPMU	TDR1_HUMAN	TDR1_MOUSE	Y076_HUMAN	VG41_BPML5	VG41_BPMD2	CYOA_BUCAI	QOX2_ACEAC	CYOA_PSEPU	DCUP_YEAST	D12_CREAL	MANA_RHIME	RK_BOVIN	RK_HUMAN	RK_MOUSE	RK_RAT	GRK6_HUMAN	GRK6_MOUSE	GRK6_RAT	GRK4_HUMAN	GRKS_BOVIN	GRK5_HUMAN
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GRKS_RAT YOR1_CAEEL GPKZ_DROME BCEL_MOUSE BCEL_RAT CRAA_BACUH AMPM_LACUH BPA3_CHICK BPA3_THUAN BPA3_HUMAN BPA3_HUMAN BPA3_MOUSE BPA3_RAT GUNG
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ALIGNMENTS

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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=97394468; PubMed=9252186;
DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
"A cytokine-responsive IkappaB kinase that activates the transcription
                    TISSUE-Cervical carcinoma;
MEDLINE-96258427; PubMed-8777433;
Connelly M.A., Marcu K.B.;
"CHUK, a new member of the helix-loop-helix and leucine zipper families of interacting proteins, contains a serine-threonine kinase catalytic domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L., Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.; "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for NF-kappaB activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hu M.C.-T., Wang Y.-P., "IkappaB kinase-alpha and -beta genes are coexpressed in adult and embryonic tissues but localized to different human chromosomes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97386461; PubMed=9244310;
Regrifucer C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe I
"Identification and characterization of an IkappaB kinase.";
Cell 90:373-3884(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
745 AA.
PRT;
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MEDLINE=99032998; PubMed=9813230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 388:548-554(1997).
STANDARD;
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IKK PHOSPHORYLATION.
MEDLINE-99038238; PubMed=9819420;
MEDLINE-99038238; PubMed=9819420;
Nemoto S., DiDonato J.A., Lin A.;
"Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
Mol. Cell. Biol. 18:7336-7343(1998).
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-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: Widely expressed.
-!- FTM: Phosphorylated by MAPSK14/NIK, AKT and to a lesser extent by MEKK1, and dephosphorylated by PP2A. Autophosphorylated.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21968797; PubMed=11971985; MCOA2; NCOA3; IKKB AND IKBKG. MEDLINE=21968797; PubMed=11971985; MV R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J., O'Malley B.W.; Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator activity by I kappa B kinase "; Mol. Cell. Biol. 22:3549-3561(2002).

-!-FUNCTION: Phosphorylates inhibitor/NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates
                                                                                                                 AND SER-180.
MEDLINE-98188283; PubMed=9520446;
Ling L., Cao Z., Goeddel D.V.;
"NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-99212141; PubMed-10195894;
Delhase M., Hayakawa M., Chen Y., Karin M.;
"Positive and negative regulation of IkappaB kinase activity through
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                                                                               PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "NF-kappaB activation by tumour necrosis factor requires the Akt serine-threonine kinase.";
Nature 401:82-85(1999).
                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
MEDLINE-99413720; PubMed=10485710;
Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M.,
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                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998)
Biol. Res. 41:537-549(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lammation and protection.";
J. Physiol. 278:C451-C462(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IKKbeta subunit phosphorylation.";
Science 284:309-313(1999).
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TKKA_MOUSE STANDARD; PRT; 745 AA.

§60680, §902x3;

16-0CT-2001 (Rel. 40, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

15-SEP-2003 (Rel. 42, Last annotation update)

15-SEP-2003 (Rel. 42, Last annotation update)

16-Keppa-B kinase alpha) (IkBKA) (IKK-alpha) (IKK-A) (Ikappa-B kinase)

(I-kappa-B kinase alpha) (IKKI) (Conserved helix-Loop-helix ubiquitous (Kinase) (Nuclear factor NFKappa-B inhibitor kinase alpha) (NFKBIKA).

CHUK OR IKKA.
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K-AM. LOSS OF AUTOPHOSPHORYLATION.
S-AA. LOSS OF PHOSPHORYLATION AND OF
ACTIVITY.
T-AS. NO CHANGE IN PHOSPHORYLATION.
S-AS. NO CHANGE IN PHOSPHORYLATION.
E -> G (IN REF. 5).
L -> AY (IN REF. 5).
TS -> AY (IN REF. 5).
F -> AY (IN REF. 5).
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PHOSPHORYLATION (BY PKB/AKT1).
PHOSPHORYLATION (BY MAP3K14).
                                                                                                                                               MIM; 600664; -. Grytoplasm; TAS. GO; GO:0065737; C:cytoplasm; TAS. GO; GO:0005737; C:cytoplasm; TAS. GO; GO:0005737; F:IkappaB kinase activity; TAS. GO; GO:0007285; P:I-kappaB phosphorylation; TAS. GO; GO:0007252; P:I-kappaB phosphorylation; TAS. GO; GO:0006955; P:Immune response; TAS. InterPro; IPR002290; Ser thr pkinase. InterPro; IPR002290; Ser thr pkinase. InterPro; IPR00245; Tyr pkinase. Pfam; PF00069; pkinase; 1. PR01109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                              Probom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKc; 1.
PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
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83.3%; Pred. No. 1.2e+02;
ive 1; Mismatches 0; Indels
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NEMO-BINDING.
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ATP (BY SIMILARITY).
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EMBL, AF012890; AAC51662.1; -.
EMBL, AF00225; AAC51671.1; -.
EMBL, AF080157; AAD08996.1; -.
EMBL, U22512; AAC50713.1; -.
HSSP; Q63450; 1A06.
Genew; HGNC:1974; CHUK.
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  Carrainescape, Shibata K., Yoshino M., Itoh M., Ishii Y., Shibata K., Yoshino M., Itoh M., Ishii Y., Shibata K., Yoshino M., Itoh M., Ishii Y., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arawai J., Shinagawa A., Shibata K., Yoshino H., Adachi J., Pukuda S., Arawawa T., Hara A., Pukunishi Y., Konno H., Kantawa T., Pukuda S., Anto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Adach M., Gasterland T., Gissi C., King B., Kochiwa H., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Anchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bakai K., Okido T., Puruno M., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Chenstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H., Lonnan M., Machima J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wayshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Maturica A., Nordon annocation of a full-length mouse cDNA collection.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nemoto S., Dibonato J.A., Lin A.; "Coordinate requilation of IkappaB kinases by mitogen-activated protein kinase kinase kinase 1 and NF-kappaB-inducing kinase."; Mol. Cell. Biol. 18:7336-743(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20198447; PubMed=10733566; McKenzie F.R., Connelly M.A., Balzarano D., Mueller J.R., Geleziunas R., Marcu K.B.; Geleziunas R., Marcu K.B.; Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking leucine zipper and helix-loop-helix domains reveal that IKKalpha and IKKbeta have different activation requirements.";
                                                                                           Mock B.A., Connelly M.A., McBride O.W., Kozak C.A., Marcu K.B., "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human
                                                                                                                                                                                                                                                                                    Connelly M.A., Marcu K.B., "Churk, a new member of the helix-loop-helix and leucine zipper families of interacting proteins, contains a serine-threonine kinase
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"Positive and negative regulation of IkappaB kinase activity through
IKKDeta subunit phosphorylation.";
Science 284:309-313(1999).
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MEDLINE-98188238; PubMed-9520401;
Nakano H., Shindo M., Sakon S., Niehinaka S., Mihara M., Yagita H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Differential regulation of IkappaB kinase alpha and beta by two upstream kinases. NF kappaB-inducing kinase and mitogen-activated protein kinase/ERK kinase kinase-1."; Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
                                                                                                                                             chromosome 10 and mouse chromosome 19."; Genomics 27:348-351(1995).
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                                                                                                                                                                                                                                                                  MEDLINE=96258427; PubMed=8777433;
                                                STRAIN=BALB/c;
MEDLINE=9604444; PubMed=7558004;
[1]
SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IKK PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                     catalytic domain."
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                                                                                                                                                                                                                                              STRAIN-BALB/c;
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REVIEW.

AX MEDLINE-20178139; PubMed=10712233;

RA Jobin C., Sartor R.B.;

RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT "The I kappa B/NF-kappa B system: a inflammation and protection.";

Am. J. Physiol. 278-c45-(2000).

CC -1- FUNCTION: Phosphorylates inhibitor/NF-kappa-B complex and
the dissociation of the inhibitor. Also phosphorylates
ultimately the degradation of the inhibitor. Also phosphorylates

CC Ultimately the degradation of the inhibitor. Also phosphorylates

MCA3.
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                                                                                                                                                                                                                                                                                                                                                                                             when dephosphorylated.
SUBDNIT: Preferentially found as a heterodimer with IKK-beta but subUNIT: Preferentially found as a heterodimer. Birectly interacts with IKK-gamma/NEMO. Heterodimers form the active complex. The tripartite complex can also bind to MARBAIA/NIK, MEKKI, IKAP and IKB-alpha-P65-P50 complex. A weak interaction with TRARZ cannot be excluded. Part of a complex composed of NCOA2, NCOA3, IKKB, IKBKG and CREBBP (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=3: Synonyme=Delta H;
IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;
TISSUE SPECIFICITY: Ubiquitcous only for isoform 1, isoforms 2 and 3 are expressed predominantly in brain and T-lymphocytes.
DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by E11, E15 and E17 days. In the limb development, its expresseion predominates in the limb buds at E12.5 day.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent MEKK1, and dephosphorylated by PP2A. Autophosphorylated.
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ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (BY PKB/AKT1)
(BY SIMILARITY).
PHOSPHORYLATION (BY MAP3K14)
(BY SIMILARITY).
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Prodom; PD00001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
PROSITE; PS0011; PROTEIN KINASE DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphorylation; Alternative spliting.

DOMAIN 15 476 LEUCINE-ZIPPER (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=2; Synonyms=Delta LH;
IsoId=060680-2; Sequence=VSP_004866, VSP_004867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEMO-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q60680-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:99484; Chuk.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR01245; Tyr pkinase.
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EMBL; AK018671; BAB31335.1; -.
PIR; I49101; I49901.
HSSP; Q63450; IA06.
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MEDLINE-98008814; PubMed=9346485;
Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;
"IkappaB kinase-bera: NF-kappaB activation and complex formation with IkappaB kinase-alpha and NIK.";
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14920; 075327; 16-077-201 (Rel. 40, Created) 16-077-201 (Rel. 40, Last sequence update) 16-077-201 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last annotation update) 17-SEP-2003 (Rel. 43, Last an
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MEDLINE=98438415; PubMed=9763654;
Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
"Assignment of IkappaB kinase beta (IKBKB) to human chromosome band
Bpl2-->pll by in situ hybridization.";
Cytogenet. Cell Genet. 82:32-33(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181. ITSUBE-CEVTICAL CARCIDOMA; MEDIJNE-98000813; Dubmdc-9346484; Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L., Mercurio F., Zhu H., Murray B.W., Mann M., Manning A., Rao A.; ItK.-1 and IKK.-2: cytokine-activated IkappaB kinases essential for NP-kappaB activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hu M.C.-T, Wang Y.-P.;
"IkappaB kinase-alpha and -beta genes are coexpressed in adult and embryonic tissues but localized to different human chromosomes.";
Gene 222:31-40(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                      Missing (In isoform 2).
/FIId=VSP_004867.
DHLXSDST -> GKTLQSQY (in isoform 3)
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Pred. No. 1.2e+02;
1; Mismatches 0; Indels
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                   3FEF5582AFF92233 CRC64;
                                                                                                                                                 /FTId=VSP 004868.
Missing (in isoform 3).
/FTId=VSP 004869.
K -> E (IN REF. 3).
S -> Y (IN REF. 3).
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Best Local Similarity 83.30,
Either 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 278:866-869(1997).
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                                                                                                                                                                                                                                                                                      745 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LEWSWL 6
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                                                                                                                                                                                                                                  236
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452
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MENTIFICATION IN A COMPLEX WITH CREBBP, NCOA2; NCOA3; IKKA AND IKBKG.

MEDILINE=21968797; PubMed=11971985;

Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,

AM Malley B.W.;

Regulation of SKC-3 (pCIPACTR/AIB-1/RAC-3/TRAM-1) coactivator

Regulation of SKC-3 (pCIPACTR/AIB-1/RAC-3/TRAM-1) coactivator

Activity by I kappa B kinase.";

Mol. Call. Biol. 22:3549-3561 (2002).

-I-FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to

the dissociation of the inhibitor/NF-kappa-B complex and

ultimately the degradation of the inhibitor. Also phosphorylates

NCOA3 (By similarity).

-I-SUBUNIT: Preferentially found as a heterodimer with IKK-aipha but

also as a homodimer. Directly interacts with IKK-aipha but

also bind to MEKKI, MAP3XI4/NIK, IKAP and IKB-aipha-P65-P50

complex. Phosphorylated IKB-aipha and IKB-aipha-P65-P50

complex. Pound in a complex composed of NCOA2, NCOA3, IKBKG
Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Bramer A.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., A. Richards S., Warley K.C., Hale S., Garcia A.M., Gibbs R.A., Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Scheri J.B., Jones S.J.M., Marra M.A.; Generation and initial analysis of more than 15,000 full-length Dr. Dr. Natl Marla M. A., Schi T. G. M. A., Scholl J. B. Dr. Natl M. Marra M.A.; Dr. Marra M.A.; Dr. Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.
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MEDLINES90038238; PubMed=9819420;
MEDLINES90038238; PubMed=9819420;
Nemoto S., DiDonato J.A., Lin A.;
"Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
Mol. Cell. Biol. 18:7336-7343(1998).
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TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal
muscle, kidney, pancreas, spleen, thymus, prostate, testis and
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SIMILARITY: BELÖNGS TO THE SER/THR FAMILY OF PROTEIN KINASES. IKAPPAB KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20178139; PubMed=10712233;
Jobin C., Sartor R.B.;
"The I kappa B/NP-kappa B system: a key determinant of mucosal inflammation and protection.";
Am. J. Physiol. 278:C451-C462(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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PHOSPHORYLATION
  SEQUENCE FROM N.A.
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S-SA: DECREASE OF ACTIVITY.
WHSKYRGKEEVDIVVSEDLACTIVATION.
WHSKYRGKEEVDIVVSEDLACTIVE -> CVRMWPGTVAHS
CNPSTLGGRGRMI (IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIXEM MOUSE STANDARD; PRT; 757 AA.
088351; Q9R1J6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
(I-kappa-B-kinase beta) (IKBKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIKB)
IKBKB OR IKKB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Differential regulation of IkappaB kinase alpha and beta by two upstream kinases, NF-kappaB-inducing kinase and mitogen-activated procein kinase/ERK kinase kinase-1.";
Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI TaxID=10090;
                           GO; GO:0005737; C:cytoplasm; NAS.
GO; GO:0005737; C:cytoplasm; NAS.
GO; GO:0004674; F:ATP binding activity; NAS.
GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.
GO; GO:0016563; F:transcriptional activator activity; NAS.
GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
InterPro; IPR00219; Prot kinase.
InterPro; IPR002290; Ser Ehr pkinase.
Pfam; PF00069; pkinase; 1.
Pfam; PF00069; ubiquitin; 1.
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                                                                                                                                                                                                                              ATP (BY SIMILARITY)
BY SIMILARITY
BY SIMILARITY
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION.
K->A: LOSS OF KINASE ACTIVITY AND
EFFECT ON BINDING TO NIK.
S->A: DECREASE OF ACTIVITY.
                                                                                                                                                                   Transferase; Serine/threonine-protein kinase; ATP-binding;
Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                      Length 756;
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                               LEUCINE-ZIPPER (POTENTIAL)
NEMO-BINDING.
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P9CADF671AE9E14E CRC64;
                                                                                                                                                                                                                      (BY SIMILARITY). (BY SIMILARITY).
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                                                                                                               Pfam; PF00240; ubiquitin; 1.
Probom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE_ATP; FALSE_NEG.
PROSITE; PS00108; PROTEIN KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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Pred. No. 1.2e+02;
                                                                                                                                                                                        PROTEIN KINASE.
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MEDLINE=98188238; PubMed=9520401;
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                                                                                                                                                                                                                                                                                                                                                                                86563 MW;
                                                                                                                                                                                                                                                                                                                                                                                                   92.3%;
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          HGNC:5960; IKBKB.
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RM WALCHT, WANG Y.-P. Withial I. A. Old W.R.; Warries that Warries the Kingen V.-P. Withial I. A. Old W.R.; Warries that Kingen V.-P. Withial I. A. Old W.R.; Warries that Kingen V.-P. Withial I. A. Old W.R. Warries that Kingen V.P. Withia Sandited Adapted declaration of 188 ").

RM M.C. T. WANG Y.-P. Old W.R. Warries are response signating a Wedlings of the Confidence of the M. Wedlings of the M. W. C. T. Warries of the M. R. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W. Warries of the M. W.
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-i- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK. Weakly autophosphorylated.
    Cytoplasmic.
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STRAIN-K12 / W3110;
MEDLINE-94261430; PubMed-8202364;
                                                                                                                                                                                                                                                                                     EMBL; AF115282; AAF21978.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86866 MW;
                                                                                  IKAPPAB KINASE SUBFAMILY.
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MEDLINE=99038238; PubMed=9819420;
Nemoto S., DiDonato J.A., Lin A.;
"Coordinate regulation of ikappaB kinases by mitogen-activated protein kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
Mol. Cell. Biol. 18:7336-7343(1998).
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Jobin C., Sartor R.B.;
in The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";
Am. J. Physiol. 278:C451-C465(2000)
-!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but also as a homodimer. Directly interacts with IKK-gamma/NEMO. Heterodimers form the active complex. The tripartite complex can also bind to MEKKI, MAPSKI4/NIK, IKAP and IKB-alpha-P65-P50 complex. Phosphorylated IKB-alpha is further released from the complex. Pound in a complex composed of NCOA2, NCOA3, IKKA, IKBKG and CREBBP (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last annotation update)
17-OCT-2001 (Rel. 41, Last annotation update)
17-Dibitor of nuclear factor kappa B kinase beta subunit (BC 2.7.1.-)
17-Mappa-B-kinase beta) (IKBKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
17-CKC2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIKB)
17-CKB OR IKKB.
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                           TLDWSWLQMEDEERCSLEQACD -> VTA (IN REF.
                                     NEMO-BINDING.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                      Length 757;
                                                                                                                                                                                                                                                                                                                                                                                    92.3%; Score 36; DB 1; Length 757
83.3%; Pred. No. 1.2e+02;
ive 1; Mismatches 0; Indels
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Zhang Y., Sun S., Ravid K.;
"IKK bt.a in megakaryocyte differentiation ";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
PROTEIN KINASE.
LEUCINE-ZIPPER (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                        FED962F095449C5E CRC64;
                                                                                                                                                                              N -> D (IN REF. 2).
K -> B (IN REF. 2).
K -> B (IN REF. 2).
P -> Q (IN REF. 2).
K -> R (IN REF. 2).
K -> R (IN REF. 2).
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Q9QY78;
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
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PHOSPHORYLATION (BY SIMILARITY)
PHOSPHORYLATION (BY SIMILARITY)
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InterPro; IPR000719; Prot kinase.
InterPro; IPR001245; Tyr_Dkinase.
InterPro; IPR001245; Tyr_Dkinase.
InterPro; IPR001245; Tyr_Dkinase.
Pfam; PF00069; PrikINASE; I
Probom; PP00010; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
PROSITE; PS00101; PROTEIN KINASE ST; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
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92.3%; Score 36; DB 1; Lengtu.
- pred. No. 1.2e+02;
0; Indels
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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01-JUN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HOPC OR HOPC OR B0106.
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SLC2A8 OR GLUT8 OR GLUTX1.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                     NCBI_TaxID=9913;
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GTR8_HUMAN
ID _GTR8_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Probable).
-!- SIMILARITY: BELONGS TO THE PULP/OUTF/EXEF/XPSF/XCPS FAMILY.
-!- CAUTION: REF.2 AND REF.4 SEQUENCES DIFFER IN THE N- AND C-TERMINAL AS WELL AS IN THE CENTRAL PART DUE TO FRAMESHIFTS.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Solute carrier family 2, facilitated glucose transporter, member 8
(Glucose transporter type 8) (Glucose transporter type X1) (Fragment).
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-> MAVSNSGAGMAYAQVVLTT (IN REF. 1).
9D37332B87AE07D5 CRC64;
                                                                                             SEQUENCE FROM N.A.
STRAINS-RIZ / MG1657.
STRAINS-RIZ / MG1657.
STRAINS-9742617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. J. 255:35-43 (1988).
Fujita N., Mori H., Yura T., Ishihama A., "Systematic sequencing of the Escherichia coli genome: analysis of the 2.4-4.1 min (110,917-193,643 bp) region.";
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                                                                                                                                                                                                                                                                                                                                                                        "Nucleotide sequence of the gene encoding the GMP reductase of Escherichia coli K12.",
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                                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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EMBL; AE000119; AAC73217.1; -.
EMBL; X07917; -; NOT ANNOTATED CDS.
PIR; B64733; B64733. D64733. D64733. D6733.  D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D67333. D673333. D67333. D67333. D67333. D673333. D673333. D673333. D67333. D673333. D673333. D673333. D673
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                                                                                                                                                                                                                                                                                               SEQUENCE OF 165-400 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                          Andrews S.C., Guest J.R.;
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5; Conserve
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P58354;
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                                                                                                                A Augustin R. Pocar P., Navarrete-Santos A., Wrenzycki C., Gandolfi F., A Augustin R., Pocar P., Navarrete-Santos A., Wrenzycki C., Gandolfi F., Niemann H., Fischer B.;

A Augustin R., Pocar P., Navarrete-Santos A., Wrenzycki C., Gandolfi F., Niemann H., Fischer B.;

A Glucose transporter expression is developmentally regulated in in vitro derived bovine preimplantation embryos.";

I. Mol. Reprod. Dev. 60:370:376(201).

-!- FUNCTION: Insulin-regulated facilitative glucose transporter.

Binds cytochalasin B in a glucose-inhibitable manner. Seems to be a dual-specific sugar transporter as it is inhibitable by fructose (By similarity).

C -!- SUBCELLULAR LOCATION: Integral membrane protein. Principally intracellular. May move between intracellular vesicles and the plasma membrane. The dileucine internalization motif is critical for intracellular sequestration (By similarity).

C -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
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InterPro; IPR007114; MFS.
InterPro; IPR005829; Sub transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR00819; Sugar tr;
PROSITE; PS00216; SuGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; PARTIAL.
Transport; Sugar transport; Transmembrane; Multigene family.
DOWAIN IL 1 CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (P
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Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                        PERGURNEE FROM N.A.

PERGURNEE FROM N.A.

MEDLINE=20138191; PubMed=10671487;

MEDLINE=20138191; PubMed=10671487;

MEDLINE=20138191; PubMed=10671487;

A libberson M.R., Uldry M.A., Thorens B.;

"GLUTX1, a novel mammalian glucose transporter expressed in the central nervous system and insulin-sensitive tissues.";

"GLUTX1, a novel nammalian glucose transporter. Sensitive Glucose transporter.

"GLUTY1, a novel nammalian glucose transporter."

"J Biol. Chem. 275:4607-4612(2000).

"I FUNCTION: Insuliar regulated facilitative glucose transporter. Sensitive Glucose (By similarity).

"I FUNCTION: Integral membrane protein. Principally intracellular. May move between intracellular vesicles and the plasma membrane. The dileucine internalization motif is critical for intracellular sequestration (By similarity).

"I ISSUE SPECIFICITY: Highly expressed in testis, but not in testicular carcinoma. Lower amounts present in most other tissues."

"INDUCTION: In testis, downregulated by estrogen.

"INDUCTION: In testis, downregulated by estrogen.

"I SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
                                                                                                                                                                                                                                                                                                                                                  Doege H., Schuermann A., Bahrenberg G., Brauers A., Joost H.-G.; "GLUTB, a novel member of the sugar transport facilitator family with glucose transport activity."; "Biol. Chem. 275:16275-16280(2000).
                                                                                             œ
                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Solute carrier family 2, facilitated glucose transporter, (Glucose transporter type 8) (Glucose transporter type XI)
SLCZA8 OR GLUT8 OR GLUTXI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transport; Sugar transport; Transmembrane; Glycoprotein; Multigene family.
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1 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005887; C:integral to plasma membrane; TAS. GO; GO:0005355; F:glucose transporter activity; TAS. GO; GO:0005975; P:carbohydrate metabolism; TAS. GO; GO:0015758; P:glucose transport; TAS.
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CYTOPLASMIC (POTENTIAL)
3 (POTENTIAL).
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PROSITE; PS00216; SUGAR TRANSPORT 1; 2.
PROSITE; PS00217; SUGAR TRANSPORT 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR003663; Sugar_transpt.
Pfam; PP000083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
                                                                                                                                                                                                                                                                                                        TISSUE=Testis;
MEDLINE=20283667; PubMed=10821868;
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Genew; HGNC:13812; SLC2A8.
MIM; 605245; -.
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46
70
91
96
                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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TISSUE=Testis;
MEDLINE=20283667; PubMed=10821868;
Doege H., Schuermann A., Bahrenberg C., Brauers A., Joost H.-G.;
"GLUT8, a novel member of the sugar transport facilitator family with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                               . .) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=129; TISSUE=Embryonic carcinoma; MEDLINE=20319023; PubMed=10860996; Carayannopoulos M.O., Chi M.M.-Y., Cui Y., Pingsterhaus J.M., Mcright R.A., Mueckler M., Devaskar S.U., Moley K.H.; "GLUTB is a glucose transporter responsible for insulin-stimulated glucose uptake in the blastocyst.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                DILEUCINE INTERNALIZATION MOTIF (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20138191; PubMed=10671487; Ibberson M.R., Uldry M.A., Thorens B.; "GLUTXI, a novel mammalian glucose transporter expressed in the central nervous system and insulin-sensitive tissues."; J. Biol. Chem. 275:4607-4612(2000).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation update)
Solute carrier family 2, facilitated glucose transporter, m
(Glucose transporter type 8) (Glucose transporter type XI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 1; Length 477; Pred. No. 1.6e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
11 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                         9 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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                                                         S (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
                           (POTENTIAL)
                                                                        (POTENTIAL).
                                                                                                                                                         8 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                              12 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
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FS -> LF (IN REF. 2).
T -> I (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
N-LINKED (GLCNAC.
S -> N (IN REF. 2)
                                                                                                                                                                                                                             10 (POTENTIAL).
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                                                                                                                       7 (POTENTIAL)
                                                                                                      CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glucose transport activity.";
J. Biol. Chem. 275:16275-16280(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                         Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.2%;
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377
457
462
50792 N
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Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    477 AA;
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Matches 5: Conser
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CONFLICT
SEQUENCE
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                                                                                                                                                          fructose.

-I-SUBCELLULAR LOCATION: Integral membrane protein. Principally intractose.

-Intracellular: May move between intracellular vesicles and the plasma membrane. The dileucine internalization motif is critical for intracellular sequestration (By similarity). Insulin induces a change in the intracellular localization and gives rise to insertion in the plasma membrane.

-I-TISSUB SPECIFICITY: Highest level of expression in placenta and testis. Highly expressed in adult and pubertal testis, but not prepubertal testis. Lower levels of expression in brain, liver, heart, kidney, fat and skeletal muscle.

-I-INDUCTION: Inhibited under glucose deprivation.

-I-INDUCTION: Inhibited under glucose deprivation.

-IRANSPORTERS SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                Scheepers A., Doege H., Joost H.-G., Schuermann A.;
Mouse GLUTB: genomic organization and regulation of expression in
3T3-L1 adippocytes by glucose.";
Blochem. Blophys. Res. Commun. 288:969-974(2001).
-I- FUNCTION: Insulin-regulated facilitative glucose transporter.
Bluds cytochalasin B in a glucose-inhibitable manner. Seems to be
a dual-specific sugar transporter as it is inhibitable by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1860103; SIGZ88.
GO; GO:0005887; C:integral to plasma membrane; IDA.
GO; GO:0005887; C:integral to plasma membrane; IDA.
GO; GO:000535; F:glucose binding activity; IDA.
GO; GO:001575; F:glucose transporter activity; IDA.
GO; GO:0015758; P:glucose transport; IDA.
GO; GO:0015758; P:insulin receptor signaling pathway; IDA.
GO; GO:0001666; P:response to hypoxia; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0171; SUGRTRNSPORT.
TIGROBA9; SP; 1.
PROSITE; PSO0217; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
Transport; Sugar transport; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
5 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
 Proc. Natl. Acad. Sci. U.S.A. 97:7313-7318(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR003663; Sugar_transpt.
Pfam; PP00083; sugar_tr; 1.
                      SEQUENCE FROM N.A.
STRAIN-129/Ola; TISSUE-Spleen;
MEDLINE-21547794; Pubmed=11689004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y17802; CAB89815.1; -.
EMBL; AF232061; AAF78366.1; -.
EMBL; AJ413951; CAC88690.1; -.
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Multigene family
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DOMAIN
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TRANSMEM
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SUBCELLULAR LOCATION: Integral membrane protein. Principally intracellular. May move between intracellular vesicles and the plasma membrane. The dileucine internalization motif is critical for intracellular sequestration.

TISSUE SPECIFICITY: Highly expressed in adult and pubertal testis, but not prepubertal testis. Moderate expression in hypothalamus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Doege H., Schuermann A., Bahrenberg C., Brauers A., Joost H.-G.; GLUTB, a novel member of the sugar transport facilitator family with "GLUTB, a novel member of the sugar transport facilitator family with J. Biol. Chem. 275:16275-16280(2000).
-!- FUNCTION: Insulin-regulated facilitative glucose transporter.
- Binds cytochalasin B in a glucose-inhibitable manner. Seems to be a dual-specific sugar transporter as it is inhibitable by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                  (GLCNAC. . .) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., CHARACTERIZATION, AND MUTAGENESIS OF LEU-12 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Solute carrier family 2, facilitated glucose transporter, member (Glucose transporter type 8) (Glucose transporter type X1). SLC2A8 OR GLUTS OR GLUTX1.
                                                                                                                                                                                    12 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
DILEUCINE INTERNALIZATION MOTIF (BY
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ibberson M.R., Uldry M.A., Thorens B.; "GLUTX1, a novel mammalian glucose transporter expressed in the central nervous system and insulin-sensitive tissues.";
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"Molecular cloning of a new putative glucose transporter.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 1; Length 477;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                      9 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
10 (POTENTIAL).
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39 S -> N (IN REF. 1).
429 S -> N (IN REF. 2 AND 4).
51523 MW; A3753FB34E452F9A CRC64;
                   (POTENTIAL)
                                                                                                                                                           EXTRACELLULAR (POTENTIAL)
                                                                                                                 CYTOPLASMIC (POTENTIAL).
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Last annotation update)
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                                                                                                                                        (POTENTIAL)
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sed)
15-SEP-2003 (Rel. 42, Last ann
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83.3%;
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Best Local Similarity
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kinases."
                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation her buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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DILEUCINE INTERNALIZATION MOTIF.
DILEUCINE INTERNALIZATION MOTIF.
IL->AA: CHANGES SUBCELLULAR LOCATION
MAINLY TO THE PLASMA MEMBRANE, THREREBY
INCREASING TRANSPORT ACTIVITY.
GG -> QGA (IN REF. 2).
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                  amounts present in most other tissues. SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
cerebellum, brainstem, hippocampus, and adrenal gland. Lower
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3 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
4 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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9 (POTENTIAL).
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CYTOPLASMIC (
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InterPro; IPR005829; Sug_transporter.
InterPro; IPR003629; Sug_transporter.
InterPro; IPR00362; Sugar_transpt.
Pfan; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
TIGRAMs; TIGROMS; SP; 1.
PROSITE; PS00216; SUGAR_TRANSPORT]; 2.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                     entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
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51458 MW;
                                                        TRANSPORTERS SUBFAMILY
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Matches 5, Conservative
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685 AA.

PRT;

RORI DROME STANDARD; 1 Q24488; 28-FEB-2003 (Rel. 41, Created)

HAD

RESULT 11

179 LEWRWL 184

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DE SEPER-2003 (Rel. 41, Last sequence update)

DE SEPER-2003 (Rel. 41, Last sequence update)

DE SEPER-2003 (Rel. 41, Last sequence update)

DE SEPER-2003 (Rel. 41, Last sequence update)

DE SEPER-2003 (Rel. 41, Last sequence update)

DE SEPER-2003 (Rel. 41, Last sequence update)

DE SEPER-2003 (Rel. 41, Last sequence update)

DE SEPER-2003 (Rel. 41, Last sequence update)

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NERGINES-2013 (Rel. 41, Last sequence update)

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NERGINES-2013 (Rel. 41, Last sequence update)

NERGINES-2013 (Rel. 41, Last sequence update)

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h 87.2%;
Similarity 83.3%;
5; Conservative
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16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
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       Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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R PRINTS; PRODOUGH; KAINGLE.
R PRODOM; PD000019; TYRKINASE.
Probom; PD000019; TYRKINASE.
R PRODOM; PRODOUGH; Proc Kinase; 1.
R PROSTIE; SM0019; TyrKc. 1.
R PROSTIE; PS00021; KRINGLE 1; 1.
R PROSTIE; PS00107; PROTEIN KINASE ATP; 1.
R PROSTIE; PS00107; PROTEIN KINASE TYP; 1.
R PROSTIE; PS00109; PROTEIN KINASE TYR; 1.
R PROSTIE; PS00219; PROTEIN KINASE TYR; 1.
R PROSTIE; PS00219; PROTEIN KINASE TYR; 1.
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-1- TISSUE SPECIFICITY: Expressed in neurons of the developing nervous
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TYROSINE-PROTEIN KINASE TRANSMEMBRANE
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(POTENTIAL).
(POTENTIAL).
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                                              -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. ROR
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL).
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GO; GO: 0016621; C: integral to membrane; NAS.

GO; GO: 0016621; C: integral to membrane; NAS.

GO; GO: 0001413; F: procein tyrosine kinase activity; NAS.

GO; GO: 0004417; F: central nervous system development; IEP.

GO; GO: 0006468; P: protein amino acid phosphorylation; NAS.

InterPro; IPR00024; Fz domain.

InterPro; IPR00019; Prot kinase.

InterPro; IPR001919; Prot kinase.

InterPro; IPR001919; Prot kinase.

InterPro; IPR001919; Prot kinase.

InterPro; IPR001919; Prot kinase.

InterPro; IPR001919; IPY pkinase.

Pfam; PF00069; pkinase; 1.
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BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY
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PHOSPHORYLATION (AUTO-) (BY
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ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                 EMBL, L20297; AAA28860.1; -.
EMBL, AE003628; AAF52885.1; -.
EMBL, AJ002908; CAA05743.1; -.
PIR, A48289; A48289.
HSSP, P11362; LFGK.
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SEQUENCE OF 67-777 PROM N.A.
Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
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                                                   Gape
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Morgan G., Hatfull G., Hendrix R.;
Morgan G., Hatfull G., Hendrix R.;
"Genome of bacteriophage Mu and comparison with the Haemophilus
influenzae Mu-like prophage Pluwu.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: STRONG, TO H.INFLUENZAE H11501.
                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae; Mu-like viruses.
NCBI_TaxID=10677;
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MEDLINE=2115748; PubMed=11279525;
MANDY P.J., McCarrey J.R., Yang F., Page D.C.;
"An abundance of X-linked genes expressed in spermatogonia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.6%; Score 33; DB 1; Length 512; 66.7%; Pred. No. 2.4e+02; ive 1; Mismatches 1; Indels
Score 34; DB 1; Length 685;
Pred. No. 2.2e+02;
0; Mismatches 1; Indels
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SEQUENCE 512 AA; 56888 MW; 35E1B99373DCFC36 CRC64;
                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
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28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Tudor domain containing protein 1.
                                                                                                                                                                                                                                                     512 AA.
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Best Local Similarity 66.77
Enhan 4; Conservative
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01-NOV-1997
01-NOV-1997
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Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Jobayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S., "NEDO human cDNA sequencing project.", Substance S., Substance S., Tanaka T., Fatis and ovrary specific.

-I TISSUE SPECIFICITY: Testis and ovrary specific.
-I SIMILARITY: Contains 3 Tudor domains.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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TUDOR 2.

TUDOR 3.

T -> M (IN REF. 2).

VKS -> KKKKK (IN REF. 2).

W; A733B80D3D76A8EC CRC64;
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28-FEB-2003 (Rel. 41, Last annotation update)
Tudor domain containing protein 1.
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Interpro; IPR002999; Tudor.
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28-FEB-2003 (Rel. 41, Last seq
28-FEB-2003 (Rel. 41, Last anno
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SMART; SM00333; TUDOR; 3.
PROSITE; PS50304; TUDOR; 3.
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359 4
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737 7
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Best Local Similarity
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Q99MV1;
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MEDINE-57: PubMed=12477932;

MEDINE-57: PubMed=12477932;

MEDINE-5388257;

MEDINE-5388257;

MEDINE-5388257;

MAGNER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Bhatseley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.; Homan and mouse conx sequences: "

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S.,
Seki N., Kawarabayasi Y., Ishikawa K.-I., Tabata S.,
"Prediction of the coding sequences of unidentified human genes. I
The coding sequences of 10 new genes (KIAA0041-KIAA0080) deduced analysis of cDNA clones from human cell line KG-I.";
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Pred. No. 4.2e+02;
% Mismatches 0; Indels
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(Rel. 35, Last sequence update)
(Rel. 42, Last annotation update)
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TUDOR 3.
TUDOR 4.
                                                     InterPro; IPR001097; Maternal_tudor.
InterPro; IPR002999; Tudor.
Pfam; PF00567; TUDOR; 4.
SMART; SM00333; TUDOR; 4.
PROSITE; PS50304; TUDOR; 4.
EMBL; AF285591; AAK31970.1; -.
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                              MGD; MGI:1933218; Tdrdl
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351
571
796
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CC or send an email to license@isb-sib.ch).

CC or send an email to license@isb-sib.ch).

CR EMBL; D38548; BAA07551.1; -.

DR EMBL; D38548; BAA07551.1; -.

CN Hypothetical protein.

SQ SEQUENCE 1698 AA; 191188 WW; 57B11CC478E3EEDA CRC64;

Query Match

Best Local Similarity 66.7%; Pred. No. 7.56+02; Mismatches 0; Indels 0; Gaps 0;
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Search completed: February 18, 2004, 14:28:06 Job time : 4.55263 secs

1 LEWSWL 6 |:|:|| 1446 LQWTWL 1451

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GenCore version 5.1.6
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OM protein - protein search, using sw model

February 18, 2004, 14:12:09; Search time 6.5921 Seconds (without alignments) 87.531 Million cell updates/sec Run on:

US-09-643-260-8 39

1 LEWSWL 6 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

PC1155 F70983 E90438	C1155 70983 90438	21155 70983	1155	1155 Ig heavy			T11137 NAD		Desc		
0438	0438	2000		7000	1100	1155	1101 444 444 9075 9075 1733 1733 1733 1606 1606 174 173 173 173 173 173 173 173 173 173 173	1101, 9944 9444 10075 1318 8713 8814 8874 872	1137 1101 1101 1101 1001 1001 1001 1001	33.7 0.01 0.01 0.05 0.06 0.06 0.06 0.06 0.06 0.06 0.06	1137 1137 1101 1101 1015 1015 1015 1015 1015 101
390438	90438			0983	0983	1155	149101 PPN0444 PPN0444 PPN0444 MD13426 MG1318 MG4733 GMS11 AB4606 AB4606 MG4954 TC4954 TC4954	910) 910) 940) 940) 940) 940) 940) 9413 9413 9413 9413	1137 1101 1101 1101 1101 1101 1101 1101	337 001 001 001 108 108 109 109 109 109 109 109 109 109 109 109	137 137 1444 1444 1544 160 175 1318 1313 1313 1313 1413 1413 1472 1874
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c.		hypothetical prote	hypothetical prote	protein R09E10.3 [hypothetical prote	hypothetical prote	hypothetical prote	gene 41 protein -	gp41 protein - Myc	probable phage-rel	Ig V-D-J region (M	mel-13a protein -	conserved hypothet	CT556 hypothetical	hypothetical prote
F97654	T24087	T24092	T32136 ·	F88808	T20804	T00350	AD2464	830986	F72804	AG0447	869909	S65785	A72029	H86594	T50421
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84.6		84.6	84.6	84.6	84.6	84.6	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1
33	33	33	33	33	33	33			32	32	32	32	32	32	32
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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RESULT 1

Table dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - acorn worm mitochondrion C;Species: mitochondrion Balanoglossus carnosus
C;Species: mitochondrion Balanoglossus carnosus
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C;Accession: Tall37
R;Castresana, J; Feldmaier-Fuchs, G; Yokobori, S; Satoh, N.; Paabo, S.
Genetics 150, 1115-1123, 1998
A;Title: The mitochondrial genome of the hemichordate Balanoglossus carnosus and the ev A;Title: The mitochondrial genome of the hemichordate Balanoglossus carnosus and the ev A;Testus: preliminary; translated from GB/EMBL/DDBJ
A;Accession: Till37
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-645 <CAS>
A;Cross-references: EMBL:AF051097; NID:g3065680; PID:g3065682; PIDN:AAD11945.1
C;Genetics:
A;Genome: mitochondrion
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

ö Query Match 92.3%; Score 36; DB 2; Length 645; Best Local Similarity 83.3%; Pred. No. 2e+02; Matches 5; Conservative 1; Mismatches 0; Indels

Gaps ö

|||:|| 96 LEWTWL 101 1 LEWSWL 6 ò g

RESULT 2 149101

C;Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homol C;Keywords: ATP; phosphotransferase F;13-283/Domain: protein kinase homology <KIN>

92.3%; Score 36; DB 1; Length 745; 83.3%; Pred. No. 2.3e+02; Query Match Best Local Similarity

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A,Title: Variants of a Leishmania surface antigen derived from a multigenic family.
A,Reference number: A41710; MUID:92105105; PMID:1761547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100. Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
                                                                     A;Accession: S20075
A;Molecule type: mRNA
A;Residues: 1-371 <MUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: AD3426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: AD3426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: BMEI1394
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                                                                                                                                                                                                                                                                                                                  Fixeluza, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A;Title: A general method for chimerization of monoclonal antibodies by inverse polymera
A;Reference number: PN0444; MUID:93138402; PMID:1339379
A;Accession: PN0444
A;Accession: PN0444
A;Residues: 1-150 «KAL»
A;Cross-references: GB:L02346
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promastigote surface antigen P2 (clone 2.5) precursor - Leishmania major (fragment)
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                                                                                                                                                                                                                                                    ;Species: Homo sapiens (man)
;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000;Accession: PN0444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Caenorhabditis elegans
Space: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
Accession: T27590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Leishmania major
C;Date: 13-3na-1995 #sequence_revision 06-Feb-1998 #text_change 31-Jan-2000
C;Accession: S20075; C41710
R;Murray, P.J.; Spithill, T.W.
     Gaps
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A; Reference number: 220391

A; Accession: T2590

A; Accession: T2590

A; A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A; Residues: 1-242 < WIL>
A; Residues: 1-242 < WIL>
A; Cross-references: EMBL: Z81141; PIDN: CAB03488.1; CESP: ZC47.13

A; Experimental source: clone ZC47

A; Genetics:
A; Genetics:
A; Genetics: A; Casp: ZC47.13

A; Introns: 172/3

C; Superfamily: Caenorhabditis elegans hypothetical protein ZC47.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-19/Domain: signal sequence #status predicted <SIG>
;20-150/Product: Ig heavy chain V region #status predicted <MAT>
;20-117/Domain: variable region <VRG>
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89.7%; Score 35; DB 2; Length 242;
Best Local Similarity 83.3%; Pred. No. 1.18+02;
Matches 5; Conservative 0; Mismatches 1; Indels
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  Indels
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                                                                                                                                                                                                                             Ig heavy chain V region precursor - human (fragment)
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Pred. No. 66;
2; Mismatches
  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.78;
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Best Local Similarity 66.7
Matches 4; Conservative
  Conservative
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738 LDWSWL 743
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                                                   1 LEWSWL 6
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1 MEWSWI 6
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A,Cross-references: EMBL:X57134; NID:g9580; PID:g9581
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkag, F;1-343/Product: promastigote surface antigen P2 (fragment) #status predicted <PSA-F;344-371/Domain: carboxyl-terminal propeptide #status predicted <CTP-F;343/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asp) (in mature form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.Delvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R.Delvecchio, V.G.; Kapatral, V.; Relkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens. A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cjaccession: AG2318
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Si
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mannose-6-phosphate isomerase (EC 5.3.1.8) [imported] - Brucella melitensis (strain 16M)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein all4102 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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A;Cross-references: GB:BA000019; PIDN:BAB75801.1; PID:g17133237; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-387 «KUR»
A;Cross-references: GB:AE008917; PIDN:AAL52575.1; PID:g17983392; GSPDB:GN00190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Brucella melitensis
C;Date: 01-Feb_2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
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                                                                                                                                                                                                                                                                      89.7%; Score 35; DB 2; Length 371; 100.0%; Pred. No. 1.6e+02; Artive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.7e+02;
tive 0; Mismatches 0;
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A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from , A;Reference number: A02157; MUID:80120716; PMID:6766534 A;Contents: a allele
                                                                                                                                                                                                                                                                                                                                                        A,Note: the sequence was determined from the germline gene
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A;Title: Structure of the constant and 3' untranslated regions of the murine gamma2b he.
A;Reference number: A26235; WUID:80081501; PMID:117548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gam. A;Reference number: A26233; MUID:82173203; PMID:6803173
A;Contents: b allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kim, H ; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahasi
J. Biol. Chem. 269, 12345-12350, 1994
A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A;Reference number: A53598; MUID:94216359; PMID:7512967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ajournous: 138/1, 236/1; 258/1; 368/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kan hain disultide bonds. In some cases, such as IgA and IgM, the subunits associate into I c;Complex: An immunoglobulin c region; immunoglobulin homology circultide bonds. In special circultide bonds: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin homology cim: p:286-257/Region: hinge produced p:287/Region: hinge produced p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: immunoglobulin homology cim: p:387-454/Domain: p:387-454/Domain: p:387-454/Domain: p:387-454/Domain: p:387-454/Domain: p:387-454/Domain: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: DNA
A,Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474 <OLL>
A,Cross-references: GB:J00461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Roesidues: 138-127, Pr,174-189, 'FP',193-376,'T',378-474 <TU1>
A;Note: Lys-474 is probably removed posttranslationally
R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.7%; Score 35; DB 1; Length 474; 66.7%; Pred. No. 2.1e+02;
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A;Residues: 1381.72,'P',174-189,'FP',193-376,'T',378-474 <TU2>
R;Ollo, R: Rougeon, F.
Nature 296, 761-763, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 206, 1303-1306, 1979
A,Title: Sequence of the cloned gene for the constant 3A,Reference number: A26232; WUID:80081502; PMID:117549
A,Accession: A26232
                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 138-161,'L',163-189,'PP',193-474 <YAM>
A;Cross-references: GB:J00461
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C;Comment: The a allele sequence is shown.
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A, Residues: 234-251 < KIM;
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A;Accession: A26235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A26233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein transport protein hofC - Escherichia coli (strain K-12)
Cispecies: Escherichia coli
Cipate: 12-Sep-1997 #sequence revision 17-Sep-1997 #text_change 01-Mar-2002
CiAccession: B64733; S45184; S45183
RiBlattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome, sequence of Escherichia coli K-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S45183
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Molecule type: DNA
A; Cross-references: EMBL:D26562; NID:g473770; PIDN:BAA05562.1; PID:g473773
A; Experimental Bource: strain K-12
C; Genetics
C; Genetics
A; Genetics
C; Superfamily: secretion protein xcpS
C; Superfamily: secretion protein xcpS
C; Superfamily: secretion protein wcpS
F; S107-183, Domain: transmembrane #status predicted <TM1>
F; 219-235, Domain: transmembrane #status predicted <TM2>
F; 219-235, Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-400 <BLAT>
A;Cross-references: GB:AE000119; GB:U00096; NID:g1786283; PIDN:AAC73217.1; PID:g1786295;
A;Experimental source: strain K-12, substrain MG1655
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Cispecies: Mus musculus (house mouse)
Cjate: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
CjAccession: 825057; A03157; A26325; A26323; A26333; A53598
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific: A;Reference number: 825057
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A;Cross-references: EMBL:D26562; NID:g473770; PIDN:BAA05563.1; PID:g473774
A;Experimental source: strain K-12
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A;Residues: 1-474 <FIS.
A;Cross-references: EMBL:X67210; NID:954826; PIDN:CAA47649.1; PID:954827
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
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    Length 391;
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; Mismatches 0;
Score 35; DB 2; I
Pred. No. 1.7e+02;
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89.7%; Score 35; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.7e+0.
Matches 5; Conservative 0; Mismatches
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                                                                                         0; Mismatches
         Score 35;
83.3%;
                                                                                    Conservative
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A;Accession: S45184
                                     Best Local Similarity
Matches 5; Conserv
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    Query Match
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Length 1379;

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F;789-810/Domain: transmembrane #status predicted <TMM>F;856-1188/Domain: protein kinase homology <KIN>F;864-872/Region: protein kinase ATP-binding motif
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83.3%;
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity
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Valternate names: Quail endothelial kinase 2; Quek 2
C;Species: Coturnix coturnix japonica (Japanese quail)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 24-Sep-1999
C;Accession: JC4954
R;Bichmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.
Gene 174, 3-8, 1996
A;Title: Molecular cloning of Quek 1 and 2, two quail vascular endothelial growth factor A;Recence number: JC4953; MUID:97017121; PMID:8863722
A;Accession: JC4954
A;Status: nucleic acid sequence not shown
A;Residues: 1-1379 cEIC>
A;Coss-references: EMEL:X83287; NID:g619865; PIDN:CAA58267.1; PID:e283815; PID:g1707416
C;Comment: This protein is an endothelial-specific receptor and binds vascular endothelial C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases, protein kinase homolo C;Keywords: App: embryo; growth factor receptor; transmembrane protein
C;Keywords: App: embryo; growth factor receptor; transmembrane protein
C;Keywords: App: embryo; growth factor receptor; transmembrane protein
C;Keywords: App: embryo; growth factor receptor; transmembrane protein
C;Keywords: App: embryo; growth factor receptor; transmembrane protein
C;Keywords: App: embryo; growth factor receptor; transmembrane protein
C;Keywords: App: embryo; growth factor receptor; transmembrane protein
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. Guss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;bate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: H82874
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
A;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
A;Bescription: The complete sequence of Ureaplasma urealyticum: Alternate views of a min A;Reference number: A82870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: H82874
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1367 <GLA>
A;Cross-references: GB:AE002155; GB:AF222894; NID:g6899572; PIDN:AAF30985.1; GSPDB:GN001
A;Experimental source: serovar 3; blovar 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conserved hypothetical ATP/GTP-binding protein UU571 [imported] - Ureaplasma urealyticum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 89.7%; Score 35; DB 2; Length 522; Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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Matches 5; Conserv
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C,Genetics:
A,Gene: UU571
A,Genetic code: SGC3
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                                                                                                                                                                                                                                                A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                A; Accession: A84606
A; Status: prelimina
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probable acetyl-CoA carboxylase (EC 6.4.1.2) W09B6.1 [similarity] - Caenorhabditis elega
C,Species: Caenorhabditis elegans
C,Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 2
A;Introna: 18/3; 50/3; 97/1; 734/2; 793/3; 1975/2; 2037/2
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin-
C;Keywords: ligase
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A;Cross-references: EMBL:AF025469; PIDN:AAB71048.1; GSPDB:GN00020; CESP:W09B6.1
A;Experimental source: strain Bristol N2; clone W09B6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein - Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
                                                      Gaps
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R; Goela, D.; Maggi, L.; Andrews, S.
submitted to the EMBL Data Library, September 1997
A; Description: The sequence of C. elegans cosmid W09B6.
A; Reference number: Z21162
A; Accession: T32413
89.7%; Score 35; DB 2; Le
100.0%; Pred. No. 5.9e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.7%; Score 35; DB 2; Le
100.0%; Pred. No. 8.8e+02;
tive 0; Mismatches 0;
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A;Molecule type: DNA
A;Residues: 1-116 <VLC>
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A;Molecule type: DNA
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Pred. No. 73;
0; Mismatches
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Ighavy chain precursor V region (VAR100) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S03289
R;Blankenstein, T.; Bonhomme, F.; Krawinkel, U.
Immunogenetics 26, 237-248, 1987
A;Title: Evolution of pseudogenes in the immunoglobulin V(H)-gene family of the mouse.
A;Reference number: S03289; MUID:88006305; PMID:2820872
A;Reference number: S03289; MUID:88006305; PMID:2820872
A;Status: translation not shown
A;Molecule type: DNA
A;Status: Lil7 *BLA>
A;Cross-references: EMBL:X06866; NID:952454; PIDN:CAA29991.1; PID:g758157
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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Search completed: February 18, 2004, 14:38:42 Job time : 8.5921 secs

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APPLICANT: Noth, Mike
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APPLICANT: Wolfe, Mike
APPLICANT: Wolfe, Mike
TILLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCE: 1
CORRESPONDENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPTRY: USA
ZIP: 94104
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                         February 18, 2004, 14:16:39; Search time 7.06579 Seconds (without alignments) 35.929 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-887-518-3
US-09-032-31-3
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US-09-032-475-3
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US-09-03-125A-2
US-09-09-125A-2
US-09-09-125A-2
US-09-09-125A-2
US-09-09-125A-2
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                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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US-09-168-629-15
US-08-910-820-9
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Maximum Match 100%
Listing first 45 summaries
                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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US-09-252-991A-28780

| Sequence 28780, Application US/09252991A
| Sequence 28780, Application US/09252991A
| Sequence 28780, Application US/09252991A
| Patent No. 6551703|
| APPLICANT: Marc J. Rubenfield et al. |
| TITLE OF INVENTION: NUCLEIC ACID ANNO AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS |
| TITLE OF INVENTION: NUCLEIC ACID ANNO AMINO ACID SEQUENCES RELATING TO UNRERT OF ILLING INVENTION: 107196.136 |
| FILE REFERENCE: 107196.136 |
| FILE REFERENCE: 107196.136 |
| FILE REFERENCE: 107196.136 |
| FILING DATE: 1999-02-18 |
| PRIOR APPLICATION NUMBER: US 60/094,190 |
| PRIOR FILING DATE: 1998-0-2-18 |
| PRIOR FILING DATE: 1998-0-2-7 |
| NUMBER OF SEQ ID NOS: 33142 |
| SEQ ID NO 28780 |
| LENGTH: 454 |
| TENGTH: 454
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100.0%; Pred. No. 1.3e+02;
iive 0; Mismatches 0;
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US-09-814-908-9
US-09-817-123
US-08-32-419-2
US-08-32-419-2
US-08-35-561-27
US-08-36-561-74
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Patent No. 5843721
GENERAL INFORMATION:
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28780
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Best Local Similarity
Matches 6; Conserv
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GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Goeddel, David V.
APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK-
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STRYE: CALLERONIA
COUNTRY: USA
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Patent No. 5854003

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

APPLICANT: Wu, Lin

TITLE OF INFORTION: NIK Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAM GROUP
                                               Score 36; DB 2; Length 745; Pred. No. 5.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 745;
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83.3%; Pred. No. 5.5e+02;
"..marches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200
                                                                                           1; Mismatches
                                                                                                                                                                                                                                           RESULT 4
US-08-890-853-4
; Sequence 4, Application US/08890853
; Patent No. 5851812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: TS
                                               92.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 745 amino acids
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                 1:|||
738 LDWSWL 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    738 LDWSWL 743
                                               Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                    1 LEWSWL 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
      US-09-023-321-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-890-853-4
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US-09-032-475-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09023321
; Sequence 3, Application US/09023321
; Patent No. 5844073
; GENERAL INFORMATION:
    APPLICANT: Rothe, Mike
; APPLICANT: Rothe, Mike
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALLFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 2; Length 745;
Pred. No. 5.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
FILING DATE:
CLASSIFICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSNAW, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEPHONE: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: A15 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
HOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
RECISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 197-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (115) 349-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 92.3
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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738 LDWSWL 743
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Gapa

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| Sequence 4, Application US/09099124A |
| Sequence 4, Application US/09099124A |
| Patent No. 5339302 |
| GENERAL INFORMATION: |
| APPLICANT: Goodel, David V. |
| APPLICANT: Goodel, John |
| TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods |
| NUMBER OF SEQUENCES: 4 |
| CORRESPONDENCE ADDRESS: |
| STREET: 268 BUSH STREET, SUITE 3200 |
| CITY: SAN FRANCISCO |
| STATE: CALIFORNIA |
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                 Score 36; DB 2; Length 745;
Pred. No. 5.5e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.3%; Score 36; DB 2; Length 745; 83.3%; Pred. No. 5.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,124A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION O:
RICAR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 35,627
REFERNCE/DOCKET NUMBER: 197-006-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                      TELEPHONE: (415) 343-4341
TELEPAK: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      92.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                              LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 745 amino acids
TYPE: amino acid
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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738 LDWSWL 743
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738 LDWSWL 743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-099-124A-4
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| Sequence 4, Application US/09099125A
| Patent No. 5916760
| GENERAL INFORMATION:
| APPLICANT: Goeddel, David V. APPLICANT: Woronicz, John TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods INVBER OF SEQUENCES:
| ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET; SUITE 3200
| CITY: SAN FRANCISCO CITY: SAN FRANCISCO CITY: SAN FRANCISCO CITY: SAN FRANCISCO CITY: SAN FRANCISCO CITY: SAN FRANCISCO CITY: BATORIC COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: WADDIM TYPE: Floppy disk COMPUTER: INP PC compatible COMPUTER: INP PC compatible COMPUTER: PSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 745;
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83.3%; Pred. No. 5.5e+02;
                                                         ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,475
FLING DATE:
RICHARD ATE:
APPLICATION NUMBER: 08/887,518
FLING DATE:
NAME: OSWAN, RICHARD A
REGISTRATION:
NAME: OSWAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,125A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 83.3.5
Lag 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: peptide
  SAN FRANCISCO
                         CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1:||||
738 LDWSWL 743
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CITY: SA
STATE: CA
COUNTRY:
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Gaps

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: 745 amino acids
amino acid
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    738 LDWSWL 743
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                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-890-854-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-023-324-4
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| Sequence 4, Application US/08890854
| Sequence 4. Application US/08890854
| Patent No. 6235512
| GENERAL INFORMATION:
| APPLICANT: Rothe, Mike
| APPLICANT: Cao, Zhaodan
| APPLICANT: R gnier, Catherine
| TITLE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods
| NUMBER OF SEQUENCES: 5
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: SIRET: 268 BUSH STREET, SUITE 3200
| STREET: Z68 BUSH STREET, SUITE 3200
| STATE: CALIFORNIA
| CONTRACTOR OF ADDRESS: COUNTRY: USA
                                                                             APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
APPLICANT: R gnier, Catherine
TITLE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
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Pred. No. 5.5e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36.627
REFERENCE/DOCKET NUMBER: 197-006-1
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 343-4341
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISICS:
LENGTH: 745 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
                   Sequence 4, Application US/09032476
Patent No. 6235492
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 92.3
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                      ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94104
COMPUTER READABLE FORM:
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US-09-032-476-4
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wedding tries: Propy disk

COMPUTER: IN PC Compatible

OREALIZATION WOMER: PC COMPACT

SOUTHABEN PREVIOUS SYSTEM: PC DOS/MS-DOS

GORRANIA PRICATION WOMER: PC COMPACT

ATTORENY AREA THOWN WOMER: 36,677

REGISTRATION WHOMER: 36,677

REGISTRATION WHOMER: 31,343,412

INFORMACONES: (1413) 343,434

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INFORMACONES: (1414) 343,434

INFORMACONES
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Score 36; DB 3; Length 745; Pred. No. 5.5e+02;
APPLICATION NUMBER: US/08/910,820
FILING DATE: 12-AUG-1997
CLASSIFTCATION: 435
ATTORNEY GRENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFENCE/DOCKET NUMBER: 36098.413C
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08810131A Patent No. 6268194
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Best Local Similarity 83.3,
                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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US-08-910-820-10
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Best Local Similarity
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US-08-810-131A-2
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APPLICANT: DiDonaco, Joseph A.
APPLICANT: DiDonaco, Joseph A.
APPLICANT: DiDonaco, Joseph A.
APPLICANT: Bibonarf, David M.
APPLICANT: Andi, Ebrahim
TITLE OF INVENTION: INB Kinase, Subunits Thereof, and Methods of Using Same
FILE REFERENCE: P-UD 3295
CURRENT APPLICATION NUMBER: US/09/168,629
CURRENT APPLICATION NUMBER: 60/061,470
EARLIER PILING DATE: 1999-10-09
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 745
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US-08-910-820-10

i Sequence 10, Application US/08910820

i Patent No. 625879

i GENERAL INFORMATION:
APPLICANT: Mercurio, Frank
APPLICANT: Zhu, Hengyi
APPLICANT: Li, Gian
APPLICANT: Li, Gian
APPLICANT: Murray, Brion W,
ITILE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
COUNTRY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                           Score 36; DB 3; Length 745; Pred. No. 5.5e+02; 1; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 3; Pred. No. 5.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09168629
Patent No. 6242253
GENERAL INFORMATION:
                                                                                                                                                        Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
                                      ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-023-324-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-168-629-2
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738 LDWSWL 743
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         STRANDEDNESS:
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Gaps
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APPLICANT: Karin, Michael
APPLICANT: Ratin, Michael
APPLICANT: Blonato, Joseph A.
APPLICANT: Blonato, Joseph A.
APPLICANT: Bandi, Ebrahim
TITLE OF INVENTION: 1-kappa-B Kinase and Methods of Using
TITLE OF INVENTION: 5ame
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Cambbell & Flores LLP
STREET: A170 La Jolla Village Drive, Suite 700
CITY: San Diego
STREET: California
COUNTRY: United States
92.3%; Score 36; DB 3; Length 745; 83.3%; Pred. No. 5.5e+02; ive 1; Mismatches 0; Indels
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APPLICATION DATA:
APPLICATION DATA:
APPLICATION STATEMENT SOFTWARE STILLING DATE: 25-FEB.1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-UD 2408
TELECOMMUNICATION INFORMATION:
TELEFRANCE (619) 535-9001
TELEFRANCE (619) 535-9001
TELEFRANCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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NUMBER OF
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                                                                                                                                                                       Sequence 4, Application US/09109966
; Sequence 4, Application US/09109966
; Patent No. 6479266
; GENERAL INFORMATION:
APPLICANT: Rothe, Mise
APPLICANT: Rothe, Mise
APPLICANT: Rotherine
; TITLE OF INVENTION: IKK-* Proteins, Nucleic Acids and Methods
; TITLE OF INVENTION: IKK-* Proteins, Nucleic Acids and Methods
; TITLE OF INVENTION: IKK-* Proteins, Nucleic Acids and Methods
; CORRESPONDENCE ADDRESS:
ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; COUNTRY: USA
; COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; COMPUTER: IBM PC compatible
; COMPUTER: IBM PC compatible
; COMPUTER: IBM PC compatible
; COMPUTER: IBM PC compatible
; COMPUTER: IBM PC compatible
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US-09-84-908-10
US-09-84-908-10
; Sequence 10, Application US/09844908
; Patent No. 6576437
; GENERAL INFORMATION:
; APPLICANT: Mercurio, Frank
; Zhu, Hengyi
; Barbosa, Miguel
Li, Glan
; Murray, Brion W.
; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 4; Length 745;
Pred. No. 5.5e+02;
1; Mismatches 0; Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,986
    ;;
  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: OSWAN, RICHARD A
REGISTRATION UNUMBER: 36,627
REFERENCE/DOCKET NUMBER: 197-C
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 343-4341
TELEPAX: (415) 343-4342
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: Si
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738 LDWSWL 743
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                                         1 LEWSWL 6
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                                                                                                                                               RESULT 14
US-09-109-986-4
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  Matches
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/844,908
FILING DATE: 27-APPL-2001
FILING PATE: 27-APPL-2001
PRIOR APPLICATION NUMBER: US/08/910,820
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 4; Length 745
Pred. No. 5.5e+02;
1; Mismatches 0; Indels
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.413C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: February 18, 2004, 14:41:47 Job time: 7.06579 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHRAACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.3%;
                                                                                                                                       ZIP: 98104
COMPUTER READABLE FORM:
                                                                       CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 92.3
Best Local Similarity 83.3
Matches 5; Conservative
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OM protein

Run on:

Sequence:

Searched:

Database

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QBbrk2 mus musculu
Q8qu52 oryza sativ
Q9s722 arabidopsis
Q9fil7 arabidopsis
Q9fil7 arabidopsis
Q9fil8 arabidopsis
Q9996 mycobacteri
Q99ik2 pseudomonas
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Lat sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase 3 (EC 4.4.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
Wambutt R., Heubner D., Mewes H.W., Weil B., Wiemann S.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ALB31955; CAD38600.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1033 AA; 114395 MW; ED4F629A229CDB6B CRC64;
                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                   PRT; 1033 AA
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                                                                    Created
                                                                                                                                                                                                                                                                                                                                 01-0CT-2002 (TrEMBLrel. 22, Cres
01-0CT-2002 (TrEMBLrel. 22, Lass
01-0CT-2002 (TrEMBLrel. 22, Lass
Hypothetical protein (Fragment)
DKFZP451G202.
  6; Conservative
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LAWSWL 562
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Best Local Similarity
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  NCBI_TaxID=9606;
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SEQUENCE
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Q9SEJ7;
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Q9SEJ7
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Q9sej7 lupinus alb
Q58ej7 lupinus alb
Q58649 methanobact
Q58039 rhiodobacter
Q503744 mycobacteri
Q81010 drosophila
Q95x81 brevibacteri
Q50005 mycobacteri
Q50005 mycobacteri
Q50017 mycobacteri
Q5137 mycobacteri
Q94515 drosophila
Q94515 drosophila
Q94515 drosophila
Q95km6 brucella su
Q92nu3 rhizobium m
Q92nu3 rhizobium m
Q8udu6 agrobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                          February 18, 2004, 14:09:39; Search time 17.3684 Seconds (without alignments) 89.145 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                          830525 segs, 258052604 residues
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                                           - protein search, using sw model
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Q26849
Q98C88
Q68039
Q05744
Q810L0
Q9KK81
Q50005
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094515
Q9VFY8
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Q92NU3
Q8UDU6
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sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_vertebrate:*
sp_unclassified:*
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sp_phage:*
sp_plant:*
sp_rodent:*
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18 VAWSWL 23
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                                                                                                                                                                                                            -i- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- MISCELLANDEOUS: IN BUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
-i- SIMILARITY: BELCHOGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
                                                                                                                                                           "Differential expression of four genes encoding 1-aminocyclopropane-1-caroboxylate synthase in Lupinus albus during germination, and in response to indole-3-acetic acid and wounding.";
                                        Rosidae;
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Rodrigues-Pousada C.;
              Eukaryota, Viriliplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosid, eurosida 1, Fabales, Fabaceae, Papilionoideae, Genisteae, Lupinus.
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MEDLINE-98037514; PubMed-9371463;

Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois ,
Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
McDougall S., Shimer G., Goyal A., Pletrovski S., Church G.M.,
Danniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
"Complete genome sequence of Methanobacterium thermoautotrophicum
"Complete genome sequence of Methanobacterium thermoautotrophicum
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Methanobacteriaceae, Methanothermobacter.
NCBI TaxID=187420;
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J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                       55026 MW; 5BB0D640DD129970 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                94.7%; Score 36; DB 10; L. 83.3%; Pred. No. 6.2e+02; Live 1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  675 AA.
                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00155; aminotran 1 2; 1.
SRINYS; PR00753; ACCSYNTHĀBE.
PROSITE; PS00105; AA TRANSPER_CLĀSS_1; 1.
Lyase; Pyridoxal phoēphate.
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01-JAN-1998 (TrEMBLrel. 05, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                                                          InterPro; IPR001176; ACC_synthase.
InterPro; IPR004839; Aminotransf1/2.
InterPro; IPR004838; NHtransf_1.
Pfam; PF00155; aminotran_1_2; 1.
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Interpro; IPR006403; ATPBRSS-1BL Cu.
Interpro; IPR006416; ATPBRS-EIB ÄVY
Interpro; IPR001757; ATPBRS-EI-EZ
                                                                                                         STRAIN=cv. Ultra;
MEDLINE=20539411; PubMed=11089679;
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Best Local Similarity 83.5-
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MEDITRE=21082930; PubMed=11214968; MEDITRE=21082930; PubMed=11214968; Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Hypochetical 12.6 Kba protein.
Rhodobacter capsulatus (Rhodopseudomonas capsulata)
Bacteria, Proteobacteria, Alphaproteobacteria; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceae; Rhodobacteraceaeae; Rhodobacteraceaeaeaeaeaeaeaeaea
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Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.7%; Score 36; DB 17; Length 675; 83.3%; Pred. No. 8.5e+02; ive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72337 MW; 56A5D4C175C0CC6F CRC64;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Exopolysaccharide production repressor, ExoX.
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                                          Pfam; PF00122; E1-E2 ATPASE; 1.
Pfam; PF0702; Hydrolase; 1.
PRINTS; PR00149; CATATPASE.
PRINTS; PR00943; CUATPASE.
TIGREAMS; TIGR01511; ATPASE-1B1 Cu; 1.
TIGREAMS; TIGR01525; ATPASE-1B hvy; 1.
TIGREAMS; TIGR01494; ATPASE E1_E2; 1.
Complete proteome.
SEQUENCE 675 AA; 72337 MW; 56A5D4C
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InterPro; IPR005834; Hydrolase.
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BMBL, AP003006; BAB51733.1; -.
COMplete proteome.
SEQUENCE 91 AA; 9887 MW; 10
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Matches 5; Conservative
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"Use of an ordered cosmid library to deduce the genomic organization
of Mycobacterium leprae.";
Mol. Microbiol. 7:197-206 (1993).
EMBL: 295151; CAB08408.1; -.
Hypothetical protein.
SEQUENCE 135 AA; 14516 MW; E7B32E2379C4888C CRC64;
                            Fonstein M.;
     STAIN=SB1003;
MEDLINE=97404404; PubMed=9256491;
WICLE C., Paces V., Maltsev N., Paces J., Haselkorn R., Fonstei Vicek C., Paces V., Maltsev N., Paces J., Haselkorn R., Fonstei Saquence of a 189-74 Begment of the chromosome of Rhodobacter capsulatus SB1003 ";
Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388 (1997).
EMBL; APO10496; AAC16125.1; -.
InterPro; IPR005133; PhaG MnhG YufB.
Pran; PP03334; PhaG MnhG YufB; 1.
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                               92.1%; Score 35; DB 2; Length 116; 83.3%; Pred. No. 2.2e+02; 1ve 1; Mismatches 0; Indels
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83.3%; Pred. No. 2.6e+02;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Badcock K., Churcher C.M.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                 Parkhill J., Barrell B.G., Rajandream M.A., Submitted (MAX-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                   Hypothetical protein.
SEQUENCE 116 AA; 12553 MW; FFB91E726D421996 CRC64;
                                                                                                                                                                                                                                                       01-JUL_1997 (TrEMBLrel. 04, Created)
01-JUL_1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1998 (TrEMBLrel. 06, Last annotation update)
Hypothetical 14.5 kDa protein.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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23,
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                   5; Conservative
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(GH04494p).
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                                                                                                                                         Local Similarity
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                                                                                                                                                                                      63 LSWSWL 68
                                                                                                                                                                     1 LAWSWL 6
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01-MAR-2003 (
01-MAR-2003 (
CG32240-PA (G
                                                                                                                               Query Match
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QBIOLO;
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Matches
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DT OO
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STRAIN=IN;
MEDLINE=21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacrolx C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
                                                                                                                                            Mycobacterium leprae.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corymebacterinee, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1769,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Poder M. M. M. Bogin M.L., Perlman P.S.;
Podar M., Mullineaux L., Sogin M.L., Perlman P.S.;
Bacterial group II introns in a deep sea hydrothermal vent
environment.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AVO'5118; AAL'8669.1;
InterPro; IRR000477; RVTSe.
Pfam; PF00078; rvt; 1.
RNA-directed DNA polymerase; Transferase.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.1%; Score 35; DB 16; Length 196; 83.3%; Pred. No. 3.6e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 92.1%; Score 35; DB 2; Length 197; Best Local Similarity 83.3%; Pred. No. 3.7e+02; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                      Smith D.R., Robison K.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Matary gen, decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL; U15.181; AAA62925.1; -.
EMBL; AL583920; CAC31422.1; -.
EMPL; ML041; -.
Hypothetical protein; Complete proteome.
SEQUENCE 196 AA; 21186 MW; 15D4AF7CDF653936 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 197 AA; 24010 MW; FA76F629B32D836A CRC64;
                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
  196 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 AA
                                        01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last seq 01-NAR-2002 (TrEMBLrel. 20, Last ann U1764V (Hypothetical protein ML1041)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
    PRT;
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Bacteria, environmental samples.
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Query Local Similarity 83.33,
Best Local Similarity 63.53,
  PRELIMINARY;
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SEQUENCE FROM N.A.
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  Q50005
Q50005;
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QBRSV7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Krubasik P., Sandmann G., "A carotenogenic gene cluster from Brevibacterium linens with novel lycopene cyclase genes involved in the synthesis of aromatic carotenoids.";
                                                                                                                                                                                                                                        Stapleron M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phonenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; BT001386; AAN71141.1; --

SEQUENCE 145 AA; 17393 MW; 4EF7D500940F762A CRC64;
                                                         Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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NCBI_TaxID=1703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.1%; Score 35; DB 5; Length 145; 83.3%; Pred. No. 2.7e+02; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.1%; Score 35; DB 2; Length 172; 83.3%; Pred. No. 3.2e+02; ive 1; Mismatches 0; Indels
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                            FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOI. Gen. Genet. 263:423-432 (2000).
EMBL; AR13916; AAF65585.1; -
InterPro; IPR006032; Ribosomal. S12_23.
InterPro; IPR004037; TspO_MBR.
PROMITE; PS000055; RIBOSOWAL_S12; 1.
Hypothetical protein.
SEQUENCE 172 AA; 18808 MW; 9F6BD848E95875F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9KK81;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 18.8 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 172 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=DSM 20426;
MEDLINE=20279196; PubMed=10821176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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91 VAWSWL 96
                                      SEQUENCE FROM N.A.
                                                                                                                     SEQUENCE FROM N.A.
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36 LSWSWL 41
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Best Loc Matches

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RESULT 8 Q9KK81

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RESULT 9 Q50005

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Drosophilidae; Drosophila.
Ephydroidea; Dro
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  Cole S.T., Brosch R., Carner J., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcdon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Rutter S., Geeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence."; Mature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1997 (TrEMBLrel. 02, Created).
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
IFC protein (LD15458P) (Sphingolipid delta 4 desaturase protein DES-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; 296072; CAB09496.1; -.
EMBL; AE007105; AAK47069.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corymebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 92.1%; Score 35; DB 16; Length 210; Local Similarity 83.3%; Pred. No. 3.9e+02; es 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tuberculist; Rv2680; -. Hypothetical proteome. Hypothetical protein; Complete proteome. SEQUENCE 210 AA; 22573 MW; 2D9429BFIFE0956A CRC64;
                                                                                                    01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Rv2680.
RV2680 OR MT2754 OR MTV010.04.
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                                                                                  210 AA.
                                                                                PRT;
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                                                                                                                                                                   Mycobacterium tuberculosis.
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123 VAWSWL 128
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172 LAWNWL 177
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1 LAWSWL 6
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Q94515;
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Matches
                                                         RESULT 11
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RAGAN = LOCALINEKE S.E., Holf R.A., Evans C.A., Gocayne J.D.,

RAGAN M.D. Celnikers S.E., Holf R.A., Evans C.A., Galle R.F.,

RAGE S.E., Scheers S.E., Lip P.W., Honkins R.A., Galle R.F.,

RAGE S.E., Scheers S.E., Andrews D., Champe M., Pfeiffer B.D.,

RAGE S.E., Rottand J.R., Yandlall M.D., Zhang O., Chen L.X.,

RAGE S.E., Rottand J.R., Yandlall M.D., England D.,

RAD Bandon R.C., Rogers Y.-H.C., Blazel R.G., Champe C.R., Miklos G.L.G.,

RAD Abril J.F., Agbasni A., An H.-J., Andrews Pfannkoch C., Baldwin D.,

RAD Ballew R.M., Bencs P.V., Berman B.P., Bhandari D., Bolahakov S.,

RAD Ballew R.M., Basun A.B., Butker H., Caddeu B., Center A., Chadra I.,

RAD Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P. B.,

RAD Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RAD Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RAD Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RAD Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RAD Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RAD Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RAD Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RAD Cherry J.M., Cawley B., Miller J., Well M.-H., Ibegwam C.,

RAD Cherry J.M., Cawley B., Miller J., Well M.-H., Ibegwam C.,

Alalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Alalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Alalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Martei B. M., Mortei B., Morintosh T.C., McLeod M.P., Morker D., Morshrefi A.,

RAD Merce J.M., Moy M., Murphy B., Murphy L., Murzhy D.M., Nelson D.L.,

Rad Resinert K., Moy M., Murphy B., Murphy L., Murzhy D.M., Nelson D.K.,

Rad Reinert K., Remington K., Saunders R., Venter B., Wang Z.-Y.,

Rad Bazzolo M., Pittuan G.S., Pan S., Pollard J., Welsenbach J.,

Rader E., Spradlind A.C., Staplecon M., Stupog K., Sun B.,

Syiekas R., Zhodra C., Marsen P., Welley C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chawpe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.B., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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Endo K., Akiyama T., Kobayashi S., Okada M.;
"Degenerative spermatocyte, a novel gene encoding a transmembrane
protein required for the initiation of melosis in Drosophila
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Ternes P., Franke S., Zaehringer U., Sperling P., Heinz E.;
"Identification and Characterization of a Sphingolipid Delta4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Gen. Genet. 253:157-165(1996).
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J. Biol. Chem. 0:0-0 (2002).
Bubl. AE003612; AAF52318.1;
EMBL, X94180; CAA63889.1; -.
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AF466379; AAM12535.1;
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STRAIN=BERKELEY;
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Query Match
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RA MEDLINE=2019/0006; Pubbace=1073132;

RA Mannatides P.G., Scherer S.E., Li P.W., Bvans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Holt R.A., Gable R.F.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballo R.M., Basu A., Baxendaled J., Baytaktaroglu L., Basaley R.M.,

RA Ballo R.W., Banch W., Bauler H.-G., Cadieu E., Center A., Chandra I.,

RA Borchan M.R., Bouck J., Brokersein P., Brottler P.,

Burtis K.C., Busam D.A., Danlac H.C., Davenport L.B., Davies P.,

Burtis K.C., Busam D.A., Danlac H., Davenport L.B., Davies P.,

Burtis K.C., Busam D.A., Danlac H., Davenport L.B., Davies P.,

Burtis K.C., Busam D.A., Danlac H., Davenport L.B., Davies P.,

Burtis K.D., Evangelista C.C., Ferraz C., Ferriaz S., Pleischman W.,

RA Gerblos B., Delcher A., Deng Z., Maya A.D., Dew I., Diletz S.M.,

Bodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

Brandlos B., Gorrell J.H., Gu Z., Glann P., Harris M.,

Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Hostin D., Houston K.A., Howland T.J., Wend M.-H., Ibegwam C.

Brandlos B., McIntosh F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Branko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Branko P., Lei Y., Marcha B., Murphy L., Muzry D.M., Nelson D.L.,

Reinert K., Remington K., Saunders R.D. Moshrefi A.,

Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.

Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri W., Wang X.,

Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri W., Marka R.,

Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri W., Wang S., Yao Q., Zhan M.,

Ralazzolo M., Waodage T., Wonley K.C., Wu D., Yang S., Zhu X., Smith H.,

Wang Z.-Y., Massarama D.A., Weinston W., Strong
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                Length 321;
                                                                                                                                                                                                                         92.1%; Score 35; DB 5; Length 321
83.3%; Pred. No. 5.88+02; ....marrhes 0; Indels
                                                                                                                                                                                                  321 AA; 37213 MW; B8DB13961BF5F38E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last annotation update)
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                  InterPro; IPR001064; Crystallin.
InterPro; IPR005804; FA_desat_fam.
InterPro; IPR005804; FA_desat_fam.
InterPro; IPR00625; Zn_WrpeptGae.
Pram; Pr00487; FA_desaturase; 1.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
PROSITE; PS00142; ZINC_PROTEĀSE; 1.
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MEDLINE=20196006; PubMed=10731132;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 83.5
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                                                                                                                                                                                                                                                                                                                                                                                                    64 LSWSWL 69
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                                                                                                                                                                          Transmembrane
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SEQUENCE FROM N.A.
STRAIN=1330 / Blovar 1;
MEDLINE=22247741; PubMed=12271122;
MEDLINE=22247741; PubMed=12271122;
MEDLINE=22247741; PubMed=12271122;
MEDLINE=22247741; PubMed=12271122;
Medlson I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F., Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.,
"The Brucella suis genome reveals fundamental similarities between
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative NADH dehydrogenase transmembrane protein (EC 1.6.99.3).
NDH OR R02079 OR SMC04452.
Rhizobium meliloti (Sinorhizobium meliloti)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Pyridine nucleotide-disulphide oxidoreductase family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
NCBI_TaxID=29461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.1%; Score 35; DB 16; Length 398; 83.3%; Pred. No. 7.2e+02; ive 1; Mismatches 0; Indels
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Rhizobiaceae, Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                92.1%; Score 35; DB 5; Length 329; 83.3%; Pred. No. 6e+02; tive 1; Mismatches 0; Indels
                                                          EMBL, AE003689, AAF54907.1; -
FlyBaes, FBGn0038120; CG10148.
InterPro; IPR001561; LRR.
InterPro; IPR001561; LRR.
FRINTS, PR00019; LEURICHRPT.
SMART; SM00169; LRR TYP, 1.
PROSITE; PS05066; LRR TYP, 1.
SROSITE; PS05066; LRR TYPICAL; 1.
SEQUENCE 329 AA; 37165 MW; C4106348E5C334DA CRC64;
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"The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
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17 LAWTWL 22
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Search completed: February 18, 2004, 14:35:43 Job time : 19.3684 secs

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Query Match
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Matches 5; Conservative
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Sequence 311, App
Sequence 311, App
Sequence 21611, A
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Sequence 21611, A
Sequence 241, App
Sequence 22, Appl
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Sequence 23948, A
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Sequence 19590
Sequence 79, A
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-17325

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Match Length
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Sequence 31699, A Sequence 30, Appl Sequence 30, Appl Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli
         Sequence 79, Appl
Sequence 80, Appl
Sequence 23585, A
Sequence 23780, A
Sequence 31, Appl
Sequence 31, Appl
Patent No. 5217891
US-08-818-111-80
US-09-056-556-79
US-09-056-556-79
US-09-052-56-79
US-09-252-991A-23565
US-08-137-117D-31
US-08-137-117D-31
US-08-252-991A-31699
US-09-252-991A-31699
US-09-252-991A-26255
US-09-023-312-3
US-09-023-312-3
US-09-033-312-3
US-09-099-125A-4
US-09-099-125A-4
US-09-099-125A-4
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ALIGNMENTS

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APPLICANT: SMITH, DOUGLAS
APPLICANT: SMITH, DOUGLAS
APPLICANT: SMITH, DOUGLAS
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES:
ADDRESSED: WOLF, GREENFIELD & SACKS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMULCATION INFORMATION:
TELEPHONE: 617/720-3500
                                                                                                                                                                                                                            6:00 ATLANTIC AVENUE
; Sequence 69, Application US/08311731A ; Patent No. 6583266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: MYCOBACTERIUM LEPRAE
US-08-311-731A-69
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INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
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amino acid
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CITY: BOSTON
STATE: MASSACHUSETTS
COINTRY: USA
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MOLECULE TYPE: protein
HYDOTHRTICAL: YES
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CATION NUMBER: 60/048,880

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1997-06-06 1997-06-06 1997-06-06

90-90-266

90-90-4661

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PPLICATION NUMBER: 60/048,882
ILING DATE: 1997-06-06
                                                                                FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,896
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,877
                                                                                                                                                      APPLICATION NUMBER: 60/049,020
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/048,899
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
                                                                                                                                                                                                APPLICATION NUMBER: 60/048,876
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LICATION NUMBER: 60/048,893
ING DATE: 1997-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICATION NUMBER: 60/048,972 ILING DATE: 1997-06-06
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PLICATION NUMBER: 60/049,374
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FILING DATE: 1997-06-06
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                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/048,895
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                                                                                                                                                                                                                                                                                                                                                                        LICATION NUMBER: 60/048,971
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                                                                                                                Sequence 319, Application US/08311731A
Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
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Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                               STATE: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: SIO
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/POCKET NUMBER: 31,616
REFERENCE/POCKET NUMBER: C0044/7125
TELEPHONE: 617/720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZOO7P1
CURRENT APPLICATION NUMBER: US/09/205,258
                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C. STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/049,375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 319:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 198 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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111 VAWSWL 116
: | | | | | |
109 VAWSWL 114
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US-09-205-258-359
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Sequence 21611, Application US/09252991A
Sequence 21611, Application US/09252991A
Sequence 21611, Application US/09252991A
Sequence 21611, Application US/09252991A
SEQUENCE INFORMATION:
TITLE OF INVENTION: WICLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
FRIOR APPLICATION NUMBER: US 60/094,190
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-02-18
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FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-02-18
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERGIANOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERGIANOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17325
LENGTH: 172
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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Pred. No. 2.3e+02;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                             ; Sequence 17325, Application US/09252991A; Patent No. 6551795
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US-09-252-991A-17325
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Best Local Similarity 100...
Then 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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                             43 AWSWL 47
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US-09-252-991A-31792
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Patent No. 6593266
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
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                                                                                                                                                                                                                                                                                                                                                                           Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02210

COMPUTER READABLE FORM:
MEDIUM TYRER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
                                                                                                                                                                                                                                                                                                                                                                        89.5%; Score 34; DB 4;
100.0%; Pred. No. 80;
tive 0; Mismatches (
                                                                                                                                                                                                                                                              ) LOCATION: (56)
) OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-359
BARLIER APPLICATION NUMBER: 60/094,657
BARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 359
LENGTH: 56
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C0044/7125
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US-08-311-731A-311
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ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: 0.0044
TELEPHONE: 617/720-340
INFORMATION FOR SEQ ID NO: 311:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 600 ATLANTIC
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
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                                                                                                                                                                                                                FEATURE:
NAME/KEY: SITE
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Length 313;
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                                                                                                                                                                                                                                                                                                                                                89.5%; Score 34; DB 4; L. 100.0%; Pred. No. 3.9e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Andersen, Lene
APPLICANT: Bjornvad, Mads.
TITLE OF INVENTION: NO. 6566114el Mannanases
FILE REFERENCE: 5440.204-US
CURRENT APPLICATION NUMBER: US/09/339,159B
CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin version 3.1
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Andersen, Lene
APPLICANT: Biornvad, Mads
TITLE OF INVENTION: No. 6566114el Mannanases
FILE REFERENCE: 5440.204-US
CURRENT APPLICATION NUMBER: US/09/339,159B
CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 331
                                                     FILE REFERENCE: 107196.136
CURRENT APPLICATION WUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR FILING DATE: 1998-02-18
FRIOR APPLICATION NUMBER: US 60/094,190
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28418
LENGTH: 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22, Application US/09339159B
Patent No. 6566114
GENERAL INFORMATION: APPLICANT: Kauppinen, Markus
APPLICANT: Schulein, Martin
APPLICANT: Schnorr, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09339159B; Patent No. 6566114; GENERAL INFORMATION: APPLICANT: Kauppinen, Markus; APPLICANT: Schulein, Martin; APPLICANT: Schorr, Kirk
                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28418
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Best Local Similarity 10v...
5; Conservative
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Best Local Similarity
Matches 5; Conserv
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US-09-339-159B-12
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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FILE REFERENCE: 107196.136

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 269

Type ...
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Pred. No. 3.4e+02;
0; Mismatches 1; Indels
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. 3.5e+02;
ches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Holland, Ross
APPLICANT: O'Toole, Paul W.
APPLICANT: Reid, Julian R.
APPLICANT: Reid, Julian R.
TITLE OF INVENTION: Polymuclectides, materi;
TITLE OF INVENTION: them and methods for us;
FILE REFERENCE: 11000.1043U1
CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT FILING DATE: 2000-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.5%; Score 34; 100.0%; Pred. No.
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; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-634-238-334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 28418, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 334, Application US/09634238
Patent No. 6544772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glenn, Matthew
Havukkala, Ilkka J.
Bloksberg, Leonard, N.
Lubbers, Mark W.
Dekker, James
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83.3%;
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APPLICANT: Marc J. F
TITLE OF INVENTION:
TITLE OF INVENTION:
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LENGTH: 280
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Sequence 4, Application US/09485648
Patent No. 6376445
GENERAL INFORMATION.
APPLICANT: Bettiol, Jean-Luc P.
APPLICANT: Showell, Michael S.
TITLE OF INVENTION: Detergent Compositions Comprising a Mannanase and a TITLE OF INVENTION: Protease
FILE REFERENCE: Mannanase and protease
CURRENT APPLICATION NUMBER: US/09/485,648
CURRENT PILING DATE: 2000-04-05
PRIOR PILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 6
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.5%; Score 34; DB 4; Length 369; 100.0%; Pred. No. 4.6e+02;
                                                                                                                              APPLICANT: Schulein, Markue
APPLICANT: Schulein, Martin
APPLICANT: Schulein, Martin
APPLICANT: Schnorr, Kirk
APPLICANT: Bjornvad, Made
TITLE OF INVENTION: NO. 6566114el Mannanases
TITLE OF INVENTION: NO. 6566114el Mannanases
CURRENT APPLICATION NUMBER: US/09/339,159B
CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 369
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Job time : 8.06579 secs
                                                                   Sequence 16, Application US/09339159B; Patent No. 6566114; GENERAL INFORMATION:
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LENGTH: 468
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US-09-485-648-4
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US-09-252-91A-23948

i Sequence 2348, Application US/09252991A

i Patent No. 6521795

i GENERAL INFORMATION:

i APPLICATION:

ITILE OF INVENTION:

ITILE OF INVENTION:

ITILE OF INVENTION:

RICHERT APPLICATION NUMBER: US/09/252,991A

CURRENT ELIGATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1999-02-18

PRIOR PLILOR DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR PLILOR DATE: 1998-02-18

SEQ ID NO 23948

LENGTH: 335
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REFERENCE: 107196.13 6
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

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US-09-339-1598-12
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                                                                                                                                                                                                                                                                                                       Chang G.-J.J., Trent D.W.;

"Nucleotide sequence of the genome region encoding the 26S mRNA of eastern equine encephalomyelitis virus and the deduced amino acid sequence of the viral structural proteins.";

J. Gen. Virol. 68:2129-2142(1987).

-!- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.

-!- PING. SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.

-!- MISCELLANBOUS: THE 6 ADD POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL.

SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL
                                                            01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Structural polyprotein (P130) [Contains: Coat protein C (EC 3.4.21.-)
(Capsid protein C); Spike glycoprotein B3; Spike glycoprotein E2;
                                                                                                                                               6 kDa peptide; Spike glycoprotein El].
Eastern equine encephalitis virus (Eastern equine encephalomyelitis
                                                                                                                                                                                            Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coat protein, Polyprotein, Transmembrane, Glycoprotein, Hydrolase,
Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW; 8C7664A405D2D41C CRC64;
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SPIKE GLYCOPROTEIN E2.
6 kDa PEPTIDE.
SPIKE GLYCOPROTEIN E1.
CHARGE RELAY SYSTEM (BY SI
CHARGE RELAY SYSTEM (BY SI
CHARGE RELAY SYSTEM (BY SI
                                 PRT; 1239 AA
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InterPro; IPR000936; Alpha E2_glycop.
InterPro; IPR000930; Alpha E2_glycop.
InterPro; IPR000930; Togavirin.
Pfam; PF00944; Alpha Core; 1.
Pfam; PF00949; Alpha El_glycop; 1.
Pfam; PF00943; Alpha El_glycop; 1.
Pfam; PF01563; Alpha E3_glycop; 1.
PRINTS; PR00798; TOGĀVIRIN.
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                                                                                                                                                                                                                                                                           STRAIN=82V-2137;
MEDLINE=87282265; PubMed=2886548;
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                                 STANDARD;
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                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                             Alphavirus.
NCBI_TaxID=11021;
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                                 POLS EEEV
P08768;
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                                                                                                                                                                               virus).
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RESULT 2
POLS EEEV
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89.5%; Score 34; DB 1; Length 1239;

Query Match

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                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          North America.";
Virology 182:774-784(1991).
-!- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.
-!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
-!- MISCELLANEOUS: THE 6 KDB POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL.
SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL
                                                                                                                                                                                                           01-AUG-1992 (Rel. 23, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Structural polyprotein (P130) (Contains: Coat protein C (EC 3.4.21.-)
(Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2;
6 kDa peptide; Spike glycoprotein E1].
Eastern equine encephalitis virus (strain va33[ten broeck]) (Eastern equine encephalomyelitis virus).
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPIKE GLYCOPROTEIN E3.
SPIKE GLYCOPROTEIN E2.
6 kDa PEPTIDE.
SPIKE GLYCOPROTEIN E1.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91220727; PubMed=2024496; Weaver S.C., Scott T.W., Rico-Hesse R.; Molecular evolution of eastern equine encephalomyelitis virus in
                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.
                             Indels
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                                                                                                                                                                  PRT; 1240 AA
                            Mismatches
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POTENTIAL.
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InterPro: IPR000936; Alpha E2_glycop.
InterPro: IPR000936; Alpha E2_glycop.
InterPro: IPR000930; Togavirin.
Pfam; PF00944; Alpha core; 1.
Pfam; PF00944; Alpha El glycop; 1.
Pfam; PF01589; Alpha El glycop; 1.
Pfam; PF01581; Alpha E3_glycop; 1.
Pfam; PF01563; Alpha E3_glycop; 1.
PRINTS; PR00798; TOGAVIRIN.
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100.0%; Pre-
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1143
211
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712
738
                                                                                        1205 AWSWL 1209
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                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=11022;
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                                                           2 AWSWL
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us-09-643-260-7.rsp

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SEQUENCE OF 1151-1402 FROM N.A.

SEQUENCE OF 1151-1402 FROM N.A.

SEQUENCE OF 1151-1402 FROM N.A.

SEQUENCE OF SUBSEGO, Pubmed=11217851;

MEDLINE=21085660; Pubmed=11217851;

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Arawawa T., Hara A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kaukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsudi F., Suzuki R., Tomita M., Wagner L., Washio T.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Anchons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodríguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Hayashizaki Y.,

"Punctional annotation of a full-length mouse cDNA collection.";

Nature 409:685-690(2001).
                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mus muscullus mRNA for gtl-13 (gene trap locus-13), similar to human KIAA0197 gene (D83781), complete cds.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21448620; PubMed=11564755;
Belgareh N., Rabut G., Bai S.W., van Overbeek M., Beaudouin J.,
Daigle N., Zatsepina O.V., Pasteau F., Labas V., Fromont-Racine M.,
Ellenberg J., Doye V.;
"An evolutionarily conserved NPC subcomplex, which redistributes in
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                0920W3; 09CZD9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Nuclear pore complex protein Nup160 (Nuclearporin Nup160) (160 kDa
nucleoporin) (Gene trap locus 1-13) (GTL-13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=129/SvJ;
Van de Putte T., Cozijnsen M., Dewulf N., Tylzanowski P., Lonnoy
Huylebroeck D.;
                  (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                    ö
   (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION, FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION MEDLINE-21541555; Pubmed=11684705;
                                                                                                    DB 1; Length 1240;
                                                                                                                                 0; Indels
                                                                   MW; AEBEB1599D083045 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION, SUBUNIT, AND SUBCELLULAR LOCATION.
                                                                                                  Score 34; DB 1; Le
Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                  PRT; 1402 AA.
                                                                                                          100.0%; Pred. nc-
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 N-LINKED (
N-LINKED (
N-LINKED (
N-LINKED (
                                                                                                  89.58;
                                                                   137290
                                                                                                                 Best Local Similarity 100.
Matches 5; Conservative
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                                  834
933
 49
638
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933
1240 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                  2 AWSWL 6
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CARBOHYD
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
Rerlavage A.R., Bult C.J., Tomb J.-F., Doughbarty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fulrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                               export.";
J. Call Biol. 155:339-354 (2001).
J. Call Biol. 155:339-354 (2001).
J. FUNCTION: Involved in poly (A) + RNA transport.
J. SUBUNIT: Forms part of the Nupl60 subcomplex in the nuclear pore which is composed of Nupl60, Nupl33, Nupl07 and Nup96. This composex plays a role in RNA export and in tethering Nup98 and Nup153 to the nucleus.
Vasu S., Shah S., Orjalo A., Park M., Fischer W.H., Forbes D.J.; "Novel vertebrate nucleoporins Nupl33 and Nup160 play a role in mRNA
                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Nuclear pore complex.
-!- CAUTION: Ref.2 sequence differs from that shown due to a frameshift in position 1157 and a stop codon in position 1396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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EMBL, AK012715; BAB28429.1; ALT_FRAME.
MGD; MGI:1926227; Nup160.
GO; GO:0005643; C:nuclear pore; IDA.
GO; GO:0005487; F:nucleocytoplasmic transporter activity; IDA.
GO; GO:0006466; P:mRNA-nucleus export; IDA.
CONFLICT 1156 1156 A -> T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 1; Length 1402;
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1314 1314 E -> G (IN REF. 2).
138 138 N -> D (IN REF. 2).
1402 AA; 158230 MW; 3BFSD9F057D28772 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No. 4.2e+02; ive '0; Mismatches 0;
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Last annotation update)
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HI1416.
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01-NOV-1995 (Rel. 32, Last seq
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28-FEB-2003
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P44188;
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Amanatides P.G., Scherer S.E., Hi P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner W., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner W., Henderson S.N.,
Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A wan K.H., Doyle C., Baxer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pamhoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Barlew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bourk J., Brockstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Ade Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
STRAIN=Canton-S; TISSUE-Larval brain;
MEDLINE=9348222; PubMed=8394009;
MEDLINE=9348222, PubMed=8394009;
"Dron C., Goberdhan D.C.I., Steller H.;
"Dror, a potential neurotrophic receptor gene, encodes a Drosophila homolog of the vertebrate Ror family of Trk-related receptor tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Yyrosine-protein Kinsse transmembrane receptor Ror precursor (EC 2.7.1.112) (dRor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN 28 118 HYPOTHETICAL PROTEIN HI1416. SEQUENCE 118 AA; 13516 MW; 96CE5D469DF8E2EB CRC64;
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                                                                                                                                                                                                                                                                                                                                                           Interpro; IPRO06481; Holin_lambda.
Pfam; PF05106; Phage_holin_3; 1.
TIGRPAMS; TIGR01594; holin_lambda; 1.
Hypothetical protein; Signal; Complete proteome.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 90:7109-7113(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.8%; Score 33; DB
83.3%; Pred. No. 63;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
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                                                                                                                                                                                                                                                     EMBL; U32821; AAC23067.1; -. PIR; I64028; I64028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5, Conservative
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Matches 5, Conserv
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Q24488;
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Note the D. Housenen K.A., in Allendan C.A., well M.-H., thegamen C.B., Kardin C. W., well M.-H., in C. Lidang V., and M.-H. in C. Lidang V. Lida Y., the Kinnell B.E., Kardine C. W. Kardin C. Kardin E. W. Man D. Lidang V. Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Lidang V., Mandragon W., Strong V., Mandragon W., Strong V., Mandragon W., Strong V., Standang V., Saunders R. D., Sadherler P., Signe H. M. G., Sheller C., Siden Kalmos II. Silmapon M., Strong K., Sunk T., Santha R., Vallang V., Santha W., Strong V., Santha W., Strong V., Standang V., Straphecon M., Strong W., Sunk H. C., Stden Kalmos II. Silmapon M., Strong W., Sunk H. C., Stden Kalmos II. Silmapon M., Strong W., Sunk H. C., Stden Kalmos II. Silmapon M., Strong W., Sunk H. C., Stden Kalmos II. Strong V., Straphecon M., Strong W., Sunk H. C., Stden Kalmos II. Strong V., Straphecon M., Strong W., Sunk H. C., Stden Kalmos II. Strong V., Strong W., Strong W., Strong W., Strong P., Strong W., Strong W., Strong P., Strong V., Strong P., Strong W., Strong W., Strong P., Strong W., Strong W., Strong P., Strong W., Strong W., Strong P., Strong W., Strong W., Strong P., Strong W., Strong W., Strong P., Strong W., Strong W., Strong P., Strong W., Strong W., Strong W., Strong W., Strong P., Strong W., Strong W., Strong P., Strong W., Strong W., Strong P., Strong W., Strong W., Strong W., Strong W., Strong W., Strong P., Strong W., Strong W., Strong W., Strong P., Strong W., Strong W., Strong W., Strong W., Strong W., Strong W., Strong W., Strong W., Strong W., Strong W., Strong W., Strong W., Strong W., Strong W., Strong W., Strong W., Strong W., Strong W., Strong W., Strong W., Strong W., Strong W., Strong W., Str
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE=97051601, PubMed=8896278,
Lum P.Y., Edwards S., Wright R.;
"Molecular, functional and evolutionary characterization of the gene
encoding HMG-CoA reductase in the fission yeast, Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=972;
MEDLINE=2184401; PubMed=11859360;
WOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Source J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Sgource G., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00239; RECEPTOR_TYR II; 1.
Transferase; Kinase; Tyrosine-protein kinase; ATP-binding; Receptor; Transmembrane; Signal; Glycoprotein; Kringle; Phosphorylation; Developmental protein.
                                                                        TYROSINE-PROTEIN KINASE TRANSMEMBRANE
RECEPTOR ROR.
EXTRACELLULAR (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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Pred. No. 3.1e+02;
0; Mismatches 1; Indels
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PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
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PHOSPHORYLATION (AUTO-) (BY
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526162D27D5FD7C7 CRC64;
                                                                                                            CYTOPLASMIC (POTENTIAL)
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Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetacee,
Schizosaccharomyces.
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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83.3%;
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63
129
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685 AA;
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                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 5; Conserv
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MOD_RES
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PROBLEMS AND STRENGE TO A COMMENT BY A HARDE E J. Angele B K.,

A MINISTER L. JORNES L. JORNES M. Leather S. MINCOMAID S. MINISTER L. JORNES M. MINISTER L. JORNES M. MINISTER L. JORNES M. MINISTER L. JORNES M. MINISTER L. JORNES M. MINISTER S. SERVICE S. SERVICE S. SERVICE M. MINISTER S. SERVICE M. MINISTER S. SERVICE M. MINISTER S. SERVICE M. MINISTER S. SERVICE M. MINISTER S. SERVICE M. MINISTER S. SERVICE M. MINISTER S. SERVICE M. MINISTER S. SERVICE M. MINISTER S. SERVICE M. MINISTER S. SERVICE M. MINISTER S. SERVICE M. MINISTER S. SERVICE M. MINISTER S. SERVICE M. MINISTER S. SERVICE M. MINISTER S. SERVICE M. MINISTER S. SERVICE M. MINISTER S. SERVICE M. MINISTER S. SERVICE M. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S. MINISTER S.
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WEDIANIE-2184401; PubMed=11859360;
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Squoros U., Peat N., Hayles J., Backer S., Bachama D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Brown D., Rowner C., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gentles S., Goble A., Hamlin N., Harris D., Hidgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
Mooney P., Moule S., Mangall K., Murphy L., Niblett D., Odell C.,
A. Hutherford K., Rutter S., Sauders R., Seeger K., Sharp S.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
Arylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
Noodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Modward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Boffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
Allbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Huts C.,
Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Potashkin J.,
Marker M., Marker D., Barrell B.G., Nurse P.;
When the Grome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- FUNCTION: INTERACTS WITH POM152 IN THE CORE STRUCTURE OF THE NUCLEAR PORE COMPLEX (NPC). INVOLVED IN THE EXPORT OF MRNA.
--- SUBSCILLULAR LOCATION: Nuclear pore complex.
--- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 1560 ONWARD AND IS LONGER (1628 AA) DUE TO A FRAMESHIFT.
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIJNE=99318821; PubMed=10388805;
Whalen W.A., Yoon J.H., Shen R., Dhar R.;
"Regulation of mRNA export by nutritional status in fission yeast.";
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N -> D (IN REF. 1).
                                                                                                          .;
0
                                                                           DB 1; Length 1053;
                                                                                                         0; Indels
                                            MW, 33E5C2365222D238 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).

Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                   OPTIME: 09Y8G4;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Nucleoporin nup184 (Nuclear pore protein nup184).
                                                                       Score 33; DB 1; 1
Pred. No. 4.6e+02;
2; Mismatches 0;
               N-LINKED (GLCNA
N -> D (IN REF.
                                                                                                                                                                                                                                           PRT; 1564 AA.
                                                                          86.8%;
66.7%;
                                              114876
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                                                                                                         4; Conservative
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1022
751
 776 77
1022 102
751 75
1053 AA;
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177 ISWSWL 182
                                                                          Query Match
Best Local Similarity
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               CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503; **
Blattner R.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Ralley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Res. 3:137-155(1996).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 1; Length 1564;
Pred. No. 6.6e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                              1219 1219 S -> P (IN REF. 1).
1564 AA; 176962 MW; 248F3AEF338C30B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein ymfR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                               EMBL; AF055035; AAD43830.1; ALT_FRAME.
EMBL; AL157917; CAB76031.1; -.
GeneDB_SPombe; SPAP27G11.10c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97061202; PubMed=8905232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000214; AAC74234.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                   86.8%;
                                                                                                                                                                                                                                                                                                              Nuclear protein; Transport.
CONFLICT 1219 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, D90749; BAA35976.1; -. EMBL, D90750; BAA35988.1; -. PIR; C64860; C64860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EcoGene; EG14336; ymfR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:||:
6 LSWSWI 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LAWSWL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YMFR OR B1150.
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                                                                                                                                                                                                                                                                                                                                              CONFLICT
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136 AA

PRT;

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STANDARD;
                     01-JAN-1990 (Rel. 13,
01-JAN-1990 (Rel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 AWSWI 39
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                                                                                      Bacteriophage T4.
                                                                                                                        NCBI_TaxID=10665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AWSWL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y4IO RHISN
P55498;
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  YO7C BPT4
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                                                                                                                                                                                                                                                                                                                                                                            Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Res. 7:331-338(2000).
-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-1- SIMILARITY: BELONGS TO THE UPP0060 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
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                                                                                                                                                                                                                                                                         Rhizobium loti (Megorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 107;
                                                           Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                  1; Indels
Hypothetical protein; Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
0C666D85212C16C3 CRC64;
                                  A41487AAFEED364A CRC64;
                                                          Score 32; DB 1;
Pred. No. 47;
0; Mismatches
                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                             107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.2%; Score 32; DB
83.3%; Pred. No. 80;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL. POTENTIAL.
             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                        STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11591 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP003012; BAB54221.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF_00010; -; 1.
InterPro; IPR003844; UPF0060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam, PF02694; UPF0060; 1.
ProDom; PD015609; UPF0060; 1.
                                                                                                                                                                                                                                                      Hypothetical protein mll7841.
                                  6381 MW;
                                                          84.2%;
                                                       Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                             STANDARD;
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60
87
107 AA;
                                                                                                       1 LAWSWL 6
| ||||
39 LFWSWL 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mesorhizobium loti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 LAWLWL 76
                                  60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LAWSWL 6
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=381;
                                                                                                                                                                                            YNFA_RHILO
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TRANSMEM
SEQUENCE
           TRANSMEM
                                  SEQUENCE
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RESULT 11 YO7C_BPT4

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
          01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical 16.0 kDa protein in segB-ipI intergenic region (ORF3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 387:394-401(1997)
-!- SIMILARITY: LOW SIMILARITY TO THE IS1111A/IS1328/IS1533 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=97305956; Pubmed=9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal
                                                                                                                                 Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid sym pNGR234a.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

BEDLINES 66037230; PubMed=4057254;
Broida J., Abelson J., Abelson In the "Sequence organization and control of transcription in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 1; Length 136;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: HIGH TO FI3; SOME, TO Y4PF/Y4SB AND Y4QE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G.
Mesyanzhinov V., Ruger W., Stidham T., Thomas E.;
"Bacteriophage T4 genome analysis.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF158101; AAD42681.1; -.
Hypothetical protein.
SEQUENCE 136 AA; 16034 MW; 02ED3B4D8D274D9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 28.6 kDa protein Y410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.2%; Sco...
80.0%; Pred. No. 1s...
1; Mismatches
                                                                                                                                                                                                                                                                                                                                              bacteriophage T4 tRNA region.";
J. Mol. Biol. 185:545-563(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhizobium sp. (strain NGR234).
Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X03016; CAA26805.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 80.0 es 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=Guatemala laboratory colony, and Hawaii laboratory colony;
MEDLINE=95261546; PubMed=7742977;
Gasparich G.E., Shapard W.S., Han H.Y., McPheron B.A., Steck G.J.;
"Analysis of mitochondrial DNA and development of PCR-based diagnostic molecular markers for Mediterranean fruit fly (Ceratitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              capitata) populations.";
Insect Mol. Biol. 4:61-67(1995).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                       ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Tephritoidea; Tephritidae; Ceratitis.
                                                                                                                                                                                                                                                                 84.2%; Score 32; DB 1; Length 252; 83.3%; Pred. No. 1.8e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 66.7%; Pred. No. 2.9e+02;
4; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam: PF00361; oxidored q1; 1.—Pfam: PF01059; oxidored q5 N; 1.
PRINTS: PR01437; NUOXDRDTASE4.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 446 AA; 50967 NW; E9AAAC06796897FD CRC64;
                                                                                                                                                             InterPro; IPR003346; Transposase 20.
Pfam; PF02371; Transposase 20; 1.
Hypothetical protein; Plasmid.
SEQUENCE 252 AA; 28552 MW; D993C7DA03E15190 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUAM CERCA STANDARD, PRT, 446 AA. 034048; 034053; Created) St. Created) St. Uru-1998 (Rel. 36, Created) St. Uru-1998 (Rel. 36, Last sequence update) St. Uru-1998 (Rel. 36, Last annotation update) MADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ceratitis capitata (Mediterranean fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003918; NADHub oxred4.
InterPro; IPR001750; Oxidored_q1.
InterPro; IPR000260; Oxidored_q5_N.
                                                                                                                                                EMBL; AE000079; AAB91710.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U12925; AAA85797.1; -. EMBL; U12924; AAA85796.1; -.
                                                                                                                                                                                                                                              190 LAWLWL 195
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE-97332569; PubMed=9188803;

MEDLINE-97332569; PubMed=9188803;

Medracteristics of the melibiose transporter and its primary structure in Enterobacter aerogenes.";

Biochim. Biophys. Acta 1326:83-91(1997).

-I FUNCTION: PROTEIN RESPONSIBLE FOR MELIBIOSE TRANSPORT. IT IS CAPABLE OF USING HYDROGEN AND LITHIUM CATIONS AS COUPLING CATIONS FOR COTRANSPORT!, DEPENDING ON THE PARTICULAR SUGAR TRANSPORTED
                                                                                                                                                                                                                                                                                                                                                                  membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inner membrane; Symport.
                                                                                                                                                                                                                                                                                                                                                          (SYMPOKE SYSTEM).
SUBCELLULAR LOCATION: Integral membrane protein. Inner membran
SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY
                                                                                                                                                      Enterobacter aerogenes (Aerobacter aerogenes).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Enterobacter.
                                                                   15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mellbiose carrier protein (Thiomethylgalactoside permease II)
(Mellbiose permease) (Na+ (Li+)/mellbiose symporter) (Mellbiose
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9755D85D91828106 CRC64;
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DOMAIN 1 11 CYTOPLASMIC (POTENTIAL).
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ILGETPO: IPRO01927; Nad Gal_symport.
TIGREAMs; TIGR00792; gph; 1.
PROSITE; PS00872; NA_GALACTOSIDE_SYMP; 1.
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RESULT 14
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CYTOPLASMIC (POTENTIAL).

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-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
-!- SUBCELLULAR ENCATION: Integral membrane protein. Inner membrane.
                                    Gaps
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INTERPRO; ITEN0192; gph; 1.
PROSITE; PSO0872; NA_GALACTOSIDE_SYMP; 1.
TRANBOOKT; Sugar transport; Transmembrane; Inner membrane; Symport.
NOMAIN 1 11 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                 Klebaiella pneumoniae.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
                                                                                                                                                                                                                   01-JTL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Melibiose carrier protein (Thiomethylgalactoside permease II)
(Melibiose permease) (Na+ (Li+)/melibiose symporter) (Melibiose
                                  ó,
84.2%; Score 32; DB 1; Length 471; 83.3%; Pred. No. 3.1e+02;
              Pred. No. 3.1e+02;
0; Mismatches 1; Indels
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MEDLINE=92406738; PubMed=1339436;
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              Best Local Similarity 83.3
Matches 5; Conservative
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Pred. No. 3.1e+02;
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6D373D09BP4BAEC7 CRC64;
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Job time : 4.55263 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 18, 2004, 14:12:09; Search time 6.5921 Seconds Run on:

(without alignments) 87.531 Million cell updates/sec

US-09-643-260-7 38 Perfect score:

1 LAWSWL 6 Seguence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

PIR 76:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	9	Query		8		
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•••	36	94.7	675	01	H69200	heavy-metal transp
.,	32	92.1	116	~	T03472	~
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• •	35	92.1	196	~	C87039	conserved hypothet
•	35	92.1	210	~	C70528	hypothetical prote
•	35	92.1	421	~	AI2824	NADH dehydrogenase
•	35	92.1	438	~	H97602	probable NADH dehy
•	35	92.1	441	ď	A13607	NADH2 dehydrogenas
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•	34	89.5	151	~	AE2249	hypothetical prote
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	34		207	~	A48608	El glycoprotein -
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• •	34	6.	264	~	H83224	phosphonate transp
•	34	φ.	266	~	C83602	prolipoprotein dia
•	34	٠	296	~	E83292	conserved hypothet
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• •	34	φ.		~	T35781	
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	34	6		Н	VHWVEV	structural polypro
	34	•		~	S26373	qenome polyprotein
	34	89.5	1242	7	S72350	structural polypro
	34	6		~	A56605	structural polypro
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ALIGNMENTS

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C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: H69200
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S.; Church, G.M.; Danlels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func A;Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Status: preliminary; nucleic acid sequence not shown; translation not shown A,Molecule type: DNA A,Molecule type: DNA A,Residues: 1-675 <MTH> A,Residues: 1-675 <MTH> A,Residues: 1-675 <MTH> A,Residues: 1-675 <MTH> A,Residues: 1-675 <MTH> A,Residues: 1-675 <MTH> A,Residues: 1-675 <MTH> A,Residues: 1-675 <MTH> A,Residues: 1-675 <MTH> A,Residues: 1-675 <MTH> A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Residues: 1-675 <MTH A,Resid
heavy-metal transporting CPx-type ATPase - Methanobacterium thermoautotrophicum (strain
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Gaps ö Length 675; 'Match 94.7%; Score 36; DB 2; Length 675 Local Similarity 83.3%; Pred. No. 2.1e+02; es 5; Conservative 1; Mismatches 0; Indels Query Match Best Local Matches

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Conserved hypothetical protein - Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C;Accession: T03472
C;Accession: T03472
R;Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB100

A; Reference number: Z14955; MUID:97404404; PMID:9256491

A;Status: preliminary; translated from GB/EMBL/DDBJ A; Accession: T03472

Query Match

92.1%; Score 35; DB 2; Length 116;

Gaps

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A;Residues: 1-210 <COL>
A;Cross-references: GB:296072; GB:AL123456; NID:g3261793; PIDN:CAB09496.1; PID:e1300031,,
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClelll; Karp, P.; Romero, P.; Zhang, S. Science 294, 2117-2233, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davila, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

Nature 393, 537-544, 1998

A;Authores: Sqares, R.; Sullston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Hitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NADH dehydrogenase ndh [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                   A;Accession: C70528
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: Rv2680
C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.1%; Score 35; DB 2; Length 421; 83.3%; Pred. No. 1.9e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35; DB 2;
Pred. No. 1e+02;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: NADH dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 83.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                 C;Accession: T51122
R;Krubasik, P.; Sandmann, G.
Mol. Gen. 2. 263, 423-432, 2000
A;Title: A carotenogenic gene cluster from Brevibacterium linens with novel lycopene cyclesterence number: 225303; MUID:20279196; PMID:10821176
A;Accession: T51122
A;Accession: T51122
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-172 <KRU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conserved hypothetical protein MIJ041 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: C87039
R;Cole, S.T.; Eiglmeier, K; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc
R; Davies, R.M.; Duthoy, K.M.
M.A.; Rutherford, K.M.
Mature 409, 1007-1011, 2001
A;Authores: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq.
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
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A;Residues: 1-196 <STO>
A;Cross-references: GB:AL450380; NID:g13093055; PIDN:CAC31422.1; GSPDB:GN00147
                                                                                                                                                                                                                                                                                  crtK protein [imported] - Brevibacterium linens
C;Species: Brevibacterium linens
C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000
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                                Gaps
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C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2680
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                                   Indels
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     d. No. 57;
Mismatches
     Pred.
                                1;
     83.3%;
Best Local Similarity 83.3
Matches 5; Conservative
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109 VAWSWL 114
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LSWSWL 68
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91 VAWSWL 96
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Les 5; Conserv
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A;Status: preliminary
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Matches
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probable NADH dehydrogenase (Y09899) [imported] - Agrobacterium tumefaciens (strain C58, G5peciess Agrobacterium tumefaciens
C;Speciess Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: H97602
A;Scodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2332-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Accession: A12824
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                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Rosidues: 1-421 <KUNA
A;Crosidues: 1-421 <KUNA
A;Crosidues: 1-8121 <KUNA
A;Crosidues: 1-8121 <KUNA
A;Crosidues: CB:ARO08688; PIDN:AAL43015.1; PID:g17740478; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
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C;Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Accession: AE249 B;Accession: AF,Eference of the Filamentous Nitrogen-fixing Cyanobacterium An. A;Reference number: AB1807; MUID:21595285; PMID:11759840 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2249 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2249 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession: AE2449 B;Accession:
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A;Experimental source: strain PAO1
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C;Species: eastern equine encephalomyelitis virus
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
C;Accession: A48608
E;Weaver, S.C.; Bellew, L.A.; Gousset, L.; Repik, P.M.; Scott, T.W.; Holland, J.J. Virology 195, 700-709, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B33635
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, 1. J. Dison, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-151 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB75247.1; PID:g17132681; GSPDB:GN00179
                                                                                                                                                                                                                                                          hypothetical protein alr3548 [imported] - Nostoc sp. (strain PCC 7120)
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100.0%; Pred. No. 1e+02;
ive 0; Mismatches 0; Indels
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Best Local Similarity 100.vv
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Best Local Similarity 100.
Matches 5; Conservative
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A;Molecule type: DNA
A;Residues: 1-162 <STO>
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                                                                      68 AWSWL 72
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A;Gene: PA0085
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Reference number: AD3252; PMID:11756688
A;Recession: A13607
A;Recession: A1407
A;Redocule type: DNA
A;Redocule type: DNA
A;Redocule type: DNA
A;Redocule type: DNA
A;Redocule type: DNA
A;Cross-references: GB:AE008918; PIDN:AAL54028.1; PID:g17984981; GSPDB:GN00191
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A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
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                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                           A Residues: 1-438 «KUR»
A;Cross-references: GB:AE007869; PIDN:AAK87777.1; PID:g155148; GSPDB:GN00169
C;Genetics:
A;Gene: AGR C 3667
A;Gene: AGR C 1667
C;Superfamily: NADH dehydrogenase
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: A10124
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Pred. No. 2e+02;
1; Mismatches 0; Indels
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Pred. No. 2e+02;
1; Mismatches
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89.5%; Score 34; DB 2;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches (
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3%;
Matches 5; Conservative
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C,Superfamily: NADH dehydro
C,Keywords: oxidoreductase
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413 VAWSWL 418
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410 VAWSWL 415
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A; Molecule type: DNA
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Gene: BMEII0786
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A;Molecule type: DNA
A;Residues: 1-266 <STO>
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Cyfacesion: #83224
RyStover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Lory, S.; Olson, M.W.
Nature 406, 959-964, 2000
A.Title: Complete genome sequence of Pseudomonas aeruginosa PAOI, an opportunistic patho
A.Title: Complete genome sequence of Pseudomonas aeruginosa PAOI, an opportunistic patho
A.Title: Complete genome sequence of Pseudomonas aeruginosa PAOI, an opportunistic patho
A.Title: Day
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A,Title: Diversity within natural populations of eastern equine encephalomyelitis virus.
A,Reference number: A48608; MUID:93331728; PMID:8101674
A,Contents: 215-85, MD85B
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Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 22-Oct-1999
Accession: C48652; S33428
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C;Date: 15-Sep_2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-224 < HAG>
A, Cross-references: EMBL: Z19593; NID: G298051; PIDN: CAA79641.1; PID: G298054
C, Genetics:
                                                                                                                 A;Accession: A48608
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-207 <NEA.
A;Cross-references: GB:S63996; NID:g400551; PIDN:AAB27576.1; PID:g400552
A;Ouce: sequence extracted from NCBI backbone (NCBIN:135481, NCBIP:135482)
C;Superfamily: togavirus structural polyprotein
C;Keywords: glycoprotein
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Gaps

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prolipoprotein diacylglyceryl transferase PA0341 [imported] - Pseudomonas aeruginosa (st
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                       Cjaccession: C83602
Kristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Baddy, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 95-964, 2000
A.jritle: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: GB:AE004472; GB:AE004091; NID:g9946188; PIDN:AAG03730.1; GSPDB:GN001
A,Experimental source: strain PAO1
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Pred. No. 1.8e+02;
0; Mismatches 1; Indels
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C;Superfamily: prolipoprotein diacylglyceryl transferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 89.5
Best Local Similarity 83.3
Matches 5; Conservative
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Q8fqz9 corynebacte
Q9aza caubidopsie
Q9xgz2 arabidopsie
Q914x2 streptomyce
Q8nbw1 homo sapien
Q94jm4 arabidopsie
Q940d6 arabidopsie
Q940d6 arabidopsie
Q95170 arabidopsie
Q95170 arabidopsie
Q95170 arabidopsie
Q95170 arabidopsie
Q96wt 6 arabidopsie
Q96wt 8 chizosacch
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Q96wt 8 chizosacch
Q96wt 3 chizosacch
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O9pa54 xylella fas
O9e117 meleagrid h
O9dptl meleagrid h
O801y6 hypocrea sc
O00005 trichoderma
Q96ab7 homo sapien
Q8mmj0 apis cerana
Q9cyu6 mus musculu
                                                O9btv6 homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22067395; PubMed=12073090; Godgebur FROM N.A. MeDLINE=22067395; PubMed=12073090; Godgebur F., Powler T., Phillips J., van der Kley P., Godgebur F., Powler T., Phillips J., van der Kley P., Van Solingen P., Dankmeyer L., Power S.D.; "Cloning and relational analysis of 15 novel fungal endoglucanases from family 12 glycosyl hydrolase."; Curr. Genet. 41:89-98 (2005). EMBL; AR435065; AAM77708.1; ... InterPro; IPR002594; Glyco hydro_12. Femi, PF01670; Glyco hydro_12. Femi, PF01670; Glyco hydro_12. Femi, PF01670; Glyco hydro_12. 1. SEQUENCE 236 AA; 26024 MW; C3DBA7E33F0C41D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bionectria ochroleuca.
Eukaryota; Pungl; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Bionectriaceae; Bionectria.
MCBI_TaxID=29856;
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Pred. No. 1.8e+02;
1; Mismatches 0; Indels
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Last sequence update)
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PRT;
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83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
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Q8d59 bifidobacte
Q9g59 bifidobacte
Q92x130 filazobium m
Q92mi5 rhizobium m
Q92mp drosophila
Q9vyp2 drosophila
Q9vyp2 drosophila
Q94712 streptomyce
Q91389 pseudomonas
Q9acr5 streptomyce
Q91x88 homo sapien
Q91y88 cullex nigri
Q8bit9 mus musculu
G8D100 prunus arme
Q9p100 pseudomonas
Q8p401 xanthomonas
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                                                                                                      February 18, 2004, 14:09:39; Search time 17.3684 Seconds (without alignments) 89.145 Million cell updates/sec
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Q92K30
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Q81XK8
Q81XK8
Q81YK8
Q81YK9
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Minimum DB Maximum DB

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PRELIMINARY;
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01-MAR-2003
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Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
EMBL; AE014701; AAN24605.1; -.
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Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boitsraf P., Becker A., Rahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
"Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
            01-MAR-2003 (TrEMBLrel. 23, Created) · 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Probable dihydroorotate dehydrogenase electron transfer subunit. PYRK OR BLO790.
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                                                                                        Bifidobacterium longum.
Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
                                                                                                                                                                                 STRAIN-NCC 2705;
MEDINE-22294977; PubMed=12381787;
SChell M.A., Karmixrantzou M., Snel B., Vilanova D., Berger B. Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M., Pridmore R.D., Arigoni F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein R02283.
R02283 OR SMC01671.
R02283 OR SMC01671.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiaces; Rhizobiaces; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                      Match 92.5%; Score 37; DB 16; Length 274; Local Similarity 83.3%; Pred. No. 2.1e+02; les 5; Conservative 1; Mismatches 0; Indels
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SEQUENCE 437 AA; 48372 MW; 950E0B3DA963CE78 CRC64;
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157 ADWNWA 162
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Matches 5; Conserv
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SEQUENCE 274 AA;
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RESULT 4 Q92MI5

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STRAINE-1021;
MEDLINE-21305507; PubMed=11481430;
A Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
A Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
A Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
A Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium mellioti strain 1021.";
EMBL, AL591791; CAC47210.1;
EMBL, AL591791; CAC47210.1;
R InterPro; IPR003439; AMP-bind.
PEMBL, PR00501; AMP-bind.
PEMBL, PR0501; AMP-DINGNGTER, 1.
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Stapleton M., Broketein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Drokett V., Dresnek D., Farfan D., Frise E.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
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Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota,
Neoptera, Endopterygota, Diptera; Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                R02631 OR SMCÕ0741.
Rhizobium mellioti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 548;
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EMBL; AY118818; AAM50678.1; -.
FlyBase; FBgn0037896; CG6728.
InterPro; IPR000172; GMC_oxred.
Interpro; IPR000169; SHprot_acsite.
Pfan: PPR072, CMC_oxred: 3
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PROSITE; PS00639; THIOL PROTEASE HIS; 1.
SEQUENCE 581 AA; 63475 MW; AZF13BEBC25E496D CRC64;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last amnotation update)
Putative fatty-acid-CoA ligase protein (EC 6.-.-.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.5%; Score 37; DB 16; Le
83.3%; Pred. No. 4.1e+02;
....ematches 0;
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SEQUENCE 548 AA; 59383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=382;
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RX MEDLINE=20196006; PubMed=10731132;
RATAN=BERKELEY;
RA Adama M.D., Celniker S.E., Holt R.A., Beans C.A., Gocayne J.D.,
Radamatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,
Radamatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,
Radecoge R.A., Levis S.E., Fichardes R.A., Ashburner M., Henderson S.N.,
Radecoge R.A., Levis S.E., Richardes R.A., Champe M., Ffeiffer B.D.,
Radecon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Ffeiffer B.D.,
Radecon R.C., Bennes P.V., Bernadal W.D., Barakaroglu L., Beasley E.M.,
Benkova D., Botchan M.R., Bouck J., Byraktaroglu L., Beasley E.M.,
Radecon R., Benchen M.R., Bouck J., Brokstein P., Botchiarkov S.,
Radecon R., Doup L.E., Downes M., Dugaln Roches P., Chandra I.,
Radecon R.J., Evangelista C.C., Ferraz C., Ferriera S., Plaischman W.,
Radecon R.J., Evangelista C.C., Ferraz C., Ferriera S., Plaischman W.,
Radecon R.J., Gabriellan A.E., Gasy N.S., Gelbart W.M., Glasser K.J.
Robin R.J., Barocy D., Heiman T.J., Hernandez J.R., Houck J.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kalp D., Lai Z.,
Liang Y., Lin X.,
Liakov P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Matteil B., McIntosh T.C., McLeod M.P., McPherson D.L.,
Radion D.R., Nathon R.A., Nixon K., Nusskern D.R., Pacteb J.M.,
Radion R.M., Moy M., Wurphy E., Wurzhy D.M., Nathon D.L.,
Radion D.R., Wattenn G.S., Pan S., Pollacu Y., Rennicon D.L.,
Radion D.R., Wattenn G.S., Pan S., Pollacu Y., Shen H.,
Spier E., Spradining A.C., Stapleton M., Stupski M.P.,
Radion D.R., Wooder T., Water E., Wang A.,
Radion R.R., Woodes T., Water E., Wang A.,
Radion D.R., Watere E., Wardy S., Yung D.,
Radion D.R., Watere E., Wang A., Wang G.,
Radion R.R., Wasserman D.A., Weissenbach J.,
Radion D.R., Watere E., Spradining A.C., Stapleton M., Stupski M.P.,
Radion R.C., Stander E., Wang G., Zhu X., Smith H.O.,
Radion R.R., Wasserman D.A., Weilse R.D.C., Shang S., Physe R., Shu B.C., Saden-Rise R., Rubin G.,
Radione R.G., Shang S., Pollack C., 
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                                            Gape
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0
                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
  Score 37; DB 5; Length 581;
Score 37; L. ...
Pred. No. 4.40+02;
Pred. no. 4.40+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase, FBGN00137896, CG6728.
InterPro, IPR000172, GMC_oxred.
InterPro, IPR000169, SHprot_acsite.
Pfam, PF00713, GMC_oxred; 1.
PROSITE, PS00624, GMC_OXRED 2; 1.
PROSITE, PS00639, THIOL_PROTEASE HIS; 1.
SEQUENCE 597 AA; 65274 MW; 8G4C362AFFA0902A CRC64;
                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                             597 AA
                                        1; Mismatches
                                                                                                                                                                                                                         PRT;
92.5%;
83.3%;
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                 Best Local Similarity 83.3
Matches 5, Conservative
                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                            158 SDWSWA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                 1 ADWSWA 6
                                                                                                                                                                                                                                                                                                                                CG6728 protein.
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Query Match
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                                                                                                                                                                                     RESULT 6
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STRAINS-ATC. 15692 / PAO1;
STRAINS-ATC. 15692 / PAO1;
STOWER C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowallik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Waselbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Polger K.R., Kas A., Larbig K., Lim R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=1196410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Marren T., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Mature 417:141-147(2002).

EMBL; AL93128; CAA20627.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 610 AA; 67368 MW; 052CEA90DB589021 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Streptomycineae, Streptomycetaceae, Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.5%; Score 37; DB 16; Length 610; 83.3%; Pred. No. 4.6e+02; ive 1; Mismatches 0; Indels
Length 597;
                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical profess SC05530.
SC05530 OR SC5C7.15.
Streptomyces coelicolor.
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Last sequence update)
Last annotation update)
                                4.5e+02;
   Score 37; DB 5;
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                                                                 1; Mismatches
                                   Pred. No.
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   92.5%;
83.3%;
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KDPD OR PA1636.
                          Best Local Similarity 83.3
Matches 5, Conservative
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                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                   :|||||
158 SDWSWA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                               1 ADWSWA 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ADWSWA 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hopwood D.A.;
      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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086712
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STRAIN-Florida1997;
MEDLINE=21488685; PubMed=11602755;
Afonso C.L., Tulman B.R., Lu Z., Balinsky C.A., Moser B.A.,
Bernel J.J., Rock D.L., Kuitsh G.F.;
"Genome Sequence of a Baculovirus Pathogenic for Culex nigripalpus.";
J. Virol. 75:11157-11165(2001).
                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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STRAIN=Florida1997;
Afonso C.L., Tulman B.R., Lu Z., Balinsky C.A., Moser B.A.,
Becnel J.J., Rock D.L., Kutish G.F.;
Submitted (JuL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF403738; AAK94146.1;
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.0%; Score 36; DB 12; Length 242; 100.0%; Pred. No. 2.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC040173; AAH40173.1; -.
Hypothetical protein.
SEQUENCE 227 AA; 25487 MW; F11A71EA57062A05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 AA; 27222 MW; 6014967531110E52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Culex nigripalpus baculovirus.
Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to hypothetical protein BC017335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.0%; Score 36; DB 4; Le
100.0%; Pred. No. 2.4e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUN068 hypothetical protein
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nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                            10 ADWSW 14
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                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
  ADWSW
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01-DEC-2001
01-DEC-2001
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QBIXK8;
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Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitesh B., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Complete genome sequence of the model actinomycete Streptomyces
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Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBL_TaxID=1902;
                                                                                                           -!- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS. EMBL; AE004591; AAG05025.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50109; HIS_KIN; 1.
Kinase; Phosphorylation; Sensory transduction; Transferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.5%; Score 37; DB 16; Length 88:
83.3%; Pred. No. 6.7e+02;
wiemafches 0; Indels
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Nature 417:141-147(2002).
EMBL; AL590464; CAC3679).;
Hypotherical protein; Plasmid; Complete proteome.
SEQUENCE 205 AA; 23051 MW; 6602396CFF93F2D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         885 AA; 97019 MW; 20FC8E2B2AB876C0 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 AA
                                                                                                                                                                            InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR004358; Bact sens pr C.
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                                                                                                                                                                                                                      InterPro; IPR003018; GAF.
InterPro; IPR003661; His kinA.
InterPro; IPR005467; His kinAs.
InterPro; IPR003852; KdpD.
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01-0CT-2002 (TrEMBLrel. 22, La
Hypothetical protein SCP1.253.
SCP1.253.
                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00344; BCTRLSENSOR.
SMART; SM00065; GAF; 1.
SMART; SM00387; HATPaec; 1.
SMART; SM00388; HisKA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
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                                                                                                                                                                                                                                                                                                                 Pfam; PF02518; HATPase
Pfam; PF00512; HisKA; ī
                                                              opportunistic pathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          563 ADWAWA 568
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SEQUENCE 885 AA
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STRAIN=ATCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043;

MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X. Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman P.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
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STRAINS-ATCC 33913 / NCPPB 528;
MEDLINE-22022145; PubMed=12024217;
MEDLINE-22022145; Perro J.A., Reinach F.C., Farah C.S., Furlan L.R., Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F., Alves L.M.C., do Amaral A.M., Berrolini M.C., Camargo L.B.A., Caracoli R.B., Coutinho L.L., Cursino-Santos D.F., Giapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T., Fornighieri B.F., Franco M.C., Gruber A., Fornighieri B.F., Franco M.C., Gruber A., Lemos M.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F., Locali B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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Pred. No. 4e+02;
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                                                 Indels
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Hypothetical protein; Complete proteome.
SEQUENCE 374 AA; 42269 MW; 31EF185C4F683884 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical protein PA3230.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Cationic amino acid transporter.
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    Pred. No. 3.8e+02;
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100.0%; Pred. No. ac.
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                                                 0; Mismatches
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    100.0%;
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                    108 ADWSW 112
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Q8P4A1;
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STRAINANOD; TISSUB-Thymus;
STRAINANOD; TISSUB-Thymus;
MEDLINE-223546813; Pubmed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length conse transcriptome based on functional annotation of 80,770 full-length conse transcriptome based on functional annotation of 60,770 full-length conse transcriptome based on functional annotation of SEMBL; AK087998; BAC40084.1; --
EMBL; AK087998; BAC40084.1; --
EMBL; AK087998; BAC40084.1; --
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STRAIN=Bergeron; TISSUE=Mesocarp, and Exocarp;
STRAIN=A-Mberguie D., Gomez R.-M., Fils-Lycaon B.;
Sequence of AFTRI, a Cysteine Proteinase From Apricot Fruit
(Accession No. U93166). Gene Expression During Fruit Ripening. (PGR97-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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PROSITE; PROGNOSS; HIM 1; 1.
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PROSITE; PROGNOSS; THIOL. PROTEASE THIOL. PROGNOSITE; PROGNOSS; THIOL. PROTEASE THIOL. PROFESSE THIOL. PROTEASE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFESSE THIOL. PROFE
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Mitochondrial ribosomal protein L41 homolog.
Mus musculus (Mouse).
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InterPro; 1PR000668; Peptidase Cl.
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Plant Physiol. 115:1730-1730(1997).
EMBL; U93166; AAB97142.1; -.
HSSP; P07711; 1CJL.
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01-JUN-1998 (TrEMBLrel. 06,
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A Pereira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

A Pereira H.A., Rossa A., Sana J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.P.,

RA Setubal J.C., Kitajima J.P.;

RT "Comparison of the genomes of two Xanthomonas pathogens with differing

RT host specificities.",

Nature 417:459-463(2002).

REMBL, AE012502; AAM43483.1; --

DR InterPro; IPR004841; Permease.

InterPro; IPR004841; Permease.

RW Complete proteome.

SQ SEQUENCE 433 AA; 45128 MW; EF217D2A7C516533 CRC64;
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                          Virology 193:868-876(1993).

-!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.
-!- CATALVITC ACTIVITY: Hydrolysis of alpha-(2-3)., alpha-(2-56)-, alpha-(2-8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
                                                           Gaps
                                                                                                                                                                                                                                                                                                                          Saito T., Kawaoka Y., Webster R.G.; "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURPACE OF THE VIRION.
-!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL).
398 N-LINKED (GLCNAC. . .) (POTENTIAL.)
51989 MW; DIAGF07460F6F8AD CRC64;
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                                     Length 470;
                                                                                                                                                                                                                                          Influenza A virus (strain A/Duck/Chabarovsk/1610/72).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANCHOR (BY SIMILARITY).
HYPERVARIABLE STALK REGION.
HEAD OF NEURAMINIDASE.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .))
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                                                          Indels
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Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
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                                     1;
                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Neuraminidase (EC 3.2.1.18).
                                  DB 1
62;
                                                                                                                                                                470 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed.
                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement ((or send an email to license@isb-sib.ch)
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                                   Score 36;
Pred. No.
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N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001860; Glyco_hydro_34.
                                                                                                                                                                                                                                                                                                                 MEDLINE=93212520; PubMed=8460490;
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                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
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                                  90.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L06573; AAA43367.1; -.
HSSP; P06820; 2BAT.
                      Query Match
Best Local Similarity 100.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Homotetramer.
                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00064; neur;
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398
470 AA;
           470 AA;
                                                                                                      453 ADWSW 457
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                                                                                 1 ADWSW
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Q07571;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.

CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93212520; PubMed=8460490;
Saito T., Kawaoka Y., Webster R.G.;
"Phylogenetic analysis of the N8 neuraminidase gene of influenza
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
Indels
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52015 MW; E1C1D3E2C650B93C CRC64;
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Hydrolase; Glycosidase; Glycoprotein; Transmembrane
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Mismatches
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100.0%; Pred
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5; Conservative
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Gaps

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Mismatches

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STANDARD;

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virules.";
Virology 193:868-876(1993).

Virology 193:868-876(1993).

-!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.

-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-glycopidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
                                                                                                                                                                                                                        MEDLINE-93212520; PubMed-8460490;
Saito T., Kawaoka Y., Webster R.G.;
"Phylogenetic analysis of the N8 neuraminidase gene of influenza A
                                                                                                                                 Influenza A virus (strain A/Duck/Ukraine/1/63).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
                                                        01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
Neuraminidase (EC 3.2.1.18).
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                               NCBI_TaxID=11374;
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                                        007599;
 RESULT 5
NRAM_IADU3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                       VIROLOGY 193:868-876(1993).

-1- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.

-1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-56)-, alpha-(2-8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoteins, glycolipids, colominic acid and synthetic substrates.
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
BEDILNES-23125.20; PubMed=8460490;
Saito T., Kawaoka Y., Webbier R.G.;
"Phylogenetic analysis of the N8 neuraminidase gene of influenza A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBCELLULAR LOCATION: VIRAL MEMBRANE, FORMS A MUSHROOM-SHAPED SPIKE ON THE SURPACE OF THE VIRION.
-i- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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HRAD OF NEURAMINIDASE.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (POTER N-LINKED (GLCNAC. . . ) (POTEN N-LINKED (GLCNAC. . . ) (POTEN N-LINKED (GLCNAC. . . ) (POTEN N-LINKED)
                                                                                                                                                                                        Influenza A virus (strain A/Duck/Memphis/928/74).
Viruses, ssRNA negative-strand viruses, Orthomyxoviridae,
Influenza A viruses, Influenzavirus A.
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(GLCNAC...)
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Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
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                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pduraninidase (EC 3.2.1.18).
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                                                                                       470 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L06575; AAA43404.1; -. HSSP; P06820; 2BAT.
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                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00064; neur;
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398
470 AA;
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ADWSW 457
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nes 5; Conserv
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01-FEB-1995 (
28-FEB-2003 (
                                                                                    NRAM IADM2
Q07573;
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-!- SUBCELLULAR LOCATION: VIRAL MEMBRANE, FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION.
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62;
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Pfam; PF00064; neur; 1.

ProDom; PD000431; Glyco_hydro_34; 1.

Hydrolase; Glycosidase; Glycoprotein; Transmembrane.

TRANGNEM 38 HYPERVARIABLE STALK REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51960 MW; B46D54A03AC84CCE CRC64;
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100.0%; Pred. No. v...
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Q07574;
01-FEB-1995 (Rel. 31, Created)
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Gaps

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0; Indels

Conservative

ADWSW 457

453

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Viriology 193:868-876(1993).

-!- FUNCTION: Removes the terminal static acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.
-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->6)-sh)-glycosidic linkages of terminal static residues in cligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
                                                                                            MEDLINE=93212520; PubMed=8460490;
Saito T., Kawaoka Y., Webster R.G.;
"Phylogenetic analysis of the N8 neuraminidase gene of influenza A
Influenza A virus (strain A/Herring gull/DE/677/88).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
                                                                               SEQUENCE FROM N.A.
                                              NCBI_TaxID=38964;
                                                                                                                                           viruses.";
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    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                Virology 193:868-876(1993).

-!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.
-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycopsidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
                                                                                                                                                      MEDLINE=93212520; PubMed=8460490;
Saito T., Kawaoka Y., Webster R.G.;
"Phylogenetic analysis of the N8 neuraminidase gene of influenza A
                                                                                                                                                                                                                                                                                                                                                                        -i-SUBCELLULAR LOCATION: VIRAL MEMBRANE, FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION.
-i-SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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(POTENTIAL).
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                                                             Influenza A virus (strain A/Guinea fowl/New York/4-3587/84).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 470;
                                                                          Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANCHOR (BY SIMILARITY). HYPERVARIABLE STALK REGION.
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BY SIMILARITY.
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Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
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(GLCNAC. . .)
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 Last sequence update)
Last annotation update)
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                   28-FEB-2003 (Rel. 41, Last a
Neuraminidase (EC 3.2.1.18).
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293
398
470 AA;
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Best Local Similarity
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                (Rel.
                                                                                                            NCBI_TaxID=38963;
                28-FEB-2003
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CARBOHYD
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SÜBUNIT: Homotetramer.
SUBCELLÜLAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
SPIKE ON THE SURFACE OF THE VIRION.
SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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HEAD OF NEURAMINIDASE.
BY SIMILARITY.
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N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED (GLCNAC. . .) (POTEN N-LINKED M-LINKED 
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probom; PF00064; neur; 1.
Probom; PD000431; Glyco hydro 34; 1.
Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
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Neuraminidase (EC 3.2.1.18).
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NRAM_IAHJI
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Gaps

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Indels

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100.0%; Pred. No. 62; ive 0; Mismatches

5; Conservative

Matches

453 ADWSW 457

1 ADWSW 5

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01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Neuraminidase (EC 3.2.1.18).

470 AA

PRT;

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RESULT 7

of influenza

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                                         Viriology 193:868-876(1993).

-!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.

-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycopteins, glycolipids, colominic acid and synthetic substrates.
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Virology 193:868-876(1993).
-!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION. SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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MEDLINES-2312520; PubMed=8460490;
Saito T., Kawaoka Y., Webster R.G.;
"Phylogenetic analysis of the N8 neuraminidase gene of influenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
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HEAD OF NEURAMINIDASE.
BY SIMILARITY.
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557630C3E11F2765 CRC64;
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Pfam; PF00064; neur; 1.
Pfam; PD000431; Glyco hydro_34; 1.
Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
Hydrolase; Glycosidase; ANCHOR (BY SIMILARITY).
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  neuraminidase gene
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Pred. No. 62;
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Last annotation update)
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"Phylogenetic analysis of the N8
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01-FEB-1995 (Rel. 31, Last seq
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Neuraminidase (EC 3.2.1.18).
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            SEQUENCE FROM N.A.
MEDLINE=93212520; PubMed=8460490;
Saito T., Kawaoka Y., Webster R.G.;
"Phylogenetic analysis of the N8 neuraminidase gene of influenza A
                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION. SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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Influenza A viruses; Influenzavirus A.
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HYPERVARIABLE STALK REGION
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01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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100.0%; Pred. ...
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MEDLINE-93212520; PubMed=8460490;
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Neuraminidase (EC 3.2.1.18).
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HSSP; P06820; 2BAT.
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                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia
               envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection. CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligoasccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
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"The family of major royal jelly proteins and its evolution.";
J. Mol. 8vol. 49:290-297(1999).
-!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN HONEYBEE NUTRITION. IT IS
FOUND IN THE ROYAL JELLY WHICH IS THE POOD OF THE QUEEN HONEY BEE
LARVA. THE ROYAL JELLY DETERMINES THE DEVELOPMENT OF THE YOUNG
LARVA. AND IS RESPONSIBLE FOR THE HIGH REPRODUCTIVE ABILITY OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Hymenoptera, Apocrita, Aculeata, Apoidea,
NCBI_TAXID=7460;
                                                                                                                                                              SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FFB-2003 (Rel. 41, Last sequence update)
28-FFB-2003 (Rel. 41, Last amocation update)
Major royal jelly protein 5 precursor (MRJP-5) (Bee-milk protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL). (POTENTIAL). (POTENTIAL).
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                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 470;
62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEAD OF NEURANINIDASE.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (1)
N-LINKED (GLCNAC. .) (1)
N-LINKED (GLCNAC. .) (1)
N-LINKED (GLCNAC. .) (1)
N-LINKED (GLCNAC. .) (1)
N-LINKED (GLCNAC. .) (1)
N-LINKED (GLCNAC. .) (1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANCHOR (BY SIMILARITY)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001860; Glyco_hydro_34. Pfam; PF00064; neur; 1. ProDom; PD000431; Glyco_hydro_34; 1. Hydrolase; Glycosidase; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99373663; PubMed=10441680;
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100.0%; Pre
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                                                                                                                                              SUBUNIT: Homotetramer.
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398
470 AA;
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             453 ADWSW 457
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ACT_SITE
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HONEYBEE QUEEN.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: HYPOPHARYNGEAL GLANDS OF NURSE HONEY BEES.
-!- DEVELOPMENTAL STACE: PRODUCED BY THE CEPHALIC GLANDULAR SYSTEM OF THE NURSE HONEY BEE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribon A.B., Coelho J.L.C., Barros E.G., Araujo E.F.;
"Cloning and characterization of a gene encoding the endopolygalacturonase of Penicillium griseoroseum.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBU databases.
-!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-galactosiduronic linkages in pectare and other galacturonans.
-!- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES (POLYGALACTURONASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
                                                                                                                                          -!- SIMILARITY: BELONGS TO THE MAJOR ROYAL JELLY PROTEIN FAMILY.
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30-MAY-2000 (Rel. 39, Last annotation update)
Polygalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAJOR ROYAL JELLY PROTEIN 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.0%; Scur.
100.0%; Pred. No. '''
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InterPro; IPR000743; Glyco_hydro_28.
InterPro; IPR006626; PbH1.
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AF004842, AAD01205.1; -.
InterPro; IPR003534; Royaljelly.
Pfam; PF03022; MRJP; 2.
SIGNAL; PR01366; ROYALJELLY.
Signal; Repeat; Glycoprotein.
SIGNAL
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70236 MW;
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30-MAY-2000 (Rel. 39, Last seq
30-MAY-2000 (Rel. 39, Last anno
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181
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598 AA;
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Best Local Similarity
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Wood V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,
Wood V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,
Bouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
A Brook R., Brown D., Brown S., Chillingworth T., Churcher C.M.,
A Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gonles S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
A Holroyd S., Hornby T., Howarth S., WcDonald S., McLean J.,
A Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
A Nitherford K., Zhores M., Squares R., Stevens K.,
A Retlon J., Simmonds M., Squares R., Squares S., Stevens K.,
A Taylor R.G., Trivey A., Walsh S.V., Warren T., Whitehead S.,
Rwelton J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Ra Goble C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
Ra Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Ra Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Ra Goffeau A., Cadieu B., Dreano S., Gloux S., Lelaure V., Mottier S.,
                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21363051; PubMed=11470243; Yokoyama K., Saltoh S., Ishida M., Yamakawa Y., Nakamura K., Inoue K., Yokoyama K., Saltoh S., Ishida M., Yamagida M., Setaka M.; Taguchi R., Tokumura A., Nishijima M., Yanagida M., Setaka M.; "Very long-chain fatty-acid-containing phospholipida accumulate in fatty acid synthase temperature-sensitive mutant strains of the fisation yeast Schizosaccharomyces pombe fas2/1sd1."; Biophys. Acta 1532:223-238(2001).
                                                                                                                                                                                                                                                                                    PAS2_SCHPO STANDARD; PRT; 1842 AA.

Q10289, O14163; P78973;

L15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fatty acid synthase subunit alpha (EC 2.3.1.86) (p190/210) [Includes: Acyl carrier; 3-oxoacyl-[acyl-carrier protein] reductase
(EC 1.1.1.100) (Beta-ketoacyl reductase); 3-oxoacyl-[acyl-carrier protein] synthase (EC 2.3.1.41) (Beta-ketoacyl synthase)].
FAS2 OR LSD1 OR SPAC4AB.11C.
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96354912; PubMed=8769419; Saitoh S., Takahashi K., Nabeshima K., Yamashita Y., Nakaseko Y., Saitoh S., Takahashi K., Nabeshima K., Yamagida M.; Hirata A., Yamagida M.; Harata A., Yamagida M.; Saberrant mitosli in fission yeast mutants defective in fatty acid synthetase and acetyl CoA carboxylase."; J. Cell Biol. 134:949-961(1996).
                                                                                                                                                     ö
                                                                                                                       Length 376;
                                                                                                                                                     0; Indels
                    SMART; SMUULLU; FURT, J.
PROSTIE; PSO0502; POLYGALACTURONASE; 1.
Hydrolase; Glycosidase; Cell wall; Signal.
SIGNAL 1 20 POTENTIAL.
CHAIN 21 376 POLYGALACTURONASE.
SEOURNCE 376 AA; 38068 MW; IEDBIEC56ED56928 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                    85.0%; Score 34; DB 1;
66.7%; Pred. No. 1e+02;
ive 2; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast)
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Pfam; PF00295; Glyco_hydro_28; 1.
SMART; SM00710; PbH1; 5.
                                                                      21 376 PC
376 AA; 38068 MW;
                                                                                                                                  Local Similarity 66.7
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Matches
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J. Biol. Chem. 269:14103-14110(1994).

J. Biol. Chem. 269:14103-14110(1994).

J. Biol. Chem. 269:1403-14110(1994).

J. Biol. Chem. 269:1403-14110(1994).

J. SINDER STAY ACID SYNTHETASE. CATALYZES THE FORMATION OF LONG-CHAIN PATTY ACID STORM ACETYL.-COA, MALONYL-COA AND NADPH.

J. OXOACYL-(ACYL-CARRIER PROTEIN) REDUCTASE, AND 3-OXOACYL-(ACYL-CARRIER-PROTEIN) SYNTHASE. THIS SUBBULT COORDINATES THE BINDING OF THE SIX BETA SUBBULTS TO THE ENZYME COMPLEX.

J. CATALYTIC ACTIVITY: Acetyl-CoA + N malonyl-CoA + ZN NADPH = a long-chain acyl-CoA + N (COA + N CO(2) + ZN NADP(+).

J. CATALYTIC ACTIVITY: Acetyl-carrier protein] + malonyl-[acyl-carrier protein] + CO(2) + CATALYTIC ACTIVITY: Acetyl-carrier protein] + CO(2) + CATALYTIC ACTIVITY: ACETYL-CATALYTIC ACETYL-CATALYTY: ACETYL-CATALYTY: ACETYL-CATALYTY: ACETYL-CATALYTY: ACETYL-CATALYTY: ACETYL-CATALYTY: ACETYL-CATALYTY: ACETYL-CATALYTY PHOSPHOPANTETHEINE (BY SIMILARITY).

BETA-KETOACYL SYNTHASE (BY SIMILARITY).
5 -> A (IN REF. 4).
K -> R (IN REF. 1). Kaeslin E., Heyer W.-D.; "Schizosaccharomyces pombe fatty acid synthase mediates DNA strand CATALYTIC FOOTEN - CATALYTIC FOOTEN FOOTEN FOOTEN CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-{acyl-carrier protein}
NADP(+) = 3-oxoacyl-{acyl-carrier protein} + NADPH.
SUBUNIT: {Alpha(6)beta(6)} hexamers of two multifunctional subunits (alpha and beta).
SIMILARITY: TO THE PATTY ACID SYNTHETASE, SUBUNIT ALPHA PROM TIGRFAMS; TIGRO0556; pancethn trn; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
FRUTY acid biosynthesis; Multifunctional enzyme; Oxidoreductase;
Transferase; NADP; Phosphopantetheine. Koken M.H.M., de Rooij J.; Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases. ACYL CARRIER (ACP). BETA-KETOACYL REDUCTASE. BETA-KETOACYL SYNTHASE. InterPro; IPR000282; ACPS.
InterPro; IPR000794; Ketoacyl-synt.
InterPro; IPR0001568; Pantethn.tm.
InterPro; IPR006162; Ppantne_attach.
Pfam; PF01648; ACPS; 1.
Pfam; PF02801; ketoacyl-synt.; 1.
Pfam; PF02801; ketoacyl-synt.; 1.
ProDom; PD004282; ACPS; 1.
TIGRFAM8; TIGR00556; pantethn.tm; 1. SEQUENCE OF 1-20. MEDLINE=94245730; Pubmed=8188691; PIR; A54083; A54083. PIR; T34781; T38781. PIR; T43409; T43409. GeneDB_SPombe; SPAC4A8.11c; -. EMBL, D83412; BAA11913.1; -.
EMBL, AB013747; BAB62029.1; -.
EMBL, 298762; CAB11481.1; -.
EMBL, U82216; AAB39943.1; -. SEQUENCE OF 1-215 FROM N.A. 1262 107 422 OTHER FUNGI ACT SITE CONFLICT BINDING DOMAIN

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Search completed: February 18, 2004, 14:28:04 Job time : 3.55263 secs
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                                                                                                                                                                                                          30-MXY-2000 (Rel. 39, Created)
30-MXY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type III) (NOSIII) (Endothelial NOS) (EONSTILUTIVE NOS) (CNOS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nitric oxide + N NADP(+).

COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Aguan K., Weiner C.P.;

"Effect of hypoxia on the microvasculature of developing fetal brain of sheep: a studies on the expression pattern of constitutive forms of nitric oxide synthase.";

Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN VASCULAR SMOOTH MUSCLE RELAAATION THROUGH A CGMP-MEDIATED SIGNAL TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF02898; NO_synthase; 1.
PROSITE, P8650001; NOS; PARTIAL.
Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Calcium-binding;
Heme; Multigene family.
                                                                                                                                                                                                                                                                                               NOS3 OR ENOS.
Ovis aries (Sheep).
Bukaryota, Metazooa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinee, Ovis.
                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE ENZYME (BY SIMILARITY).
-!- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN (BY
                             Length 1842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 1; Length 99;
Pred. No. 43;
1; Mismatches 0; Indels
                                                       Indels
202168 MW; E4019F2D133EE571 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 AA; 11034 MW; 82C3C765557031DA CRC64;
                        85.0%; Score 34; DB 1; Le:
66.7%; Pred. No. 4.3e+02;
live 2; Mismatches 0;
                                                                                                                                                                                    99 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: Homodimer (By similarity).
-!- SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR004030; NO synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U76738; AAB40705.1; -.
HSSP; P29473; 1D0C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.5%;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Endothelial cells;
                                                         4; Conservative
                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
 1842 AA;
                                                                                                              400 SDWNWA 405
                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                   1 ADWSWA 6
                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P29473
                                                                                                                                                                                   NOS3 SHEEP
P79209;
                                                                                                                                                                                                                                                                                      (Fragment)
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NON TER
SEQUENCE
 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interPro;
                             Query Match
                                                                                                                                                                     SHEEP
                                                      Matches
                                                                                                                                                        RESULT 14
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEDLINE=96337999; Dubmed=8688087;
MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Button G.G., Blake J.A., FitzGerald L.M., Clayron R.A., Gocayne J.D.,
Kerlavage A.R., Bougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: TO M.JANNASCHII MJ1220 AND MJECL42.
-!- SIMILARITY: WITH TYPE I RESTRICTION SYSTEM ADENINE METHYLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003356; NG_DNA_Mtase.
Pfam, PP02384; NG Mtase; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 220 AA; 25766 MW; 710DDAE4C7A47954 CRC64;
                                                                                                                                                                                                                                                                                         Archaea, Euryarchaeota, Methanococci, Methanococcales, Methanocaldococcaceae, Methanocaldococcus.
                                                                        (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
   220 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U67470; AAB98113.1; -. PIR; D64316; D64316.
                                                                                                                                                                               Hypothetical protein MJ0132.
MJ0132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 273:1058-1073(1996)
                                                                                                                                                                                                                                                              Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ADWSW 5
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                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2190;
                                                                        01-NOV-1997
                                                                                                                  01-NOV-1997
                                                                                                                                                16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               annaschii.
Y132 METJA
Q57596;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 18, 2004, 14:12:09; Search time 6.5921 Seconds (without alignments) 87.531 Million cell updates/sec Run on:

US-09-643-260-6 40 ·

1 ADWSWA 6 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	hypothetical prote	two-component sens	conserved hypothet	TonB-dependent rec	hypothetical prote	probable protein k		fatty acid synthas	mel-13a protein -	conserved hypothet	restriction modifi	CD1b protein - she	hypothetical prote	conserved hypothet	hypothetical prote	probable cytochrom	L-fucose-specific	vegetatible incomp	oligopeptide ABC t	gene CD1 protein -	cysteine proteinas	probable proteinas	lycopene cyclase -	hypothetical prote	sugar ABC transpor		probable phosphata	hypothetical prote	
ID	T35222	C83441	B83241	E87304	T05822	C84922	T43409	T38781	S65785	B82531	D64316	S58353	D90470	D87152	B75337	F83632	JC7853	AB3548	E72424	847246	871923	H90998	D75475	AE1844	AE1460	AF1097	T38242	T31511	G82697
08																	7									0	7	N	7
Length	610	882	374	883	275	617	1842	1842	132	198	220	232	239	257	276	304	310	324	328	333	320	368	410	415	418	418	421	433	467
& Query Match		92.5	0.06	90.0	Š.	85.0	ď.						82.5				82.5						•			ď	ď	٠	٠
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Result No.	7	7	m	4	ហ	9	7	60	თ	10	11	12	13	14	15	16	17		19		21	22	23	24	25	56	27	28	53

6-phospho-beta-glu 6-phospho-beta-glu	aerolysin precurso	probable GMP synth	hypothetical prote	restriction modifi	GMP synthase (glut	type I restriction	type I restriction	hypothetical prote	conserved hypothet	nitric-oxide synth	nitric-oxide synth	nitric-oxide synth	conserved hypothet	alkaline phosphata
E89790 I39953	803098	C86958	T15256	C64452	S72813	C69226	E75221	876795	D82177	S71424	A47501	A38943	D87226	S74916
0 0	~	~	~	~	~	~	~	~	7	~	-	-	N	~
478	492	529	539	578	290	616	623	765	836	1202	1203	1205	1329	1409
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82.5 82.5	82.5	82.5	82.5	82.5	82.5			82.	82.		82.	82.	82.	82.
33 82.5 33 82.5			33 82.5				82.					33 82.	33 82.	33 82.

ALIGNMENTS

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1930thetical protein SC5C7.15 SC5C7.15 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Spaces coelicolor
C;Accession: T3522
R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, September 1998
A;Reference number: Z21572
A;Reference number: Z21572
A;Reference number: Z21572
A;Reference number: Z21572
A;Residues: Jreliminary; translated from GB/EMBL/DDBJ
A;Robecule type: DNA
A;Robidues: 1-610 <SEE>
A;Cross-references: EMBL:AL031515; PIDN:CAA20627.1; GSPDB:GN00070; SCOEDB:SC5C7.15
A;Experimental source: strain A3(2)
C;Genetics:
A;Genetics:
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ö Сарв ö Length 610; 0; Indels Query Match 92.5%; Score 37; DB 2; Best Local Similarity 83.3%; Pred. No. 1e+02; Matches 5; Conservative 1; Mismatches

|||:|| 83 ADWAWA 88 1 ADWSWA 6

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Component sensor KdpD PA1636 [imported] - Pseudomonas aeruginosa (strain PAO1)
CiSpecies: Pseudomonas aeruginosa
CiSpecies: Pseudomonas aeruginosa
CiSpecies: Pseudomonas aeruginosa
CiSpecies: Pseudomonas aeruginosa
CiSpecies: Pseudomonas aeruginosa
CiSpecies: Pseudomonas aeruginosa
CiSpecies: Ca3441
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path. A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Recession: C83441
A;Recession: C83441
A;Redecession:
Gape ö Query Match 92.5%; Score 37; DB 2; Length 885; Best Local Similarity 83.3%; Pred. No. 1.5e+02; Matches 5; Conservative 1; Mismatches 0; Indels

N

Page

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A;Note: 1sd1+
C;Superfamily: yeast fatty-acid synthase
C;Keywords: acyltransferase; coenzyme A
                                                                                                                                                                                                                                                                               A,Map position: 4
A,Introns: 103/3; 141/3; 169/1; 206/3
A,Note: T5X18.170
A,Accession: T05822
A,Molecule type: DNA
A,Residues: 1-275 <BEV>
A,Cross-references: EMBL:AL022580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.0%;
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Best Local Similarity 66.7%;
Matches 4; Conservative 2
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Best Local Similarity وه...
المالية عند المالية وه...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 66.7
Matches 4; Conservative
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500 ADWAWS 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-617 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ADWSWA 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: C84922
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                                                                                                                                                                                                                                                                                                                 Conserved hypothetical protein PA3230 [imported] - Pseudomonas aeruginosa (strain PAO1) (Species: Pseudomonas aeruginosa C;Species: Ba2241 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Residues: 1-374 cSTO-A;Residues: 1-374 cSTO-A;Re
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C;Species: Caulobacter crescentus
C;Date: 20.Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: E87304
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Iauh, M.T.; DeBoy, R.T.; Dodson, R.J.; Dukkin, A.S.; Owinn, M.L.; Haft, D.H.; Kolon
I, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ва
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A;Residues: 1-889 <STO>
A;Cross-references: GB:AE005673; NID:g13421615; PIDN:AAK22433.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC0446
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92;
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Best Local Similarity 100...
5, Conservative
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                                                                                                 563 ADWAWA 568
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Best Local Similarity
Matches 5; Conserv
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C,Accession: T43409
R,Saitoh, S.; Takahashi, K.; Nabeshima, K.; Yamashita, Y.; Nakaseko, Y.; Hirata, A.; Yar
R,Saitoh, S.; Takahashi, K.; Nabeshima, K.; Yamashita, Y.; Nakaseko, Y.; Hirata, A.; Yar
A,Title: Aberrant mitosis in fission yeast mutants defective in fatty acid synthetase an A,Reference number: Z22433; MUID:96354912; PMID:8769419
A,Accession: T43409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. Buss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
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A;Cross-references: EMBL:D83412; NID:g1199959; PIDN:BAA11913.1; PID:g1199960
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C'Species: Schizosaccharomyces pombe
C'Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84922
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Pred. No. 1.4e+02;
2; Mismatches 0; Indels
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Pred. No. 3.1e+02;
2; Mismatches 0; Indels
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Pred. No. 9.4e+02;
2; Mismatches 0; Indels
A; Experimental source: cultivar Columbia; BAC clone T5K18 C; Genetics:
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Gaps

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A;Residues: 1-198 <SIM>
A;Crose-references: GS:AED04072; GB:AED03849; NID:g9107884; PIDN:AAF85463.1; GSPDB:GN001
A;Crose-references: GS:AED04072; GB:AED03849; NID:g9107884; PIDN:AAF85463.1; GSPDB:GN001
A;Crose-references: GS:AED0405; Rcinario, B.; Archae, F.; Brinnes, M.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, I.E.A.; Carraro, D.M.; Carrer, I Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, I.E.A.; Carraro, D.M.; Carrer, I submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Franca, S.C.; Franco, M.C.; Frohm. J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laignidado, M.A.; Madeira, A.M.B.N.; Madeira, H.W.F.; Marino, C.L.; Marquee, M.V.; Martine, A.A., A.Authors: Martine, E.M.F.; Mateukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunee, L.R.; Oliveira, M.C.; Go Oliveira, R.C.; Palmieri, D.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sal. R.G.; Santelli, R.V.; Sawasal, A.A.thors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.C. da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai, A.R.; da Silvai
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: B82531
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Best Local Similarity 80.0-
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135 DWNWA 139
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Cispecies: Mus muscules (house mouse)
Cispecies: Mus muscules (house mouse)
Cispecies: Mus muscules (house mouse)
Cispecies: Mano, R.; Taniguchi, M.; Kanno, M.
Biochim. Biophys. Acta 1305, 109-112, 1996
A;Title: Cloning and characterization of two transcripts generated from the mel-13 gene A;Reference number: S65785
A;Accession: S65785
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
C;Accession: B82531
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide SequenNature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T38781
R;Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
Bubmitted to the EMBL Data Library, August 1997
A;Reference number: Z21751
A;Reference number: Z21751
A;Reference number: Z21751
A;Recession: T38781
A;Reference preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Roser-references: EMBL:Z98762; PIDN:CAB11481.1; GSPDB:GN00066; SPDB:SPAC4A8.11c
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                fatty acid synthase, subunit alpha – fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Schizosaccharomyces pombe
19ate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
Accession: T38781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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80.0%; Pred. No. 96;
Live 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: SPDB:SPAC4A8.11c
A,Map position: 1
C,Superfamily: yeast fatty-acid synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A/Gene: mel-13
C/Superfamily: mouse mel-13a protein
C/Keywords: alternative splicing
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C;Genetics:
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Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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400 SDWNWA 405
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400 SDWNWA 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ADWSWA 6
                                                                                                         1 ADWSWA 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ADWSW 5
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C;Accession: D64316
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A;Rieference number: Afalso, WUID:96337999; PMID:8688087
A;Accession: D64316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-220 <BUL>
A;Cross-references: GB:U67470; GB:L77117; NID:g2826247; PIDN:AAB98113.1; PID:g1592267;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: type I site-specific deoxyribonuclease chain hsdM (associate member)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restriction modification enzyme subunit M1 homolog - Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDIb protein - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000
C;Accession: S58353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2002
                                                                                                                                                Gaps
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                                                                  Score 33; DB 2; Length 198; Pred. No. 1.4e+02; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.5%; Score 33; DB 2; Length 220;
80.0%; Pred. No. 1.6e+02;
ive 1; Mismatches 0; Indele
C; Superfamily: conserved hypothetical protein MJ1677
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Gaps

; 0

Score 33; DB 2; Length 257; Pred. No. 1.9e+02; 0; Mismatches 1; Indels

0; Mismatches

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Query Match
Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 4; Conser
                                                                                                                                                                                                                                                                                                     11 ATWSWA 16
                                                                                                                                                                                                            1 ADWSWA 6
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C.Species: Mycobacterium leprae
C.Species: Mycobacterium leprae
C.Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C.Accession: D87152
R.Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A.Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A.Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A.Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A.Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A.Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A.Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A.Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A.Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A.Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A.Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A.Residues: preliminary
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-257 <STO>
A.Genetics.
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A.Description: Sulfolobus solfataricus complete genome.

A.Reference number: A99139

A.Accession: D90470

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-239 «KUR»

A.Cross-references: GB:AE006641; NID:g13816282; PIDN:AAK43019.1; GSPDB:GN00155

G.Genetics:

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A.G
R;Ferguson, E.D.; Dutia, B.M.; Hein, W.; Hopkins, J.
submitted to the EMBL Data Library, July 1995
A;Description: The ovine CD1 gene family contains at least four CD1B homologues.
A;Reference number: 858353
A;Accession: S58353
A;Accession: S58353
A;Accession: S58353
A;Accession: S58353
A;Return preliminary
A;Molecule type: mRNA
A;Residues: 1-232 <FBR>
A;Cross=references: EMBL:300567; NID:9945010; PIDN:CAA62187.1; PID:9945011
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;115-180/Domain: immunoglobulin homology <IMM>
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.Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
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;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1100
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Pred. No. 1.7e+02;
1; Mismatches 0; Indels
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Pred. No. 1.7e+02;
1; Mismatches 0; Indels
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Best Local Similarity 80.0%;
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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156 ADWTW 160
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hypothetical protein - Deinococcus radiodurans (strain R1)
(Species: Deinococcus radiodurans
(C)Species: Deinococcus radiodurans
(C)Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
(C)Accession: B75337
(R)White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-276 <MHI->
A;Residues: 1-276 <MHI->
A;Cross-references: GB:AE002032; GB:AE000513; NID:g6459715; PIDN:AAF11479.1; PID:g645971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1 A,Reference number: A75250; MUID:20036896; PMID:10567266
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Job time : 7.5921 secs
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80.0%;
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83.3%;
                                                                            5; Conservative
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Gaps

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Length 276; 0; Indels

Score 33; DB 2; Pred. No. 2e+02;

Mismatches



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Sequence 22368, A
Sequence 21704, A
Sequence 274, App
Sequence 2, Appli
Sequence 2, Appli
Sequence 10, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 11, Appli
Sequence 11, Appli
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Sequence 11, Appli
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Sequence 163, App
Sequence 162, App
Sequence 3, Appli
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Sequence 18367, A
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                                                                                   ; Search time 7.06579 Seconds (without alignments) 35.929 Million cell updates/sec
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Sequence
Sequence
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-18367
US-09-325-991A-1833
US-09-325-991A-162
US-09-325-991A-162
US-09-325-932A-162
US-09-325-932A-168
US-09-252-991A-22168
US-09-252-991A-221704
US-08-252-991A-221704
US-08-252-991A-221704
US-08-325-991A-221704
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US-08-325-991A-23817
US-08-332-846C-10
US-08-332-846C-10
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US-08-332-846C-10
US-08-332-846C-10
US-08-332-846C-10
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US-09-216-295-1
US-09-633-084-1
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US-09-146-770-3
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                                                                                   February 18, 2004, 14:16:39
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Maximum Match 100%
Listing first 45 summaries
                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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40
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Match Length
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No.
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US-09-25-991A-23882

i Sequence 23882, Application US/09252991A

i Sequence 23882, Application US/09252991A

i Sequence 23882, Application US/09252991A

i Sequence 23882, Application US/09252991A

i GENERAL INFORMATION:

i TITLE OF INVENTION:

i PRIOR APPLICATION NUMBER: US 60/074,788

i PRIOR APPLICATION NUMBER: US 60/094,190

i PRIOR PILING DATE: 1998-02-18

i PRIOR PILING DATE: 1998-07-27

i NUMBER OF SEQ ID NOS: 33142

i ENGRAH: 938

i TYPE: PRT

i ORGANISM: Peeudomonas aeruginosa

US-09-252-991A-23882
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Sequence 18367, Application US/09252991A

Sequence 18367, Application US/09252991A

Sequence 18367, Application US/09252991A

Sequence 18367, Application US/09252991A

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 18367
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                                Sequence 3, Applisequence 4, Applisequence 4, Applisequence 3, Applisequence 3, Applisequence 6, Applisequence 15, Applisequence 15, Applisequence 2, Applisequence 2, Applisequence 2, Applisequence 2, Applisequence 2, Applisequence 2, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 10, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Appliseq
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Pred. No. 2.9e+02;
US-09-146-770-4
US-09-216-295-3
US-09-216-295-3
US-09-633-084-3
US-10-075-872-3
US-10-075-872-3
US-10-075-872-3
US-10-261-997-3
US-10-261-997-3
US-10-261-997-4
US-09-252-991A-17312
US-09-252-991A-17312
US-09-252-991A-22079
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Best Local Similarity 83.3.
       581 ADWAWA 586
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                                           US-09-252-991A-18367
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Sequence 162, Application US/09325932A

Patent No. 6451604

GENERAL INFORMATION:

APPLICANT: Lasham, Annette

TITLE OF INVENTION: Compositions affecting programmed cell

TITLE OF INVENTION: death and their use in the modification of forestry plant develo

FILE REFERENCE: 1022

CURRENT APPLICATION NUMBER: US/09/325,932A

CURRENT PILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 206

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant develo
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APPLICANT: Becnel, James J.
APPLICANT: Tukuo, Fukuda
APPLICANT: Tukuo, Fukuda
APPLICANT: Occburur, Andrew
APPLICANT: Occburur, Andrew
APPLICANT: White, Susan E.
APPLICANT: Undeen, Albert H.
APPLICANT: One of S21454el Baculoviruses, Insecticidal
TITLE OF INVENTION: Compositions, and Methods for Control of Invertebrates
FILE REPERBNCE: 21042.0004
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100.0%; Pred. No. 1e+02;
/ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/345,236B
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 148
SEQ ID NO 3
LENGTH: 242
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CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
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; Patent No. 6451604
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; Sequence 3, Application US/09345236B
; Patent No. 6521454
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                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100..
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                          SEQ ID NO 162
LENGTH: 225
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Patent No. 6451604

GENERAL INFORMATION:
APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant develc
TITLE OF INVENTION: US/09/325,932A
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 163
LENGTH: 174
                                                                                                                                                                                                                                                                                                                                        APPLICANT: MATCH J. Rubenfield et al.
APPLICANT: MATCH J. Rubenfield et al.
APPLICANT: MATCH J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
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                                                                DB 4; Length 68; 32;
                                                                                                              Indels
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                                                             Query Match 90.0%; Score 36; DB Best Local Similarity 100.0%; Pred. No. 32; Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 90.0%; Score 36; DB Best Local Similarity 100.0%; Pred. No. 79; Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                     US-09-252-991A-31533
; Sequence 31533, Application US/09252991A
; Patent No. 6551795
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
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ORGANISM: Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 5; Conservative
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LENGTH: 142
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Gaps
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Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Daclert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: sig_peptide
LOCATION: -26...1
LOCATION: PETION NETHOD: Von Heijne matrix
OTHER INFORMATION: score 9.6
OTHER INFORMATION: seq WLIALASWSWALC/RI
                                                                                                                                                                                                                                                                                                                                         E: Knobbe, Martens, Olson & Bear
501 West Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
                                                                                                                                                         ; Sequence 274, Application US/08905223; Patent No. 6222029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08379538
Patent No. 5804554
GENERAL INFORMATION:
APPLICANT: Volkmann, Robert A.
APPLICANT: Saccomano, Nicholas A.
APPLICANT: Nason II, Deane M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: BEAGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: 125.655
TELECHOWINICATION INFORMATION:
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 274:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.0%;
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Beet Local Similarity 83.3%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE TYPE: Brain
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Diego
STATE: California
                                                          169 DWSWA 173
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                       2 DWSWA 6
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COUNTRY: USA
                                                                                                                       RESULT 10
US-08-905-223-274
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US-08-379-538-2
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANTON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22368
LENGTH: 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: OS EQ ID NOS: 33142
SEQ ID NOS: 33142
SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.0%; Score 36; DB 4; Length 462; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                           Length 378;
                                                                                                                                                                                                 0; Indels
                                                                                                                                                         DB 4; Le:
                                                                                                                                                                                                 0; Mismatches
SEQ ID NOS: 206
FastSEQ for Windows Version 3.0
                                                                                                                                                           90.0%; Score 36;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
                                                                         ; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-325-932A-158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 5; Conservative
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 5; Conservative
NUMBER OF SEQ ID NOS:
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    SOFTWARE: Fast
SEQ ID NO 158
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APPLICANT: MA.C. 3231/73

GENERAL INCORMATION:
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196, 136
CURRENT PAPLICATION NUMBER: US 60/074, 788
PRIOR APPLICATION NUMBER: US 60/074, 788
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-27
NUMBER: OS 60/094, 190
RIOR FILING DATE: 1998-07-27
NUMBER: OS 23817
LENGTH: 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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83.3%; Pred. No. 2.1e+02;
cive 0; Mismatches 1
                                                                                                                                                  SOFTWARE: FASTEM: DOS SOFTWARE: FASTEM DOS SOFTWARE: FASTEM FOR WINDOWS Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/774,065 FILING DATE: PRIOR APPLICATION DATA: FILING NATE: FILING NATE: FILING NATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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US-08-032-848C-10
Sequence 10, Application US/08032848C
; Patent No. 5475101
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Glaister, Debra J.
REGISTRATION NUMBER: 33,888
REPERENCE/DOCKET NUMBER: GC36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-846-7620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23817
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFRA: 415-684-6504
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                     COUNTRY: UNITED STATES
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 83.5
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US-08-774-065-2
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Best Local Similarity
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US-09-252-991A-23817
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Patent No. 598899
GENERAL INFORMATION:
APPLICANT: Larkson, Kathleen
APPLICANT: Clarkson, Kathleen
APPLICANT: Larenas, Edmund
APPLICANT: Larenas, Edmund
APPLICANT: Mard, Michael
ITILE OF INVENTION: NOVEL OVERSIZED CELLULASE COMPOSITIONS
ITILE OF INVENTION: IN THE TREATMENT OF TEXTILES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: 16
ADDRESSE: 16
ADDRESSE: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: STREET: 925 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                        APPLICANT: Ronau, Robert T.
TITLE OF INVENTION: CALCIUM CHANNEL BLOCKING POLYPEPTIDES
TITLE OF INVENTION: FROM FILISTATA HIBERNALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.5%; Score 33; DB 1; Length 74; 80.0%; Pred. No. 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,538
FILING DATE: 3-MAY-1995
CLASSIFICATION NUMBER: US 07/887073
FILING DATE: 12-MAY-1992
APPLICATION NUMBER: PCT/US93/03921
FILING DATE: 30-APRIL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Zielinski, Bryan
REGISTRATION NUMBER: 9C8175A
TELEFRONE: (212) 573-1399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LUMPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LUMPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LUMPORMATION FOR SEQ ID NO: 2:
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LUMPORTAL NO SECONDER SEQ ID NO: 2:
LUMPORMATION FOR SEQ ID NO: 2:
LUMPORTAL NO SEQ ID NO: 2:
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                                                                                                          NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER: Fizer Inc
STREET: 235 East 42nd Street
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Filistata hibernalis
; TISSUE TYPE: Venom
US-08-379-538-2
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 80.0-
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MOLECULE TYPE: protein
HYPOTHETICAL: No
                                                                                                                                                                                                                                                                                                                   ZIP: 10017
COMPUTER READABLE FORM:
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52 DWSWS 56
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APPLICANT:
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US-08-774-065-2
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PatentIn Release #1.0, Version #1.25
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             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,870
FILING DATE: May 10, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Christopher L. Stone
REGISTRATION NUMBER: 35,696
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 742-7217
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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MOLECULE TYPE: protein
US-08-438-870-10
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Sequence 10. Application US/08438870

Patent No. 5753484

GENERAL INFORMATION:
APPLICANT: Ward, Michael
APPLICANT: Clarkson, Kathleen A.
APPLICANT: Larenas, Edward
APPLICANT: Lorch, Jeffrey D.
TITLE OF INVENTION: Purification and Molecular Cloning of EG
TITLE OF INVENTION: III Cellulase
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSES: Genemor International
STREET: 180 Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
             APPLICANT: Ward, Michael
APPLICANT: Ward, Michael
APPLICANT: Clarkson, Kathleen A.
APPLICANT: Weiss, Geoffrey L.
APPLICANT: Larenas, Edward
APPLICANT: Lorch, Jeffrey D.
TITLE OF INVENTION: Purification and Molecular Cloning of
TITLE OF INVENTION: EG III Cellulase
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Genencor International
STREET: BO Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.5%; Score 33; DB 1; Length 218; 66.7%; Pred. No. 2.7e+02; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                 STATE: CA
COMPUTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOCTWARE: Patentin Nelease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/032,848C
FILING DATE: MAR 17 1993
CLASSIFYCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HORN, Margaret A.
RESISTATION NUMBER: 33,401
TELEPHONE: 415 742-7356
TELEPAX: 415 742-7217
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
TRANTH: 218 amino acids
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ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 66.7
Matches 4; Conservative
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Gaps

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Length 218; 2; 1; Indels

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influenza a
aeromonas t
catharanthu
salmonella
                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                      February 18, 2004, 13:39:39; Search time 3.55263 Seconds (without alignments) 79.423 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                     127863
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                 127863 segs, 47026705 residues
                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPA3_CHICK
EPA3_HUMAN
EPA3_MOUSE
EPA3_MOUSE
EPA3_MOUSE
EPA3_MOUSE
EPA3_MOUSE
EPA3_MOUSE
EPA3_CATE
OVEC_BUCAI
NRAM_IAWIL
NRAM_IAWIL
NRAM_IAWIC
VEXE_SALTI
VPHI_YEAST
FAAS_SCHPO
VEXE_SALTI
VPHI_YEAST
FAAS_SCHPO
VEXE_CHPOWN
STEL_RHUWE
GGDIR_CAGEU
CHI_SCHPO
CYI_RHORU
                                                                                                                                                                                                                                                                                                                                                                                     DCUP_YEAST
MRJS_APIME
IKKA_HUMAN
IKKA_MOUSE
IKKB_HUMAN
IKKB_MOUSE
IKKB_MOUSE
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Maximum Match 100%
Listing first 45 summaries
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HUMAN
BUCAI
ACEAC
                                    OM protein - protein search, using sw model
                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
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40
                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                             SwissProt_41:*
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Match Length
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1842
                                                                                                                 1 LDWSWA 6
                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
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                                                                                                                   Sequence:
                                                        Run on:
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No.
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0 influenza a	'2 influenza a	9 influenza a 4 influenza a	7 influenza a 8 influenza a	13 influenza a 15 influenza a	13 bacillus su 18 escherichia
00757	Q07572 Q07573	Q0759 Q0757	Q0757 Q0757	Q0758 Q0758	P4297;
NRAM_IADBU	NRAM_IADH2 NRAM_IADM2	NRAM_IADU3 NRAM_IAGFN	NRAM_IAHGD NRAM_IAHJI	NRAM_IAMAE NRAM_IATKL	BGLA_BACSU PROP_ECOLI
470	470	470	470	470	479 500
80.0	80.0	80.0 80.0	80.0 80.0	80.0 80.0	80.0
32	332	32 32	32	35 35	32
0. U 1. U	36	3 8 3 6 6	40 41	4 4 4 3	4 4 5

ALIGNMENTS

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[5]
SEQUENCE OF 32-745 FROM N.A.
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                                                                                                                                                                                                                                 CARBOHYD
SEQUENCE
                                                                                                                                                                                                             CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Albert S., Bhattacharya D., Klaudiny J., Schmitzova J., Simuth J.;
"The family of major royal jelly proteins and its evolution.";
J. Mol. Evol. 49:290-297(1999).
-! FUNCTION: MAY PLAY AN IMPORTANT ROLE IN HONEYBEE NUTRITION. IT IS
FOUND IN THE ROYAL JELLY WHICH IS THE FOOD OF THE QUEEN HONEY BEE
LARVA. THE ROYAL JELLY DETERMINES THE DEVELOPMENT OF THE YOUNG
IARVAE AND IS RESPONSIBLE FOR THE HIGH REPRODUCTIVE ABILITY OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIPICITY: HYPOPHARYNGEAL GLANDS OF NURSE HONEY BEES.
DEVELOPMENTAL STAGE: PRODUCED BY THE CEPHALIC GLANDULAR SYSTEM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Hymenoptera, Apocrita, Aculeata, Apoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Major royal jelly protein 5 precursor (MRJP-5) (Bee-milk protein)
MRJP5.
                                                                                                                                                                                                                                                                                                                                    Porphyrin biosynthesis; Heme biosynthesis.

9 - Y [IN HEM12-14].

1 -> I (IN HEM12-14).

1 -> S (IN HEM12-3 AND HEM12-13).

5 -> N (IN HEM12-3 AND HEM12-13).

6 -> D: INACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE NURSE HONEY BEE.
-!- SIMILARITY: BELONGS TO THE MAJOR ROYAL JELLY PROTEIN PAMILY.
             EMBL; X63721; CAA45253.1; -.
EMBL; Z19089; CAA79514.1; -.
EMBL; Z49209; CAA79078.1; -.
EMBL; S23471; S23471.
HSSP; P06132; 1URO.
SGD; S0002454; HEM12.
GO; GO:0004853; F:urrporphyrinogen decarboxylase activity; IMP.
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100.0%; Pred. No. ...
                                                                                                                                                                                   InterPro; IPR006361; HemE.
InterPro; IPR000257; Uro_decarbxyls.
PtcDom; PF01208; URO-D; 1.
PrcDom; PF01208; URO-D; 1.
TIGRFAMs; TIGR01464; hemE; 1.
PROSITE; PS00906; UROD 1; 1.
PROSITE; PS00907; UROD 2; 1.
Lyase; Decarboxylase; Porphyrin biosynu VARIANT
59 S-P (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99373663; PubMed=10441680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apis mellifera (Honeybee)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 LDWSW 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LDWSW 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apidae; Apis.
NCBI_TaxID=7460;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MRJS APIME
097432;
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VARIANT
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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MRJ5_APIME
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CCC
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DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.; "A cytokine-responsive IkappaB kinase that activates the transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IKKAH HUMAN STANDARD; PRT; 745 AA.

1KKAT-1014666; Q13132; Q92467;

16-0CT-2001 (Rel. 40, Created)

16-0CT-2003 (Rel. 42, Last annotation update)

15-SEP-2003 (Rel. 42, Last annotation update)

15-SEP-2003 (Rel. 42, Last annotation update)

16-Mappa-B kinase alpha) (IKBKA) (IKK-alpha) (IKK-alpha) (IKK-alpha) (IKK-alpha) (IKK-alpha) (IKM-alpha)                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Cervical carcinoma;
MEDLINE=98008813; PubMed=9346484;
MEDLINE=98008813; PubMed=9346484;
MEDLINE=98008813; PubMed=9346484;
Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
"IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hu M.C.-T., Wang Y.-P.;
"Ikappab kinase-alpha and -beta genes are coexpressed in adult and embryonic tissues but localized to different human chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                              (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
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Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;
"Identification and characterization of an IkappaB kinase.";
Cell 90:373-383(1997)
                                                                                                                                                                                       (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                   Length 598;
                                                                                                                                                            MAJOR ROYAL JELLY PROTEIN 5.
N-LINKED (GLCNAC. . .) (POTE
N-LINKED (GLCNAC. . .) (POTE
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75;
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                                                                                                                                                                                                                                                                                                                                90.0%; Scor.
100.0%; Pred. No. 'c,
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                                                                                                                                                                                                                                       N-LINKED
                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97394468; PubMed=9252186;
                InterPro; IPR003534; Royaljelly.
Pfam; PF03022; MRJP; 2.
SYRINTS; PR01366; ROYALJELLY.
Signal; Repeat; Glycoprotein.
sIGNAL
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                                                                                                                                                                                                                                                                324
70236 MW;
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.v.
Best Acad 5, Conservative
EMBL; AF004842; AAD01205.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 278:860-866(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 388:548-554 (1997).
                                                                                                                                                            598
148
164
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598 AA;
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MEDLINE=99038238; PubMed=9819420;
Nemocto S., DiDonato J.A., Lin A.;
"Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase 1 and MF-kappaB-inducing kinase.";
MOI. Cell. Biol. 18:7336-7343(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator activity by I kappa B kinase.";
Mol. Cell. Blol. 22:3549-3561(2002).
-!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT OF A COMPLEX CONTAINING CREBBP; NCOA2; NCOA3; IKKB AND IKBKG. MEDILTBE-21968797; PubMed=11971985; Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J., O'Malley B.W.;
                                                                                                          MEDLINE-98188283; PubMed-9520446;
Ling L., Cao Z., Goeddel D.V.;
"NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
                                                                                                                                                                                                                                                                                         Delhase M., Hayakawa M., Chen Y., Karin M.; "Positive and negative regulation of IkappaB kinase activity through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENZYME REGULATION: Activated when phosphorylated and inactivated
                                            a serine-threonine kinase
                                                                                     PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179
                                                                                                                                                                                                                       "NF-kappaB activation by tumour necrosis factor requires the Akt serine-threonine kinase."; Nature 401:82-85(1999).
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Connolly M.A., Marcu K.B.;

"CHUK, a new member of the helix-loop-helix and leucine zipper families of intracting proteins, contains a serine-threonine katalytic domain.";

Cell. Mol. Biol. Res. 41:537-549(1995).
                                                                                                                                                                          PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
MEDLINE=99413720; PubMed=10485710;
Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Jobin C., Sartor R.B.;
"The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";
Am. J. Physiol. 278:C451-C462(2000).
                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998)
                                                                                                                                                                                                                                                                                                              IKKbeta subunit phosphorylation.";
Science 284:309-313(1999)
                                                                                                                                                                                                                                                                               MEDLINE=99212141; PubMed=10195894;
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20178139; PubMed=10712233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IKAPPAB KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                   IKKA-IKKB BINDING.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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060680; Q9D2X3;
16-OCT-2001 [Rel. 40, Created)
15-SEP-2001 [Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
110-SEP-2003 (Rel. 43, Last annotation update)
110-SEP-2003 (Rel. 40, Created)
110-SEP-2003 (Rel. 40, Created)
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K->M: LOSS OF AUTOPHOSPHORYLATION.
S->A: LOSS OF PHOSPHORYLATION AND OF ACTIVITY.
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T->A: NO CHANGE IN PHOSPHORYLATION
S->A: NO CHANGE IN PHOSPHORYLATION
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PHOSPHORYLATION (BY PKB/AKT1).
PHOSPHORYLATION (BY MAP3K14).
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ProDom; PD000001; Prot_kinase; 1.
SWART; SM00220; S TKK; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE ST; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0007345; P:embryogenesis and morphogenesis; TAS. GO; GO:0007252; P:I-kappaB phosphorylation; TAS. GO; GO:0006955; P:I-kappaB phosponse; TAS. Intervo; IPR00279; Prot. kinase. Intervo; IPR002290; Ser thr pkinase. Intervo; IPR001245; Tyr pkinase. PF00069; pkinase: 1.
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P -> A (IN REF. 3 AND 5)
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ATP (BY SIMILARITY).
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GO:0005737; C:cytoplasm; TAS.
GO:0008384; F:IkappaB kinase activity; TAS.
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100.0%; Pred. No. 92;
J., o, Mismatches
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EMBL; AF009225; AAC5.671.1; -...
EMBL; AF080157; AAD08996.1; -...
EMBL; U22512; AAC50713.1; -...
HSSP; Q63450; 1A06.
Genew; HGNC:1974; CHUK.
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RA Arawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alazawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Saito R., Brischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Rochima H., Staubli F., Suuki R., Tomita M., Wagner L., Washio T., Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Barak J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Bromstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Lowns P., Marchionni L., Mashima J., Mazzarelli J., Momberts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sabaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                       Mock B.A., Connelly M.A., McBride O.W., Kozak C.A., Marcu K.B.; "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome 10 and mouse chromosome 19.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99212141; PubMed=10195894;
Delhase M., Hayakawa M., Chen Y., Karin M.;
"Positive and negative regulation of IkappaB kinase activity through IKKbeta subunit phosphorylation.";
Science 284:309-313(1999).
                                                                                                                                                                                                                                                      Connelly M.A., Marcu K.B.; "CHUK, a new member of the helix-loop-helix and leucine zipper families of interacting proteins, contains a serine-threonine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leucine zipper and helix-loop-helix domains reveal that IKKalpha and
IKKbeta have different activation requirements.";
(Nuclear factor NFkappaB inhibitor kinase alpha) (NFKBIKA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98188238; PubMed=9520401;
Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.
                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Differential regulation of IkappaB kinase alpha and beta by two upstream kinases, NF-kappaB-inducing kinase and mitogen-activated protein kinase/ERK kinase kinase-1."; Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20198447; PubMed=10733566;
McKenzie F.R., Connelly M.A., Balzarano D., Mueller J.R.,
Geleziunas R., Marcu K.B.;
                                                                                                                                                                                                                                                                                              catalytic domain.";
Cell. Mol. Biol. Res. 41:537-549(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell. Biol. 20:2635-2649(2000).
                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Colon;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                         MEDLINE=96258427; PubMed=8777433;
                                                                                                                        MEDLINE=9604444; PubMed=7558004;
                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION BY MAP3K14/NIK
                                                                                                                                                                                 Genomics 27:348-351(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE SPLICING.
                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IKKA-IKKB BINDING.
                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki Y.;
                                                                                                              STRAIN=BALB/C
                                                                                                                                                                                                                             STRAIN=BALB
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              CHUK OR
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Name=2; Synonyms=Delta LH;

Name=3; Synonyms=Delta H;

Name=3; Synonyms=Delta H;

IsoId=Q60680-2; Sequence=VSP_004868, VSP_004869;

IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;

IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;

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IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;

In IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;

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IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;

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In IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;

IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;

IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;

In IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;

IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;

In IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;

IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;

IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;

IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;

IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;

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IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;

IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;

IsoId=Q60680-3; Sequence=VSP_004868, VSP_004868, VSP_004869;

IsoId=Q60680-3; Sequence=VSP_004868, VSP_004868, VSP_004869;

IsoId=Q60680-3; Sequence=VSP_004868, VSP_004868, 
                                    Nemoto S., Dibonato J.A., Lin A.; "Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase 1 and NF-kappaB-inducing kinase."; Mol. Cell. Biol. 18:7336-7343(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENEXTME REGULATION: Activated when phosphorylated and inactivated when dephosphorylated.
SUBUNIT: Preferentially found as a heterodimer with IKK-beta but also as an homodimer. Directly interacts with IKK-gamma/NEMO.
Heterodimers form the active complex. The tripartite complex can also bind to MADRIAI, MEKKI, IKAP and IKB-alpha-P65-P50
complex. A weak interaction with TRAP2 cannot be excluded. Part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Physiol. 278:C451-C462(2000). Whysiol. 278:C450:Physiol. 278:C450:Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates
                                                                                                                                                                                                                                                                                                                                                                                                      Jobin C., Sartor R.B., "The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Transferase; Serine/Chreonine-protein kinase; ATP-binding; Phosphorylation; Alternative splicing.
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NEMO-BINDING.
ATP (BY SIMILARITY).
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EMBL; KO18671; EAB31335.1; -.
FIR; 149101; 149101.
HSSP; 063450; 1A66.
MGD; MGI:99484; Chuk.
InterPro; IPR000179; Prot_kinase.
InterPro; IPR002299; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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SUBCELLULAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS:
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MEDLINE=20178139; PubMed=10712233;
MEDLINE=99038238; PubMed=9819420;
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PRINTS; PR00109; TYRKINASE.
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Cytogenet. Cell Genet. 82:32-33(1998)

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MLSLLRYNANLTKMKNTLIS -> IFRKNVKSMERNGRKGH
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10-071-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 42, Last sequence update)
11-SEP-2003 (Rel. 42, Last annotation update)
11-SEP-2003 (Rel. 42, Last annotation update)
11-SEP-2003 (Rel. 42, Last annotation update)
11-SEP-2003 (Rel. 42, Last annotation update)
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11-SEP-2003 (Rel. 43, Last annotation update)
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"IKappaB Kinaee-bear NF-kappaB activation and complex formation with
IKappaB Kinaee-alpha and NIK.";
Science 278:866-869(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
"Assignment of IkappaB kinase beta (IKBKB) to human chromosome band
"Bp12-->p11 by in situ hybridization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
TISSUE-Cervical carcinoma;
MEDLINE-98008813; Pubmed=5346484;
Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
Li J.W., Young D.B., Barbosa M., Manning A., Rao A.;
"IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for NF-kappaB activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hu M.C.-T., Wang Y.-P.;
"IkappaB kinase-alpha and -beta genes are coexpressed in adult and
embryonic tissues but localized to different human chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                Missing (In isoform 2).
/FIId=VSP_004867.
DHLYSDST -> GKTLQSQY (in isoform 3).
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92;
                                                PHOSPHORYLATION (BY PKB/AKT1) (BY SIMILARITY).
                                                                                               PHOSPHORYLATION (BY MAP3K14)
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                                                                                                                                                                                                                                                         DHLYSDST -> GKTLQSQY (in isc
/FIId=VSP 004868.
Missing (in isoform 3).
/FIId=VSP 004869.
K -> E (IN REF. 3).
S -> Y (IN REF. 3).
W, 3FEF5582AFF92233 CRC64;
    SIMILARITY).
                                                                                                                                                                        (in isoform 2).
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                             SIMILARITY
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MEDLINE=99032998; PubMed=9813230;
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400
745 AA;
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                                                                                               TISSUE-LUNG;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MISULUNE=22388257; PubMed=12477932;

MISULUNG;

MISULUNE=22388257; PubMed=12477932;

MISULUNE=22388257; PubMed=12477932;

MISULUNE=22388257; PubMed=12477932;

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MEDLINE=21968797; PubMed=11971985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal muscle, kidney, pancreas, spleen, thymus, prostate, testis and peripheral blood.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
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SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
IKAPPAB KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jobin C., Sartor R.B.; "The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                       SEQUENCE OF 1-256 FROM N.A.
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REVIEW.
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WHSKVRQKSEVDIVVSEDLNGTVKF -> CVRMWPGTVAHS
CNPSTLGGGREWI (IN REF. 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  088351; Q9R1J6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Inhibitor of nuclear factor Kappa B Kinase beta subunit (EC 2.7.1.-)
(I-kappa-B-kinase beta) (IKR-beta) (IKR-beta) (IKR-B) (I-kappa-B kinase
2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIKB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                               R GO; GO: 0005524; F: ATP binding activity; NAS.

R GO; GO: 0004674; F: Protein serine/threonine kinase activity; NAS.

R GO; GO: 0004668; F: Franscriptional activator activity; NAS.

GO; GO: 0006468; P: protein amino acid phosphorylation; NAS.

R InterPro; IPR000719; Prot kinase.

R InterPro; IPR000719; Prot kinase.

R Pfam; PF00040; ubiquitin; 1.

R Pfam; PF00140; ubiquitin; 1.

R PROSITE; PS01070; PROTEIN KINASE ATP; FALSE NEG.

R PROSITE; PS01010; PROTEIN KINASE ST; 1.

R PROSITE; PS00101; PROTEIN KINASE DOW; 1.

Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEKKI.
STRAIN=S781BL/6; TISSUB=Spleen,
MEDIJNE=98188238; Pubmed=9520401;
Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.
                                                                                                                                                                                                                                                                                                                                 K->A: LOSS OF KINASE ACTIVITY AND NO EFFECT ON BINDING TO NIK.
S->A: DECREASE OF ACTIVITY.
S->B: FULL ACTIVATION.
S->A: DECREASE OF ACTIVITY.
S->EVLL ACTIVATION.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                      ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (BY SIMILARITY)
PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 1; Length 756;
Pred. No. 94;
                                                                                                                                                                                                                                                   LEUCINE-ZIPPER (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                 Q -> H (IN REF. 1).
F9CADF671AE9E14E CRC64;
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0
                                                                                                                                                                                                                                           PROTEIN KINASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. ...
                                                                                                                                                                                                                                                              NEMO-BINDING.
email to license@isb-sib.ch)
                                                                                      GO; GO:0005737; C:cytoplasm; NAS GO; GO:0005524; F:ATP binding act
                  EMBL; AF029684; AAC51860.1; -. EMBL; AF080158; AAD08997.1; -. EMBL; AF031416; AAC64675.1; -.
                                                 BC006231; AAH06231.1; -.
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Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                               425 '
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Matches 5; Conserv
                                                EMBL; BC006231; AAI
HSSP; Q63450; 1A06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      737 LDWSW 741
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DOMAIN 15
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MOD RES
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NP BIND
BINDING
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MUTAGEN
MUTAGEN
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MIM; 603
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MOD_RES
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseaisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but also as a homodimer. Directly interacts with IKK-gamma/NEMO. Heterodimers form the active complex. The tripartite complex can also bind to MEKKI, MAPSKI4/NIK, IKAP and IKB-ALPHA-P65-P50 complex. Phosphorylated IKB-alpha is further released from the complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKBKG and CREBEP (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFFCITY: Expressed in liver, kidney and spleen.
-!- DBVELOPMENTAL STAGE: While it is expression begins to be a tell of the brain, neural ganglia, neural tube, and in liver at E12.5 day. At E15.5 day, the expression is further restricted to specific tissues of the embryo.
-!- PTW: Phosphorylated by MEKKI and probably also by MAPSKI4/NIK.
--- WASHY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
--- IKAPPAB KINASE SUBFAMILY.
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Nemoto S., Dibonato J.A., Lin A.;
"Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase i and MP-kappaB-inducing kinase.";
Mol. Cell. Biol. 18:7336-7343(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammation and profection.";
Am. J. Physiol. 278:C451-C462(2000).
-!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor.
                                                                                                                                                                                                                                                                                                             protein kinase that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hu W.C.-T., Wang Y.-P., Olu W.R., Mikhail A., Meyer C.F., Tan T.-H.; "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling pathway activates KappaB kinases (IKK-alpha/beta) and IKK-beta is a developmentally regulated protein kinase."; oncogene 18:5514-5524(1999).
    upstream kinases. NF-kappas-inducing kinase alpha and beta by two protein kinase/EKK kinase kinase-l.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20178139; PubMed=10712233;
Jobin C., Sartor R.B.;
"The I kappa B/NF-kappa B system: a key determinant of mucosal
Differential regulation of IkappaB kinase alpha and beta by
                                                                                                                                                                                                                                                                                                                                                     constitutively phosphorylates serine residues of IkB."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.; "Murine IkB kinase-B, a developmentally regulated
                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998)
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MGD; MGI:1338071; Ikbkb.
InterPro; IPR000719; Prot kinase.
InterPro; IPR001290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
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Hu M.C.-T., Wang Y.-P., Qiu W.R., N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEVELOPMENTAL STAGE
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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as a homodimer, Directly interacts with IKK-gamma/NEMO
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InterPro; IPR002209; Ser thr pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; I
                                                                                                                                                                                                                   EMBL; AF115282; AAF21978.1; -.
HSSP; Q63450; 1A06.
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747
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145
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MOD_RES
SEQUENCE
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MOD RES
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BINDING
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates
                                                                                                                                                                                                                                                                                                                                                                                                   090Y78;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-FEB-2003 (Rel. 41, Last annotation update)
Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
(I-kappa-B-Kinase beta) (IKBKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
2) (IKKZ) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIKB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jobin C., Sartor R.B.;
"The I Kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";
Am. J. Physiol. 278:C451-C462(2000).
                                                                                                                               SIMILARITY).
SIMILARITY).
SIMILARITY).
ProDom; PD000001; Prot_kinase; 1.
RKOSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
RKOSITE; PS50011; PROTEIN KINASE DOM; 1.
FROSITE; PS50011; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                       90.0%; Score 36; DB 1; Length 757;
                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhāng Y., Sun S., Ravid K.;
"IKK beta in megakaryocyte differentiation.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                         LEUCINE-ZIPPER (POTENTIAL)
NEMO-BINDING.
                                                                                                                                                                                                                                                  FED962F095449C5E CRC64;
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ATP (BY SIMILARITY)
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PHOSPHORYLATION (
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N -> D (IN REF. 2)
K -> E (IN REF. 2)
L -> F (IN REF. 2)
K -> B (IN REF. 2)
K -> B (IN REF. 2)
K -> R (IN REF. 2)
K -> R (IN REF. 2)
                                                                                                                                                                                                                                                                                    Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                           757 AA
                                                                  PROTEIN KINASE
                                                                                                                                                                                                                                                                               100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20178139; PubMed=10712233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99038238; PubMed-9819420;
                                                                                                                                                                                                                                                    86690 MW;
                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION
                                                                                                                                                                                                                                                  757 AA;
                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                     737 LDWSW 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                 1 LDWSW 5
                                                     hosphorylation
                                                                                                        BINDING
ACT SITE
MOD RES
MOD RES
MOD RES
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                       CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           IKKB RAT
                                                                                     DOMAIN
NP BIND
                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
                                                                                                                                                                                                                                                                                                                                                                               IKKB_1
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Heterodimers form the active complex. The tripartite complex can also bind to MEKKI, MAP3K14/NIK, IKAP and IKB-alpha-P65-P50 complex. Phosphorylated IKB-alpha is further released from the complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKBKG SUBCELLULAR LOCATION: Cytoplasmic.

PTM: Phosphorylated by MEKKI and probably also by MAP3K14/NIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein EPHA1 OR ETK1) (CEK4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE 5.2012/21 FROM SEQUENCE F.B., Subramani S.;
Adjiadi F.G., Pasquale E.B., Subramani S.;
"Identification of a new eph-related receptor tyrosine kinase gene
                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. IKAPPAB KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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NEWO-BINDING.
ATP (BY SIMILARITY).
BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 1; Length 757; Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3AFFE46A7DF91F9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE TY, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE.
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MOD_RES
MOD_RES
CARBOHYD
CARBOHYD
                                                              CARBOHYD
SEQUENCE
                                         CARBOHYD
                                                     CARBOHYD
                                                                                              Query Match
                                                                                                                                                                                                     EPA3 HUMAN
                                                                                                                  Matches
 RIFFFF
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                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation he European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and a sits content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                        long as its content is in no way noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R SWART; SM000bu; r...,

R SMART; SM00164; r...,

R SWART; SM00164; ryrkc; 1.

R SWART; SM00165; ryrkc; 1.

DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.

DR PROSITE; PS00109; PROTEIN KINASE_DOM; 1.

DR PROSITE; PS00790; RECEPTOR_TYR KIN V 1; 1.

DR PROSITE; PS00790; RECEPTOR_TYR KIN V 1; 1.

DR PROSITE; PS00790; RECEPTOR_TYR KIN V 2; 1.

DR PROSITE; PS00105; SAM DOWAIN; I.

RW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.

RW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
                                                           from mouse and chicken that is developmentally regulated and encodes
                               2
         at least two forms of the receptor.";

New Biol. 3:769-778(1991).

-!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS
                                        EPHRIN-A2, -A3, -A4 AND -A5.
-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDZ-BINDING MOTIF (POTENTIAL).
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIBRONECTIN TYPE-III 1. FIBRONECTIN TYPE-III 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN KINASE.
                                                                                                                                                                                                                                             entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000719; Prot kinae:
InterPro; IPR001660; SAM.
InterPro; IPR001245; TYr pkinaee.
InterPro; IPR001426; YKase receptorV.
Pfam; PF00441; EPH lbd; 1.
Pfam; PF00041; fin3; 2.
Pfam; PF00069; pkinaee; 1.
                                                                                                                                                                                                                                                                                                    HSSF; ruoscs; reference interpro; IPR006209; EGF_like.
InterPro; IPR001090; EGF_like.
InterPro; IPR0013961; FN III.
InterPro; IPR0013962; FnIII subd.
InterPro; IPR000719; Prot_Kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD001495; Ephrin receptor; 1. ProDom; PD000001; Prot kīnase; 1. SWART; SW00615; EPH lbd; 1. SWART; SW00060; FN3; 2.
                                                                                                                                                                                                                                                                            EMBL; M68514; AAA48666.1; -. PIR; B45583; B45583.
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00014; FNTYPEIII.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                    RECEPTOR SUBFAMILY.
                                                                                                                                                                                                                                                                                                  P00523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RANSMEM
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BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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MEDLINE=92147681; PubMed=1737782; Bloyd A.W., Ward L.D., Wicks I.P., Simpson R.J., Salvaris E., Wilks A., Welch K., Loudovaris M., Rockman S., Busmanis I.; Sinpson R.J., Salvaris E., Wilks A., Welch K., Loudovaris M., Rockman S., Busmanis I.; Isolation and characterization of a novel receptor-type protein tyrosine kinase (hek) from a human pre-B cell line."; J. Biol. Chem. 267:3262-3267(1992).

-: FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A2, -A3, -A4 AND -A5. COULD PLAY A ROLE IN LYMPHOID
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISOLI-P29320-2; Sequence=VSP 002995, VSP 002996;
-!- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST LEVEL IN PLACENTA.
-!- SIMILARITY: Contenins 1 stearile alpha motif (SAM) domain.
-!- SIMILARITY: Contenins 2 fibronectin type III domains.
-!- SIMILARITY: BELONGS TO THE TYR PAMILY OF PROTEIN KINASES. EPHRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPA3 HUMAN STANDARD; PRT; 983 AA.
P29320; Q9HZV3; Q9HZV4;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor ETK1) (HEK4).
EPHA3 OR ETK1 OR HEK.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Melanoma;
Chiari R., Hames G., Stroobant V., Maillere B., Texier C., Mach B.,
Boon T., Coulie P.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boon T., Coulie P.G.;
"Identification of a tumor specific shared antigen derived from an Eph-receptor and presented to CD4 T cells on HLA class II
                           (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92179233; PibMed=1311845; Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W.; Wilkinson D., Salvaris E., Boyd A.W.; Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expressed by human lymphoid tumor cell lines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
  PHOSPHORYLATION (AUTO-) (POTENTIAL)
                                                                                                        (POTENTIAL)
                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tyrosine phosphate.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1);
SECRETED (ISOFORM 2).
                                                                                                                                                                                                                                          Length 983;
                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    molecules.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                             192 N-LINKED (GLCNAC. . .) (PO1
109910 MW; E8895F0BDF77651E CRC64;
                              (AUTO-)
                                                    (GLCNAC. . .)
                                                                                                      (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                          Score 36; DB 1; Le
Pred. No. 1.2e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P29320-1; Sequence=Displayed;
                                                                             N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                             90.00.
100.08; Pr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                    Conservative
  602
779
231
336
390
403
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602
779
231
336
390
403
492
983 AA;
                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       342 LDWSW 346
                                                                                                                                                                                                                                                                                                                                                   1 LDWSW 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=1;
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us-09-643-260-5.rsp

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VARSPLIC
                       CONFLICT
                                                                     Query Match
                                                                              Best Loca
Matches
                                                                                                                                                   EPA3_MOUSE
                                                                                                                                          RESULT 10
 Etttttt8
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                                                                                                                                                                                                                                                ATP (BY SIMILARITY)

BY SIMILARITY

PHOSPHORYLATION (AUTO-) (POTENTIAL)

PHOSPHORYLATION (AUTO-) (POTENTIAL)

PHOSPHORYLATION (AUTO-) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL). (POTENTIAL). (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> CMYYFNAV (in isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDZ-BINDING MOTIF (POTENTIAL)
                                                                                                                                MIM; 179611; -. Gintegral to plasma membrane; TAS. GO; GO:0007165; P: Signal transduction; TAS. InterPro; IPR006209; EGF like.

InterPro; IPR001090; EDFIn_receptor.

InterPro; IPR001996; FN III.

InterPro; IPR001969; FN III.

InterPro; IPR001969; Frot_Kinase.

InterPro; IPR001140; Prot_Kinase.

InterPro; IPR0011426; YYz pkinase.

R InterPro; IPR0011426; YKase_receptorV.
                                                                                                                                                                                                                                                                                                                                                                                                       EPHRIN TYPE-A RECEPTOR 3. EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                      CYS-RICH.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC. . .)
(GLCNAC. . .)
(GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
SFSISGES
                                                                          EMBL, M83941; AAAS8633.1; --
EMBL, AF213459; AAG43576.1; --
EMBL, AF21460; AAG43577.1; --
EMBL, A28003; CAA01906.1; --
PIR, A38224; A38224.
HSSP, P00523; ZPTK.
Genew; HGNC; 3387; EPHA3.
                                                                                                                                                                                                                      Pfam; PF01404; EPH 1bd; 1.
Pfam; PF00041; fn3; 2.
                                                                                                                                                                                                                                     Pfam; PF00069; pkinase; 1.
Pfam; PF00536; SAM; 1.
RECEPTOR SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NP_BIND
BINDING
ACT_SITE
MOD_RES
MOD_RES
MOD_RES
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CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
DOMAIN
SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISOId=P29319-2; Sequence=VSP 002997;
-!- TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN THE BRAIN, ALSO DETECTED IN TESTIS.
-!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
-!- SIMILARITY: Contains 2 fibronectin type III domains.
-!- SIMILARITY: Contains 2 fibronectin type III domains.
-!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tyrosine phosphate.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE SHORT ISOFORM IS SECRETED.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor ETK1) (MEK4).
Enase receptor ETK1) (MEK4).
Mus musculus (Mouse).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 983;
                                                                         507 507 F -> L (IN REF. 1; CAA01906)
724 724 V -> L (IN REF. 1; CAA01906)
924 921 S -> H (IN REF. 2)
983 AA; 110086 MW; BBD900FA80FF5121 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                       Missing (In isoform 2). /FIId=VSP_002996.
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 1; Le
Pred. No. 1.2e+02;
FTId=VSP 002995
                                                                                                                                                                                                                                                                                                                                                                                  90.0%; Scorio. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. No. 100.00%; Pred. N
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IsoId=P29319-1; Sequence=Displayed;
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EMBL; M68515; AAA39522.1; ALT_SEQ.
PIR, AA5583; A45583.
HSSP, P00523; 2PTK.
MGD; MGI:99612; Epha3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
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CONFLICT
CONFLICT
SEQUENCE
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kinase receptor REK4) (TYRO-4).
EPHA3 OR REK4 OR TYRO4.
                                                                                                                                                                                                                                                          EMBL; U69278; AAC06273.1; -. HSSP; P00523; 2PTK.
                Rattus norvegicus (Rat).
                                    NCBI_TaxID=10116;
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TRANSMEM
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DOMAIN
DOMAIN
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                                                                                  Gaps
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OGT-2001 (Rel. 40, Last annotation update)
Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (AUTO-) (POTENTIAL).
PHOSPHORYLATION (AUTO-) (POTENTIAL).
PHOSPHORYLATION (AUTO-) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 983;
1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                            D (GLCNAC. . .) (POTI
(in isoform Short).
                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 983 AA; 109955 MW; BE44A6655D8107A2 CRC64;
                                                                                                                                                                                                                     BY SIMILARITY.
EPHRIN TYPE-A RECEPTOR 3.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                            POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                             CYS-KICH.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                          002997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              984 AA
                                                                                                                                                                                                                                                                                                                                                                                                              90.0%; Score 36; DB 100.0%; Pred. No. 1.2 ive 0; Mismatches
InterPro; IPR006209; EGF_like.
InterPro; IPR001090; Ephrin_receptor.
InterPro; IPR003961; FN III.
InterPro; IPR003962; FN III subd.
InterPro; IPR000719; Prot_Kinase.
InterPro; IPR001660; SAM.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR00141; EPH_lbd; 1.
Pfam; PF00041; ff3; 2.
Pfam; PF000536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                          FTIG=VSP
                                                                                                                                                                                                                                                                                                                                                                            N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                    Missing
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 LDWSW 346
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EPA3 RAT
ID EPA3 RAT
AC 008680;
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TRANSMEM
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CARBOHYD
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                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN=Sprague-Dawley;
STRAIN=Sprague-Dawley;
A Hi Y.Y., McTiernan C.F., Feldman A.M.;
Li Y.Y., McTiernan C.F., Feldman A.M.;
Li Y.Y., McTiernan C.F., Feldman A.M.;
II.-1 beta alters the expression of the receptor tyrosine kinase gene T. Febha3 in neonatal rat cardiomyocytes.";
T. Febha3 in neonatal rat cardiomyocytes.";
L. Am. J. Physiol. 274:H331-H34 (1998).
C. -1 FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A2, -A3, -A4 AND -A5.
C. -1 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
C. CATALYTIC ACTIVITY: ATP + a protein tyrosine protein
C. -1 SUBCELLUIAR LOCATION: Type I membrane protein.
C. -1 TISSUE SPECIFICITY: MOST ABUNDANT IN THE HEART, BRAIN, AND LUNG.
MANOCYMPES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO014; FITTPEILI.

R PRINTS; PRO0109; TYRKINASE.

R PRODOM; PD001409; EDHILD. receptor; 1.

R Probom; P000109; EDHILD. receptor; 1.

R MART; SM00615; EPHILD. 1.

R SMART; SM00615; EPHILD. 2.

R SMART; SM0019; TYKC; 1.

R SMART; SM0019; TYKC; 1.

R PROSITE; PS01017; PROTEIN KINASE ATP; 1.

R PROSITE; PS01019; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.

R PROSITE; PS00790; RECEPTOR TYR KIN V. 2; 1.

R PROSITE; PS00791; RECEPTOR TYR KIN V. 2; 1.

R PROSITE; PS00791; RECEPTOR TYR KIN V. 2; 1.

R PROSITE; PS00791; RECEPTOR TYR KIN V. 2; 1.

R PROSITE; PS00791; RECEPTOR TYR KIN V. 2; 1.

R PROSITE; PS00791; RECEPTOR TYR KIN V. 2; 1.

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--- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
--- SIMILARITY: Contains 2 fibronectin type III domains.
--- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN RECEPTOR SUBFAMILY.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPHRIN TYPE-A RECEPTOR 3. EXTRACELLULAR (POTENTIAL)
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CYS-RICH.
FIBRONECTIN TYPE-III 1.
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InterPro; IRR001090; Ephrin_receptor.
InterPro; IRR001090; Ephrin_receptor.
InterPro; IRR003961; FN III.
InterPro; IRR003961; FN III.
InterPro; IRR000719; Prot_Kinase.
InterPro; IRR001245; Tyr_pkinase.
InterPro; IRR001245; Tyr_pkinase.
InterPro; IRR001426; Xfase_receptorV.
Pfam; PF00441; EBH_lbd; 1.
Pfam; PF00441; fn3; 2.
Pfam; PF00639; pkinase; 1.
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RESULT 13
PGLR_PENGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                         Gaps
                                       ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

PHOSPHORYLATION (AUTO-) (POTENTIAL).

PHOSPHORYLATION (AUTO-) (POTENTIAL).

PHOSPHORYLATION (AUTO-) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Tokyo 1998;
MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids

    -1- SIMILARITY: Belongs to the folylpolyglutamate synthase family.

                                                                                                                                                                                                                                                                                                                                                                                                              symbiotic bacterium).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
FolC bifunctional protein [Includes: Folylpolyglutamate synthase (EC 6.3.2.17) (Folylpoly-gamma-glutamate synthetase) (FPGS);
Dihydrofolate synthase (EC 6.3.2.12)].
                                                                                                                                        (POTENTIAL) (POTENTIAL)
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                                                                                                                                                                                  DB 1; Length 984;
                               PDZ-BINDING MOTIF (POTENTIAL)
                                                                                                                                                                                                       0; Indels
                                                                                                                                                 193 N-LINKED (GLCNAC. . .) (POT 110227 MW; F170C49312F7A0AB CRC64;
 FIBRONECTIN TYPE-III 2.
                                                                                                                                                                                  Score 36; DB 1; Le
Pred. No. 1.2e+02;
0; Mismatches 0;
           PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001645; Fpolygl synthtse.
InterPro; IPR000713; Mur_ligase.
Pfam; PF01225; Mur_ligase; 1.
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                                                                                                                                                                                             100.001
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                                                                                                                                                                                  90.06;
                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                              984 AA;
                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                 343 LDWSW 347
                                                                                                                                                                                                                                                                                                                                                                                                                                              MCBI_TaxID=118099;
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780
232
337
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P57265;
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PROSTIE; PS01011; FOLYLPOLYGLU SYNT 1; 1.
PROSTIE; PS01012; FOLYLPOLYGLU SYNT 2; FALSE NEG.
Multifunctional enzyme; Ligase; One-carbon metabolism; ATP-binding;
Folate biosynthesis; Complete protecome.

50 ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
NCBI_TaxID=84562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CCT 6421;
Ribon A.B., Coelho J.L.C., Barros B.G., Araujo E.F.;
Ribon A.B., Coelho J.L.C., Barros B.G., Araujo E.F.;
"Cloning and characterization of a gene encoding the endopolygalacturonase of Penicillium griseoroseum.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-galactosiduronic linkages in pectate and other galacturonans.
-!- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES
(POLYGALACTURONASES).
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Polygalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase)
                                                                                                                                                                                                   85.0%; Score 34; DB 1; Length 411; 80.0%; Pred. No. 1.1e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 376;
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Pred. No. 1.46+02;
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                                                                                                                                             SDDC2DC66539935A CRC64;
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InterPro; IPR000743; Glyco_hydro_28.
InterPro; IPR006626; PbH1.
PFam; PF00295; Glyco_hydro_28; 1.
SWART; SM00710; PbH1; 5.
PROSITE; PS00502; POLYGALACTURONASE; 1.
                                                                                                                                                411 AA; 46970 MW;
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nes 4; Conservative
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les 4; Conservative
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219 IDWSW 223
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ID NRAM IAWIL
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                                                                                                                                                SEQUENCE
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Nature 290:213-217(1981).

-!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.

-!- CATALYMIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and surface.
                                                                                                            Fields S., Winter G., Brownlee G.G.; "Structure of the neuraminidase gene in human influenza virus
Influenza A virus (strain A/Puerto Rico/8/34).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
                                                                [1] SEQUENCE FROM N.A. MEDLINE=81148841; PubMed=7010182;
                                            NCBI_TaxID=11455;
                                                                                                                                            A/PR/8/34.";
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                                                                                                                                                                                                                                               J. Virol. 41:730-734(1982).

-!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.

-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in synthesic substrates.
                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION.
                                                                                                                                                                      SEQUENCE FROM N.A. MEDINBE-82192605; PubMed=7077751; Hiti A.L., Nayak D.P.; Hiti A.L., Nayak D.P.; "Complete nucleotide sequence of the neuraminidase gene of human influenza virus A/WSN/33.";
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
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Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
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             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Neuraminidase (EC 3.2.1.18).
                                                                                         Influenza A virus (strain A/Wilson-Smith/33)
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HSSP; P03472; 2QWC.
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453 AA;
                                                                                                                                          NCBI_TaxID=11487;
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                 SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPERVARIABLE STALK REGION.
HEAD OF NEURAMINIDASE.
PROBABLE.
PROBABLE.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                              SPIKE ON THE SURFACE OF THE VIRION. SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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ProDom; PD000431; Glyco_hydro_34; 1.
Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
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Pred. No. 1.7e+02;
1; Mismatches 0;
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HSSP; P03472; 2QWC.
SUBUNIT: Homotetramer.
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Search completed: February 18, 2004, 14:28:04 Job time : 4.55263 secs

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Gaps

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Conservative

437 VDWSW 441

1 LDWSW 5

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Best Local Similarity Matches 4; Conserv

21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Neuranthidase (EC 3.2.1.18)

STANDARD;

NRAM IAPUE P03468;

GETTTE

NRAM IAPUE

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Q91719 pseudomonas
Q85478 aranthomonas
Q85478 aranthomonas
Q45498 caenorihabdi
Q8p955 xanthomonas
Q91210 pseudomonas
Q91210 pseudomonas
Q91210 pseudomonas
Q8mmj0 apis carana
Q8c9k6 mus musculu
Q8c9k6 mus musculu
Q9vgp2 drosophila
Q9vgp2 drosophila
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Q9skv1 bos taurus
Q8cb13 mus musculu
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Q8bgw8 aaccharops
Q9tc2 marek's dis
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Q9t2t2 caenorhabdi
Q9u2t2 caenorhabdi
Q8c91 yersila pe
Q8c91 yersila pe
Q8c91 bifidobacte
Q8d751 bifidobacte
Q8d751 bifidobacte
Q8d751 streptococc
Q8d5u3 streptococc
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021903 bacteriopha
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STRAIN=Florida1997;
MEDLINE=21488685; PubMed=11602755;
Afonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,
Becnel J.J., Rock D.L., Kultsh G.F.;
"Genome Sequence of a Baculovirus Pathogenic for Culex nigripalpus.";
J. Virol. 75:11157-11165(2001).
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STRAIN=Florida1997;
ATRAIN=Florida1997;
Bernel G.L., Tulk E.R., Lu Z., Balinsky C.A., Moser B.A.,
Bernel J.J., Rock D.L., Kutish G.F.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Bypothetical protein.
Hypothetical protein.
SEQUENCE 242 AA; 27222 MW; 6014967531110E52 CRC64;
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Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CUN068 hypothetical protein.
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100.0%; Score 40; DB 12;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0;
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QBCRF5
QBZC91
QBG751
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QBG771
QBE5U2
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Q8H2P9
Q8N241
Q8BG50
Q9F163
Q9F163
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  PRELIMINARY;
  NCBI_TaxID=130556;
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LDWSWA

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438 AA
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EMBL; AB012502; AAM43483.1; -.
InterPro; IPR002293; AA/rel_permeasel.
InterPro; IPR064041; Permease.
Pfam; PF00324; aa_permeases; 1.
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Matches 5; Conservative
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182 VDWSWA 187
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MEDLINE-22022145; PubMed=12024217;

da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

Quaggio R.B., Monteiro-vitorello C.B., Van Sluys M.A., Almeda N.F.,

A lives L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

A lives L.M.C., do Amaral A.M., Bertolini M.C., Canargo L.B.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., Bl-Dorry H.,

Ratia J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martines E.C., Machadis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Martines E.C., Mardianis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Martines E.C., Martine, W.W., Olivaira M.C., Olivaira V.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; Pubmed=10984043;
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
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                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 92.5%; Score 37; DB 16; Length 304; Best Local Similarity 83.3%; Pred. No. 2e+02; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 AA; 33430 MW; DC278071764B671C CRC64;
                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
probable cytochrome c oxidase assembly factor.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Cationic amino acid transporter.
                                                                     PRT; 304 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         433 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AE004449; AAG03503.1; -.
InterPro; IPR006369; CyOE_CtaB.
InterPro; IPR000537; UbiA.
Pfam; PF01040; UbiA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             opportunistic pathogen.";
                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa.
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259 LDWAWA 264
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                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=287;
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                                                                                                 091719;
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                                                                  091719
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Q8P4A1
RESULT 2
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ANDLINE=2202145; PubMed=12024217;

REDINE=22022145; PubMed=12024217;

REDINE=22022145; PubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Cicarelli R.M.B., Coutinho L.L., Curgino-Santog J.R., El-Dorry H.,

RA Earia J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Exteyana A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

RA Locali B.C., Machado M.A., Madira R.B., M., Martinez-Rossi N.M.,

Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Everira H.A., Rossi A., San J.A.D., Silva C., de Souza R.F.,

Spinola L.A.R., Takita M.A., Tamura R.E., Teixcira B.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Setubal J.C., Kitajima J.P.,

RY "Comparison of the genomes of two Xanthomonas pathogens with differing

RY "Comparison of the genomes of two Xanthomonas pathogens with differing

RME, AED12036; AAM33706.1;

RMEL PED201 PRR004293; AA/rel_permeasel.
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Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitajima J.P., "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.5%; Score 37; DB 16; Length 433; 83.3%; Pred. No. 2.88+02; ive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      433 AA; 45128 MW; EF217D2A7C516533 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Cationic amino acid transporter.
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Nature 417:459-463(2002).

EMBL, AE012305; AAM41300.1; -.

InterPro; IPR002656; Acyl transf_3.

Pfam, PF01757; Acyl transf_3; 1.

Complete protecome.

SEQUENCE 361 AA; 39147 MW; 37AB
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Best Local Similarity 100....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        opportunistic pathogen."
Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                     117 LDWSW 121
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Q9M3F6;
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Q9HZ10
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Q9M3F6
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SEQUENCE FROM N.A.

STRAIN=ATCC 33913 / NCPPB 528;

X MEDLINE=2022145; PubMed=12024217;

A Ballva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeda N.F.,

A Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

A Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Caracolli R.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Ratsuyama A.M., Kishi L.T., Leiter R.P., Lemos E.G.M., Lemos M.V.F.,

Locali E.C., Machado M.A., Madeira A.M.B.N., Marrinez-Rossi N.M.,

Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                              Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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Xanthomonadaceae; Xanthomonas.
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                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 283:2012-2018 (1998). EMBL; 292834; CAB07386.1; -.
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                                                                                                                                                                                                                                                     Dobson k.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30897 MW; 820D4D73DC5CB060 CRC64;
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                                                                                 Last sequence update)
Last annotation update)
                                258 AA
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                                                                 Created)
                                PRT;
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InterPro; IPR000980; SH2.
InterPro; IPR001960; SGS.
Pfam; PF00017; SH2; 1.
ProDom; PD000093; SH2; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50001; SH2; 1.
                                                              01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2003 (TrEMBLrel. 23, F3982.5 protein.
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ses 5; Conservative
                                PRELIMINARY;
                                                                                                                                           Caenorhabditis elegans.
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Matches
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Q8P955
RESULT 5
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Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitajima J.P.; "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.";
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X. Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X. Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Brainkman P.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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Hypothetical protein; Complete proteome.
SEQUENCE 374 AA; 42269 MW; 31EF185C4F683884 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            361 AA; 39147 MW; 37AB21791BE0393F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical protein PA3230.
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01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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100.0%; Pred. No. 3.5e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.0%; Score 36; DB 16; I
100.0%; Pred. No. 3.4e+02;
Live 0; Mismatches 0;
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Gaps

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STRAIN-CS7BL/6J; TISSUB=Thymus;

MEDLINE=22354693; PubMed=12466851;
The FANTOM COnsortium.

the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cONAs.";
Nature 420:563-573(2002).

BMBL; AK041935; BAC31104.1; -.

SRQUENCE 538 AA; 60659 MW; EEDAB12E0369E419 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise B., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.0%; Score 36; DB 11; Length 538; 100.0%; Pred. No. 56+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 581;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEAN; PP00732; GMC oxred; 3.
PROSITE; PS00639; THIOL PROTEASE HIS; 1.
SEQUENCE 581 AA; 63475 MW; AZF13BEBC25E496D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
CG6728 protein.
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Pred. No. 5.4e+02;
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100.0%; Pred. No. s.
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Interpro; IPR000169; SHprot_acsite.
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Matches 5; Conservative
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nes 5; Conservative
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                                                                                                                                            SEQUENCE FROM N.A.
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Best Local S
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Q8MSH3
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TISSUE-Nurse heads;
Sittipraneed S., Imjongjirak C.;
Sittipraneed S., Imjongjirak C.;
Wolecular Cloning of Major Royal Jelly Protein (MRJP2) cDNA from Apis cerana in Thailand.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF525777; AAM82822.1;
InterPro; IPR003534; Royaljelly.
Pfam; PF03022; MRJP; 1.
PRINTS; PR01366; ROYALJELLY.
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Hymenoptera, Apocrita, Aculeata, Apoidea,
                                                                                                                                            Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R., Welcheelgatrner M., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Salancubat M.; Cotter F., Salancubat M.; Cotter F., Salancubat M.; Cotte EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                        EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL132909; CAB87132.1; -.
Interpro; IRR003871; DUF223.
Pfam; PF02721; DUF223; 2.
SEQUENCE 409 AA; 45738 MW; ADDC4EF5597E4EE4 CRC64;
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SEQUENCE 463 AA; 52412 MW; D648AE2BAF1EDDE9 CRC64;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Major royal jelly protein MRJP2 precursor.
MRJP2.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.0%; Score 36; DB 10; I 100.0%; Pred. No. 3.8e+02;
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Best Local Similarity 100.0
Post Local Si Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                SEQUENCE FROM N.A.
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NCBI_TaxID=7461;
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RA SEQUENCE FROM N.A.

RA ROLtenberg S., Dobbelaere D.A.E., Heussler V.T.;

RA ROttenberg S., Dobbelaere D.A.E., Heussler V.T.;

RIGENTIfication and characterisation of the bovine IKB kinases (IKKs)

RI Jaha, Dete and gamma.";

RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

C. -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL, AJ414555, CAC93686.1; -.

DR InterPro; IPR000719; Prot kinase.

DR InterPro; IPR000220; Ser thr_pkinase.

PROSITE; PS00109; Prot kinase; 1.

DR PROSITE; PS00107; PROTEIN KINASE_DM; 1.

DR PROSITE; PS00108; PROTEIN KINASE_DM; 1.

DR PROSITE; PS00109; PROTEIN KINASE_ST; 1.

KW ATP-binding; Kinase; Serine/Checonine-protein kinase; Transferase.

SQ SEQUENCE 740 AA; 84343 MW; 01903BE11F44DI76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).

EMBL; AK035326; BAC29034.1; -
SEQUENCE 745 AA; 84770 MW; 48C9E01C17A61184 CRC64;
                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos. MCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.0%; Score 36; DB 6; Length 740; 100.0%; Pred. No. 6.8e+02; ive 0; Mismatches 0; Indels
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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100.0%; Pred. No. 6.9e+02;
iive 0; Mismatches 0;
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MEDLINE=22354683; PubMed=12466851;
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01-DEC-2001 (TrEMBLrel. 19, Created)
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                                                         Bos taurus (Bovine).
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          IkB kinase-alpha.
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Q95KV0
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                                                                                                                                                                                                                                          RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Ramanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George B.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Sutton G.G., Wortenan J.R., Yandell M.D., Zhang O., Chen L.X., Ratadon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Feleffer B.D., Mandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Feleffer B.D., Randon R.C., Bazen A.A. An H.-J., Andrews-Fennkoch C., Baldwin D., Ballew R.M., Baul A., Barendal J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Baul A., Ballew B.P., Barman B.P., Bhandari D., Bolshakov S., Rokova D., Botchan M.R., Bouch J., Evoketein P., Brothar J., Rokova D., Botchan M.R., Bouch J., Broketein P., Brothar J., Raman B.D., Burtler H., Cadieu E., Center A., Chadra I., Rabendari D., Bolshakov S., Rabendari D., Botchan M.R., Bouch E., Davies P., Andrews B.D., Burtler M., Cawley S., Dahlke C., Davenport L.B., Davies P., Rabendon K., Doug L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P. Dodson K., Doug L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P. Botchar A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K., Albotar C., Gabrielian A. G., Garger C., Ferraz C., Ferraz C., Ferrar S., Pletschman W., Ralleh F., Karpen G.H., Wei M.-H., Ibegwan C., Juladi M., Kalush F., Karpen G.H., Wei M.-H., Ibegwan C., Lasko P., Lei Y., Leviteky A.A., Li J., Wei M.-H., Ibegwan C., Julang Y., Lin X., Marterla N., McIntceh T.C., McLeod M.P., McBherson D.L., McKulov G., Milbhina N.V., Mobarry C., Morris J., McBherei M., Rallah M., Rallah M., Rallah M., Rallah M., Rallah M., Rallah M., Rallah M., Rallah M., Rallah M., Rallah M., Rallah M., Rallah M., Rallah M., Rallah M., Rallah M., Rallah M., Rallah M., Rallah M., McIntceh T., Morbherson D.L., Rallah M., Manday M., Millam S.M., Millams S.M., Modaled R.A., Nixon K., Nixon M., Sullah M., Sullah M., Shue B.C., Siden-Kamos I. Simpson M., Strong R., Sullah M., Sallah M., Sallah M., Sallah M., Wei S., Sallah M., Wei S., Sallah M., Sallah M., Wei S., Sallah M., Sallah M.,
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Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.0%; Score 36; DB 5; Length 597; 100.0%; Pred. No. 5.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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PROSITE; PS00624; GMC_OXRED_2; 1.
PROSITE; PS00639; THIOL_PROTEASE HIS; 1.
SEQUENCE 597 AA; 65274 MW; 8C4C362AFFA0902A_CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
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InterPro; IPR000169; SHprot_acsite.
                                                                                                                                                                                                   STRAIN=BERKELEY,
MEDLINE=20196006; Pubmed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003691; AAF54634.1; -
FlyBase; FBgn0037896; CG6728.
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(TrEMBLrel. 19, I
(TrEMBLrel. 23, I
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                                                                                                                                                                                SEQUENCE FROM N.A.
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01-DEC-2001
01-MAR-2003
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Gaps

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0; Indels

095KV1 095KV1;

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RESULT 13

Best Loc Matches

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Length 745;

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Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;

Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;

"Identification and characterisation of the bovine IKB kinases (IKKs)
"Identification and gamma.";
"I alpha, beta and gamma.";
"I submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
"I SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
"INTERPRO; IPR001290; Prot kinase.
"INTERPRO; IPR001290; Ser_Chr_pkinase.
"INTERPRO; IPR001290; Ser_Chr_pkinase.
"INTERPRO; IPR001290; Prot kinase; I."
"INTERPRO; PS000109; Prot kinase; I."
"INTERPROSITE; PS000109; PROTEIN KINASE_DOM; I."
"ROSITE; PS000109; PROTEIN KINASE_DOM; I."
"ROSITE; PS000109; PROTEIN KINASE_DOM; I."
"ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
"SEQUENCE 756 AA; 86647 MW; A072D15614A176E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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7e+02;
hes 0; Indels
01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) IKB kinase-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 90.0%; Score 36; DB Best Local Similarity 100.0%; Pred. No. 7e+ Matches 5; Conservative 0; Mismatches
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Search completed: February 18, 2004, 14:35:40 Job time : 19.3684 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Pebruary 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec Run on:

US-09-643-260-5 40 1 LDWSWA 6 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	probable cytochrom		uroporphyrinogen d	conserved hypothet	probable replicati	conserved helix-lo	receptor tyrosine	protein-tyrosine k	receptor tyrosine	gene e12 protein -	tetrahydrofolylpol	hypothetical prote	NADH2 dehydrogenas	probable potassium	conserved hypothet	probable integral	hypothetical prote	hypothetical prote	dipeptide ABC tran	NADH2 dehydrogenas	vegetatible incomp	ferric exochelin b	hypothetical prote	hypothetical prote	סי	exo-alpha-sialidas	exo-alpha-sialidas	hypothetical prote	aerolysin precurso
		er i	F83632	T21987	523471	B83241	T47298	149101	B45583	A38224	A45583	T03355	E84949	T31511	T14235	AI0379	B82531	T36162	T05822	AB2931	D98351	AI3395	AB3548	S60888	AE1844	T31787	E69371	NMI V3	NMIV	\$75362	803038
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dР	Query	Match	92.5	90.0	0.06		90.0	90.0	90.0	90.0	90.0	85.0	85.0	85.0	85.0	85.0	82.5	82.5	82.5	82.5	82.5	82.5	82.5	82.5	82.5	82.5	82.5	82.5	82.5	82.5	82.5
		Score	37	36	36	36	36	36			36			34	34	34														33	
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cytochrome P450 (C cytochrome P450 -	probable cytochrom hypothetical prote hypothetical prote	Vi polysaccharide Vi polysaccharide conserved hypothet	H+-exporting ATPas two-component sens probable multi-dom	lysobactin synthet probable fatty-aci fatty acid synthas	H+-transporting tw Ig alpha chain - h
T10000 T09999	T09944 T15256 T35222	A56975 AF1040 D82177	A42970 C83441 T50568	T18545 T43409 T38781	T11353 S24712
01 01	~ ~ ~	000	- 2 2	0 0 0	0 0
516 524	524 539 610	656 656 836	840 885 1334	1575 1842 1842	53 83
82.5 82.5	82.5 82.5 82.5	82.5 82.5 82.5	82.5 82.5 82.5	82.5 82.5 82.5	80.0
33	n n n	3333			32
30	0 0 0 2 0 4	35 34 37	338 439	4 4 4 4 3 3	4 4 5 5

ALIGNMENTS

RESULT 1 P83632	probable cytochrome c oxidase assembly factor PA0113 [imported] - Pseudomonas aeruginos C;Species: Pseudomonas aeruginosa	C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: P83632	R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbiq, K.; Lim,	.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000	A;Title: Complete genome sequence of Peeudomonas aeruginosa PA01, an opportunistic path: A:Reference number: A82950; MUID:20437337; PMID:10984043	A,Accession: F83632	A; Status: preliminary	A.Residues: 1-304 <sto></sto>	A;Cross-references: GB:AE004449; GB:AE004091; NID:g9945928; PIDN:AAG03503.1; GSPDB:GN001	A; Experimental source: strain PAO1	C; Genetics:	A;Gene: PA0113	C;Superfamily: heme O synthase	92.58;	*; Pred. No. 50;	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
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|||:|| 259 LDWAWA 264 1 LDWSWA 6 g ò

Argon transcript protein F39B2.5 - Caenorhabditis elegans C,Species: Caenorhabditis elegans C,Species: Caenorhabditis elegans C,Species: Caenorhabditis elegans C,Species: Caenorhabditis elegans C,Species: T21997 C,Accession: T21987 C,Accession: T21987 C,Accession: T21987 C,Accession: T21987 C,Accession: T21987 C,Accession: T21987 C,Accession: T21987 C,Accession: T21987 C,Accession: T21987 C,Accession: T21987 C,Accession: T21987 C,Accession: T21987 C,Accession: T21987 C,Accession: T21987 C,Accession: T21987 C,Accession: T21987 C,Accession: T21987 C,Accession: T21987 C,Accession: T21987 C,Accession: T39B2 C,Accession: T39B2 C,Accession: T39B2 C,Accession: T39B2 C,Accession: T39B2 C,Accession: T39B2 C,Accession: T39B2 C,Accession: T39B2 C,Accession: T39B2 C,Accession: T39B2 C,Accession: T3B2 C,Ac

90.0%; Score 36; DB 2; Length 258; Query Match

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A;Residues: 1-409 <NYA>
A;Cross-references: EMBL:AL132909
                                                                                 90.08;
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Best Local Similarity 100..
نام 5; Conservative
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Matches 5; Conserv
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    A;Gene: PA3230
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                                                                                 Query Match
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Aritle: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho A;Accession: B83241
A;Accession: B83241
A;Accession: B83241
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-374 <STO>
A;Accossion: B83241
A;Residues: 1-374 <STO>
A;Accossion: B83241
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A;Residues: B
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C,Accession: S23471; S33965; S54031; S27348; S31312
R,Garey, J.R.; Labbe-Bois, R.; Chelstowska, A.; Rytka, J.; Harrison, L.; Kushner, J.; LaBur, J. Biochem. 205, 1011-1016, 192
Eur. J. Biochem. 205, 1011-1016, 192
A;Title: Uroporphyrinogen decarboxylase in Saccharomyces cerevisiae. HEM12 gene sequence A;Reference number: S23471; MUID:92249304; PMID:1576986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Readdues: 1-362 cdR>
A;Crose-references: EMBL:X63721; NID:g3766; PIDN:CAA45253.1; PID:g3767
A;Crose-references: EMBL:X63721; NID:g3766; PIDN:CAA45253.1; PID:g3767
R;Diflumeri, C.; Larocque, R.; Keng, T.
Yeart, 9, 613-623, 1993
A;Title: Molecular analysis of HEMG (HEMI2) in Saccharomyces cerevisiae, the gene for A;Reference number: S33965; MUID:93348774; PMID:8346678
                                                                                                                                                                                                                                                                                                                                                                                       uroporphyrinogen decarboxylase (EC 4.1.1.37) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YD9609.03; protein YDR047w
C;Species: Saccharomyces cerevisiae
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C;Superfamily: uroporphyrinogen decarboxylase
C;Keywords: carbon-carbon lyase; carboxy-lyase; porphyrin biosynthesis
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                                        Indels
Pred. No. 61;
0; Mismatches
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A,Reference number: S54031
A,Accession: S54033
A,Molecule type: DNA
A,Residues: 1-362 «HUN»
C,Genetics: EMBL:Z49209; NID:g798897,
    83.3%;
                                        5; Conservative
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Similarity
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A;Residues: 1-362 <DIF>
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Matches 5
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Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homolc
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: 149101
R;Mock, B.A.; Connelly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.
Rsmock, B.A.; Connelly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.
A;Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome A;Reference number: 149101; MUID:9604444; PMID:7558004
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                                                                                                                                                                                                                                                                                                                   N,Alternate names: protein T14K23.110 °
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
                                                         Gaps
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A;Introns: 47/3; 95/3; 131/2; 175/3; 240/2; 281/3; 304/1; 336/3
A;Note: T14K23:110
     Length 374;
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90.0%; Score 36; DB 1; Lei
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                             probable replication protein - Arabidopsis thaliana
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A;Molecule type: mRNA
A;Residues: 1-745 <RES>
Score 36; DB 2;
Pred. No. 89;
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                     100.0%; Preu. ...
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us-09-643-260-5.rpr

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A,Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse ar A,Reference number: A45583; MUID:92031278; PMID:1657122
                                                              A;Accession: A45583
A;Status: preliminary
A;Nolcule type: mRNA
A;Residues: 1-983 <SAJ>
A;Cross-references: GB M68513; NID:g199119; PIDN:AAA39521.1; PID:g199120
A;Cross-references: GB M68513; NID:g199119; PIDN:AAA39521.1; PID:g199120
A;Cross-references: GB M68513; NID:g199119; PIDN:AAA39521.1; PID:g199120
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat in C;Superfamily: autophosphorylation; phosphoprotein; transmembrane protein
F;619-885/Domain: protein kinase homology <RIN>
F;627-635/Region: protein kinase ArP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Accession: T03355
R;Crutz-Le Coq, A.M.; Cesselin, B.; Commissaire, J.; Anba, J.; Kyriakidis, S.; Chopin, : submitted to the EMBL Data Library, June 1997
A;Description: Sequence and organization of the lactococcal isometric bIL170 phage geno. A;Reference number: Z14903
A;Accession: T03355
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R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
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Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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100.0%; Pred. No. 2.4e+02;
iive 0; Mismatches 0;
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A;Molecule type: DNA
A;Residues: 1-211 <CRU>
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C;Superfamily: folylpolyglutamate synthase
C;Keywords: ligase
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A;Residues: 1-411 <STO>
A;Cross-references: GB:AP000398; (
A;Experimental source: strain APS
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5; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LDWSWA 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: E84949
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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A,Gene: e12
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T03355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-tyrogine kinage (EC 2.7.1.112) hek precursor - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999
C;Accession A38224; B38224
R;Micks, I.P.; Wilkinson, D.; Salvaris, E.; Boyd, A.W.
Proc. Natl. Acad. Sci. U.S.A. 89, 1611-1615, 1992
A;Title: Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expresse A;Reference number: A38224; WUID:92179233; PMID:1311845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule trype: mRNA
A; Residues: 1-983 <WIC>
A; Residues: 1-983 <WIC>
A; Residues: 1-983 <WIC>
A; Residues: 1-983 <WIC>
A; Residues: 1-983 <WIC>
A; Rocression: Bis 24
A; Molecule trype: protein: WCBI backbone (NCBIP;86627)
A; Accession: Bis 24
A; Residues: 21-39;810-860 <WIZ>
C; Superfamily: protein: Trypes in the properties of the physical trype of the protein: phosphotransferase; C; Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C; Reywords: ATP; autophosphortylation; plycoprotein; phosphotransferase; F; 1-20/Domain: signal sequence #status predicted <GIG>
F; 1-20/Domain: signal sequence #status predicted <GIG>
F; 21-983/Product: protein-tyrosine kinase hek #status experimental <MAT>
F; 52-65/Domain: protein kinase homology <KIN>
F; 62-635/Region: protein kinase APP-binding motif
F; 222, 337, 391, 404, 493/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                    aH
                                                                                 C;Accession: B45583
R;Sajjadi, F.G.; Pasquale, E.B.; Subramani, S.
New Biol. 3, 769-778, 1991
A;Ttle: Identification of a new eph-related receptor tyrosine kinase gene from mouse ar A;Ttle: Identification of a new eph-related receptor tyrosine kinase gene from mouse ar A;Reference number: A45583; MUID:92031278; PMID:1657122
A;Reference number: A45583; MUID:92031278; PMID:1657122
A;Reference B45583
A;Residues: 1-983 <A;AJ>
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-983 <A;AJ>
A;Cross-references: GB:M68514; NID:9454809; PIDN:AAA48666.1; PID:9211447
A;Note: sequence extracted from NCBI backbone (NCBIN:62405, NCBIP:62411)
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat P;619-885/Domain: protein kinase homology <KIN>
F;617-635/Region: protein kinase ATP-binding motif
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receptor tyrosine kinase Cek4 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor tyrosine kinase Mek4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C;Accession: A45583
R;Sajjadi, F.G.; Pasquale, E.B.; Subramani, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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2.4e+02;
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Search completed: February 18, 2004, 14:38:38
Job time : 8.5921 secs
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                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                  A;Gene: YPO3129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable potassium efflux system YPO3129 [imported] - Yersinia pestis (strain CO92) C;Species: Yersinia pestis C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
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A,Accession: T31511
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: Dreliminary; translated from GB/EMBL/DDBJ
A,Residues: 1-433 <WIL>
A,Cross-references: EMBL-AL117204; PIDN:CAB55145.1; CESP:Y116A8C.9
A,Reperimental source: clone Y116A8C
C,Genetics:
C,Genetics:
A,Gene: CESP:Y116A8C.9
A,Gene: 16/2, 42/2; 75/2; 107/3; 173/3; 230/3; 262/3; 318/3; 373/1; 398/1
C;Superfamily: Caenorhabditis elegans hypothetical protein Y116A8C.9
                                                                                                                                                                                           hypothetical protein Y116A8C.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Sate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
C;Accession: T31511
R;McMurray, A.
submitted to the EMBL Data Library, October 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .Variety: strain PCC 7002
.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
.Accession: T14235
                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 2; Length 433;
Pred. No. 2.2e+02;
2; Mismatches 0; Indels
                                 Indels
. 2.1e+02;
0;
                                 Mismatches
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                Pred.
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66.7%;
              80.08;
                               4; Conservative
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174 VDWTWA 179
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115 MDWGWA 120
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Best Local Similarity
Matches 4; Conserv
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              Best Local Similarity
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219 IDWSW 223
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
C;Accession: BB2531
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Recession: B82531
A; Readuse: preliminary
A; Status: preliminary
A; Status: preliminary
A; Readuse: 1-198 «SIM»
A; Residuse: 1-198 «SIM»
A; Residuse: 1-198 «SIM»
A; Residuse: 1-198 «SIM»
A; Residuse: 1-198 «SIM»
A; Recession: B82531
A; Recession: B82531
A; Recession: B82531
A; Recession: Rish Records: GB: AB004072; GB: AB003849; NID: G9107884; PIDN: AAR85463.1; GSPDB: GN0011;
A; Recession: A.J. G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Camargo, M.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Alvarenga, R.; Alberto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
Briomes: M.R.S.; Bueno, M.R.P.; Camargo, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Marques, B.E.; Laigr Chado, M.A.; Madeira, A.M. B.N.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Martins, E. A; Authors: Martins, E.M.P.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Myaki, C.Y.; F.G.; Munes, L.R.; Oliveira, M.R.; de Oliveira, M.C.; Falmieri, D.Al Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak, M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z. A; Contents: annotation
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein XF2666 [imported] - Xylella fastidiosa (strain 9a5c)
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A;Cross-references: GB:AL590842; PIDN:CAC92364.1; PID:g15981067; GSPDB:GN00175
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 2; 1
Pred. No. 5.8e+02;
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C,Superfamily: conserved hypothetical protein MJ1677
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RESULT 2
US-09-847-946A-5
; Sequence 5, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
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                                                                                                                                                                   February 18, 2004, 14:36:10 ; Search time 16.6974 Seconds (without alignments) 75.239 Million cell updates/sec
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US-09-847-946A-143
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ALIGNMENTS

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Gaps
Sequence 5, Application US/09847940B
Sequence 5, Application US/09847940B
Settle No. US20020156000A1
GENERAL INFORMATION:
APPLICANT: May, Michael J.
APPLICANT: May, Michael J.
APPLICANT: Ghosh, Sankar
TITLE OF INTENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REPERBNCE: PPI-1170F
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO S: SEQ ID NO S: 27
LENGTH: 6
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ORGANISM: Artificial Sequence
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TYPE: PRT
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                           APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
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APPLICANT: Ghosh, Sankar

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mathryn

APPLICANT: Phillips, Kathryn

APPLICANT: Hannig, Gerhard

ITILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REFERENCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 160

SOUTHWARE: PATENTIN VET. 2.0

SEQ ID NOS: 160

SEQ ID NOS: 160

SEQ ID NOS: 160
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Sequence 40, Application US/09847946A

Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mark A

CURRENT PHILIPS, Kathryn

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REPERENCE: PPL-119

CURRENT APPLICATION NUMBER: US/09/847, 946A

CURRENT FILING DATE: 2000-05-02

PRIOR PILING DATE: 2000-05-02

PRIOR PLING DATE: 2000-05-02

PRIOR PLING DATE: 2000-06-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide US-09-847-946A-5
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Best Local Similarity 100.0%; Pred. No. 7e+05;
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ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.0
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LENGTH: 6
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APPLICANT: Glocal, Sankar A
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APPLICANT: Phillips, Kethryn
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TYPE: PRT
ORGANISM: Artificial Sequence
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Sequence 67, Application No. US200300549991

GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Glosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, NUMBER: 05/09/047,946A

CURRENT APPLICATION NUMBER: 60/201,261

PRIOR APPLICATION NUMBER: 60/201,261

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-02

NUMBER OF SEQ ID NOS: 160

SEQ ID NO 67

LENGTH: 8
                                                              APPLICANT: May, Michael J
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathry
APPLICANT: Phillips, Kathry
APPLICANT: Hanig, Gerhard
TITLE OF INVENTION: ANTI-INFLAWMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/641,260
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 59
LENGTH: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:NEMO binding; OTHER INFORMATION: sequence
US-09-847-946A-59
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Sequence 59, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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Use Object 1947-946-36

Usequence 30, Application Us/09847946A

Sequence 30, Application Us/09847940

SEQUENCE 30, Application No. Use 102001005499A1

SEQUENCE 30, Application No. Use 102001005499A1

APPLICANT: Phillips, Kathry
APPLICANT: Handis, Wark A

APPLICANT: Handis, Wark A

APPLICANT: Handis, Wark A

APPLICANT: Handis, Wark A

APPLICANT: Handis, Wark A

APPLICANT: Handis, Wark A

APPLICANT: Handis, Wark A

APPLICANT: Handis, Wark A

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APPLICANT: Handis, Wark A

APPLICANT: Handis, Wark A

APPLICANT: Handis, Wark A

APPLICANT: Handis, Wark A

APPLICANT: Handis, Wark A

MARK A

SEQUENCE SEQ ID NOS 2, 100 69-22

SEQ ID NO SEQ ID NOS 2, 100 69-22

SEQ ID NO SEQ ID NOS 2, 100 69-22

SEQ ID NO SEQ ID NOS 2, 100 69-22

SEQ ID NO SEQ ID NOS 2, 100 69-22

SEQ ID NO SEQ ID NOS 2, 100 69-22

SEQ ID NO SEQ ID NOS 3, 100 69-22

SEQ ID NO SEQ ID NOS 3, 100 69-22

MARCHES PECHING NAME A

APPLICANT: HANDIS SEQUENCE

ON HERBORY APPLICANTON NAMES IN USO 69-24-3-66

A APPLICANT: HANDIS SECRET PELLIS

SEQUENCE SEQ ID NOS 3, 100 69-24-3-66

A APPLICANT: HANDIS SECRET PELLIS

SEQUENCE SEQ ID NOS 3, 100 69-24-3-66

MARCHES PECHING NAMES SECRET PELLIS

SEQUENCE SEQ ID NOS 3, 100 69-24-3-66

SEQ ID NOS 5, 100 89-24-3-66

SEQ ID NOS 5, 100 89-2
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us-09-643-260-5.rapb

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Gaps

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APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
TITLE APPLICATION NUMBER: US/09/847,946A
CURRENT APPLICATION NUMBER: 00/201,261
PRIOR APPLICATION NUMBER: 09/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-08-22
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APPLICANT: Ghosh, Sankar
APPLICANT: Finderis, Mark A
APPLICANT: Philips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 40; DB 11; Length 10; 100.0%; Pred. No. 13;
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CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 00/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SEQ ID NO 60
                          Mismatches
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                                                                                                                                                                                                                                                       Sequence 57, Application US/09847946A Publication No. US20030054999A1
100.0%;
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ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.0
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Matches 6; Conserv
Best Local Similarity
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2 LDWSWA 7
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LENGTH: 10
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; Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
; APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT FILING DATE: 2000-05-02
PRIOR PLILOGATION NUMBER: 09/643,260
PRIOR PLILOGATION NUMBER: 09/643,260
PRIOR PLILOGATION NUMBER: 09/643,260
PRIOR PLILOGATION NUMBER: 09/643,260
PRIOR PLILOGATION NUMBER: 09/643,260
PRIOR PLILOGATION NUMBER: 09/643,260
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 65
LENGTH: 9
                                                                                                                                                                                                                                            APPLICANT: May, Michael J
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
ITILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
ITILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
ITILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 160
SEQ ID NOS: 160
SEQ ID NOS: 160
SEQ ID NO 64
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence:NEMO binding; OTHER INFORMATION: sequence
US-09-847-946A-64
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US-09-847-946A-65
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                                                                                                                         RESULT 10
US-09-847-946A-64
; Sequence 64, Application US/09847946A
; Publication No. US20030054999A1
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 6; Conservative
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                                  LDWSWA
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Gaps

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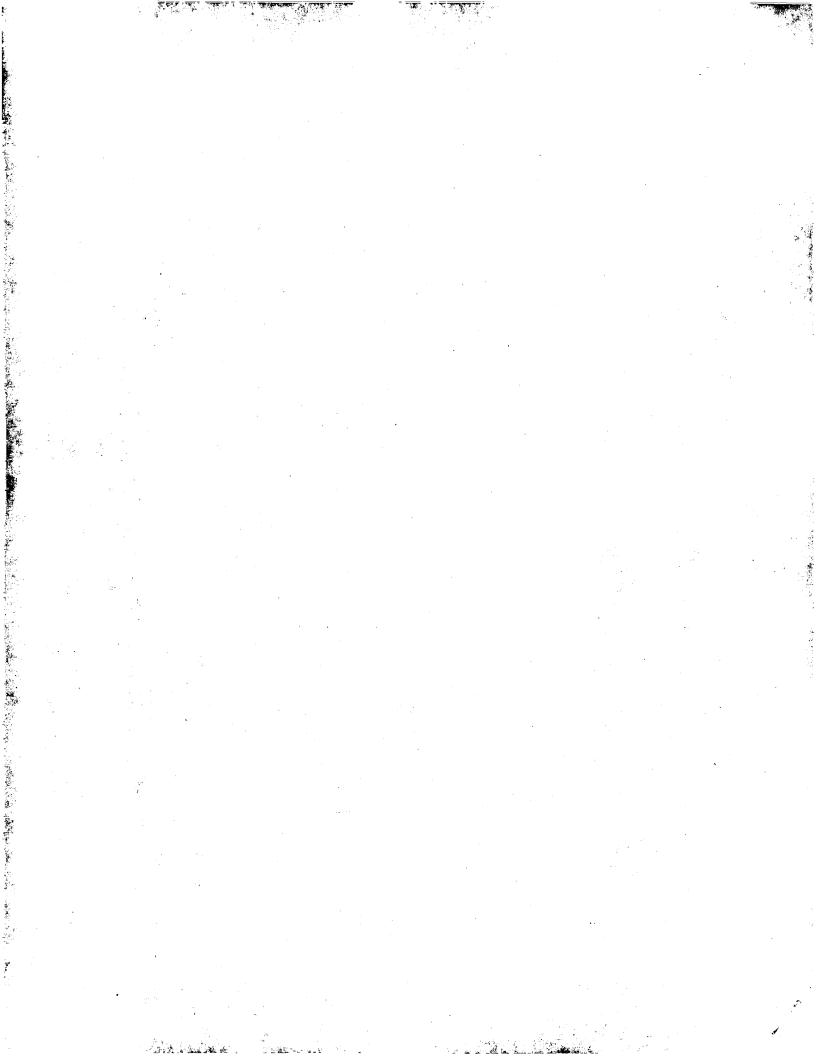
Indels

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                                                                                                                                  Sequence 2, Application US/09847940B
Patent No. US20020156000al
GENERAL INFORMATION:
APPLICANT: MAY Michael J.
APPLICANT: MAY Michael J.
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
ITLE REFERENCE: PPI-117CP
CURRENT APPLICATION NUMBER: US/09/847,940B
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR PLING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTHARE: Patentin Ver. 2.0
: SOFTHARE: Patentin Ver. 2.0
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; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-2
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                        100.0%; Score 40; DB 11; Length 10; 100.0%; Pred. No. 13;
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ORGANISM: Artificial Sequence
                       Query Match
Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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2 LDWSWA 7
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US-09-847-946A-60
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US-09-847-940B-2
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90.0%; Score 36; DB 10; Length 6;

Query Match

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Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 1 LDWSW 5
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Db 1 LDWSW 5
Search Completed: February 18, 2004, 15:41:55
Job time: 16.7529 secs
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February 18, 2004, 14:09:39; Search time 17.3684 Seconds (without alignments) 89.145 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. pp_organelle:*
sp_phage:*
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sp_plant:*
sp_rodent:*
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Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Descript
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Description	QBacrs streptomyce QBixkB homo sapien QBits mus musculu QBcab7 homo sapien QBcyu6 mus musculu QBbctv6 homo sapien QBbgd2 mus musculu QBbwg8 oncorhynchu QBwwg9 oncorhynchu QBowg9 oncorhynchu QBowg9 oncorhynchu QBowg9 oncorhynchu QBowg9 oncorhynchu QBowg9 oncorhynchu QBowg9 oncorhynchu QBowg9 oncorhynchu QBowg9 oncorhynchu QBowg9 oncorhynchu QBowg9 oncorhynchu QBowg9 oncorhynchu QBowg9 oncorhynchu QBowg9 oncorhynchu QBowg9 oncorhynchu QBowg9 oncorhynchu QBowg9 oncorhynchu QBowg9 oncorhynchuchu QBowg9 oncorhynchuchu
SUMMARIES	Q9ACR5 QB1XKB QB1TT9 QB1TT7 Q9CYU6 Q9BTV6 Q9BQD2 Q9BQD2 Q9BAXU2 Q9BAXU2 Q9BAXU2 Q9BAXU2 Q9BAXU2 Q8BAXU2 Q8BAXU2 Q8BAXU2 Q8BAXU2 Q8BAXU2 Q8BAXU2 Q8BAXU2 Q8BAXU2 Q8BAXU2 Q8BAXU2
DB	1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
% Query Match Length DB	205 227 227 452 452 477 48 108 1108 1108 1329 48 236 236 274
% Query Match	922.55 922.55 922.55 922.55 922.55 922.55 922.55 922.55 922.55
Score	444444MWWWWWWWWW
esult No.	1 2 6 4 8 0 6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

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2 Q9XBS7	16 Q8FRF1	10 050002	10 Q9F1S0	10 Q8GYG3	6 Q95KV1	11 Q8CBT3	16 069735	6 Q95KV0	17 Q97UH8	16 Q9AAZ6	2 Q9AQH0	10 Q9XGZ2	16 Q8ZC91	16 Q9L060	2 Q9X3P6	2 Q9AQG4	2 Q9X3P5	2 Q9L4X2	6 Q8SPL6	6 Q8MJT3	11 Q921P9	16 QBNS33	16 Q8FR42	6 Q9TT79	16 Q98AG0	2 Q9KJ20	5 Q8SSN6	17 027025
310	310	358	703	703	740	745	747	756	803	889	966	1005	1139	1345	1426	1751	1770	5435	49	161	161	200	241	323	562	565	296	919
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36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	32	32	35	35	35	35	32	32	35	35
17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

ap archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_inverte*
sp_mammal:*
sp_mhc:*

Database :

ACRS. Q9ACRS. Q9ACRS. Q9ACRS. Q9ACRS. Q9ACRS. Q9ACRS. Q9ACRS. Q9ACRS. Q9ACRS. Q1-UUN-2001 (TrEMBLrel: 17, Created) O1-OCT-2002 (TrEMBLrel: 22, Last annotation update) O1-OCT-2002 (TrEMBLrel: 22, Last annotation update) O1-OCT-2002 (TrEMBLrel: 22, Last annotation update) O1-OCT-2002 (TrEMBLrel: 22, Last annotation update) O1-OCT-2002 (TrEMBLrel: 32, Last annotation update) O1-OCT-2002 (TrEMBLrel: 32, Last annotation update) O1-OCT-2002 (TrEMBLrel: 32, Last annotation update) O1-OCT-2002 (TrEMBLrel: 32, Last annotation update) O1-OCT-2002 (TrEMBLrel: 32, Last annotation update) O1-OCT-2002 (TrEMBLrel: 32, Last annotation update) O1-OCT-2002 (TrEMBLrel: 32, Last annotation update) ONEL 2004 (SPI) ONEL	PRT; 205 AA.	Creat	Last	, Last annotation update) nes	233.			Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;	Streptomycetaceae; Streptomyces.			2000063.		Cerdeno-Tarraga Am., Challis G.L.,	Harber D. Bateman A. Brown S. Chandra G. Chen C.W., Collins M.,	e A., Hidalgo J., Hornsby T., Howarth S.,	rke L., Murphy L., Oliver K., O'Neil S.,	am M.A., Rutherford K., Rutter S.,	arp S., Squares R., Squares S., Taylor K.,	Woodward J., Barrell B.G., Parkhill J.,		"Complete genome sequence of the model actinomycete Streptomyces		1	mid: Complete proteome.		5; Fred. NO. 75; 0; Mismatches 0; Indels 0; Gaps
		(TrEMBLrel.	(TrEMBLrel.			tomyces coelicolor.	id SCP1.	ria; Actinobacteria;	tomycineae; Streptomy	TaxID=1902;	 INCE FROM N.A.	N=A3(2); NE_21006410. DubMod=1	The stage of the s	ey S.D., Chater K.F.,	on N.K., James A.D., r D., Bateman A., Bro	n A., Fraser A., Gob	CH., Kieser T., La	nowitsch E., Rajandre	r K., Saunders D., Sl	in T., Wietzorrek A.,	od D.A.;	lete genome sequence	COLOI A3(2).";	. (2022) (#1-1#1:(1#)	herical protein, Dlas	NCE 205 AA; 23051	ğ

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RESULT 2 Q81XK8

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STRAINS-CS7BL/6J; TISSUE-Embryo;

KM MEDLINE-21085660; PubMed-11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruell P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruell P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruell B., Lewis S., Matsuo M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
                                                                                                                                                                                                                                                                                   TISSUB-placenta;
Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suzai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Saito K., Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masubo Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; Susaki N., Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, BC01735; AAH17335. 1. -.

EMBL, AK075115; BAC11411.; -.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                              Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
2810443J12Rik protein (Mitochondrial ribosomal protein L41
                                                                                                                                                                                                    Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS00678; WD REPEATS_1; 2.

PROSITE; PS50294; WD_REPEATS_R5_1.

PROSITE; PS50294; WD_REPEATS_REGION; 1.

HYPOCHAELICAL protein; Repeat; WD repeat.

SEQUENCE 452 AA; 50575 WW; B79D255E38096733 CRC64;
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0;
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                  Hypothetical protein FLJ90634.
                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                            Homo sapiens (Human)
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Q9CYU6
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STRAIN=NOD; TISSUE=Thymus;
MEDLINE=223546683; PubMed=12466851;
The FANTOM Consortium
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to hypothetical protein BC017335.
Home sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 4; Length 227; Pred. No. 82; 0; Indels
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC040173; AAH40173.1; -.
Hypothetical protein.
SEQUENCE 227 AA; 25487 MW; F11A71EA57062A05 CRC64;
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Nature 420:563-573(2002).
BENEL; AKO87998; BAC400841.;
SEQUENCE 355 AA; 40183 WW; FEF8546127402D58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Mitcchondrial ribosomal protein L41 homolog.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
                                                                                                                                 227 AA.
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01-MAR-2003 (TrEMBLrel. 23, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
                    10 ADWSWL 15
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TISSUE=Brain;
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NCBI_TaxID=8022
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Q90WQ8
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WEDLINE-2234683; PubMed=1246681;
The FANTOM COMSONITUM,
The FANTOM COMSONITUM,
The FANTOM COMSONITUM,
The FANTOM COMSONITUM,
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
To 7.70 full-length CONNA.";
To 7.70 full-length CONNA.";
The Mebl; AK013297; BAB28775.1; ---
REMBL; AK013297; BAB28775.1; ---
REMBL; AK013297; BAB28775.1; ---
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REMBL; AK013297; BAB28775.1; ---
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Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming Wynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                   Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         484 AA.
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Best Local Similarity 100.
Matches 6; Conservative
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Matches 6; Conserv
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MEDINNE=22354683; PubMed=12466851;
The FANTOM Consortium,
The RANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK049157; BAC31480.1; -.
EMBL, AK049078; BAC33535.1; -.
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"Molecular cloning, gene organization and expression of rainbow trout
(Oncorhynchus mykiss) inducible nitric oxide synthase (1NOS) gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapa
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.5%; Score 37; DB 11; Length 154; 83.3%; Pred. No. 1.6e+02; ive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 AA; 16524 MW; A526724D4074D888 CRC64;
                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein (Fragment).
Mus musculus (Mouse).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Inducible nitric oxide synthase (EC 1.14.13.39).
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  154 AA
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EMBL; AJ300555; CAC83069.1; --
InterPro; IPR001094; Flavdoxin_like.
InterPro; IPR001205; FAD binding.
InterPro; IPR001205; Flavdoxin_like.
InterPro; IPR001709; FPW cyt_redctse.
InterPro; IPR001709; FPW cyt_redctse.
InterPro; IPR001403; Oxred FAD/NAD(P).
Pfam; PF00175; FAD_binding_1; 1.
Pfam; PF00175; FAD_binding_1; 1.
Pfam; PF00175; NAD_binding_1; 1.
Pfam; PF00175; FAD_binding_1; 1.
Pfam; PF00175; FAD_binding_1; 1.
Pfam; PF00175; FAD_binding_1; 1.
Pfam; PF00175; PR001509; FLAVODOXIN.
PRINTS; PR00175; PRCR.
PROSITE: PS60001; NOS; 1.
Oxidoreductase.
SEQUENCE 1083 AA; 123060 MW; 53E4DFD
PRT;
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PRELIMINARY;
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SEQUENCE
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Q8VKB2;
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Wang T., Bols N., Secombes C.J.;

"Two Promoters of inducible nitric oxide synthase gene exist in

rainbow trout evidenced by studies with RTG-11 and RTG-2 cell lines.";

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ295230; CAC82807.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang T., Ward M., Grabowski P.S., Secombes C.J.; Mang T. Ward M., Grabowski P.S., Secombes C.J.; Medecular cloning, gene organization and expression of rainbow trout (Oncorhynchus mykiss) inducible nitric oxide synthase (iNOS) gene."; J. Biochem. 358:747-755(2001).
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                     Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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Score 37; DB 13; Length 1083;
Pred. No. 1e+03;
1; Mismatches 0; Indels
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                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Inducible nitric oxide synthase (EC 1.14.13.39).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                           PRT; 1083 AA.
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InterPro; IPR003097; FAD_binding.
InterPro; IPR001094; Flavdoxin like.
InterPro; IPR001226; Flavdoxin.
InterPro; IPR001709; FPN cyt redctse.
InterPro; IPR004030; NO synthase.
InterPro; IPR004030; NO synthase.
Ffam; PF00667; FAD_binding_1; 1.
Pfam; PF00258; flavodoxin; 1.
Pfam; PF00175; NAD_binding_1; 1.
       92.5%;
83.3%;
                               5; Conservative
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       Query Match
Best Local Similarity
Matches 5; Conserv
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Q8AXU2
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Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Mutphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simonds M., Skelton J., Squares R., Barrell B.G.;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                      Score 37; DB 13; Length 1100;
Pred. No. 1.1e+03;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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SEQUENCE 1329 AA, 146129 MW, F8A85758D600E7D8 CRC64,
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                                                                                                                      1100 AA; 125079 MW; E4763388C97D608F CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein ML2535.
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Last annotation update)
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83.3%; Pred. No. 1.3e+03;
ive 1; Mismatches 0;
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Nature 409:1007-1011(2001).
EMBL; AL583926; CAC32066.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1329 AA
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InterPro, IPR002543; FtsK Spoilie.
Pfam; PF01580; FtsK Spoilie, 2.
SMART; SM00382; AAA; 3.
Pfam; PF02898; NO synthase; 1. PRINTS; PR00369; FLAVODOXIN. PRINTS; PR00371; FPNCR.
                                                                                                                                                                      92.5%;
83.3%;
                                                                                                                                             Query Match
Best Local Similarity 83.30,
5; Conservative
                                                                      PS60001; NOS; 1.
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                                                                                                                                                                                                                                                                                                                    419 ADWAWL 424
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NCBI_TaxID=80339
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SEQUENCE
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                                 SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
Fleisechmann R.D., Alland D.; Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09AQG7;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Glycosyl hydrolase 6 (Fragment).
Caldicellulosiruptor sp. Tok7B.1.
Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                   Gaps
                                                                                                                       "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AE006980; AAK45193.1; ---
TIGR; MT0946; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-22067395; PubMed=12073090;

MEDLINE-22067395; PubMed=12073090;

Goodgebuur F., Fowler T., Phillippa J., van der Kley P.,

van Solingen P., Dankmeyer L., Power S.D.;

"Cloning and relational analysis of 15 novel fungal endoglucanases

from family 12 glycosyl hydrolase.";

Curr. Genet. 41:89-98(2002).

EMBL; AF435065; AAM77708.1; -.

INCEPTOP, IRR002594; Glyco. hydro_12.

Prodom; PD004316; Glyco. hydro_12.1.

Prodom; PD004316; Glyco. hydro_12.1.

SEQUENCE 236 AA; 26024 MW; C3DBA7E33F0C41D8 CRC64;
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Hypocreales, Bionectriaceae, Bionectria.
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                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 48 AA; 5265 MW; COBFA9D6AA2EF8DF CRC64;
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Last sequence update)
Last annotation update)
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 5; Conservative
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Matches 5; Conservative
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           NCBI_TaxID=1773;
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CEL12C.
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EMBL, AP005276; BAB98193.1; Interpro, IPR000760; Inositol.P.
Interpro, IPR0459; inositol.P.
Complete protecome.
SEQUENCE 273 AA; 29072 MW; C132E2C67E0BBA4D CRC64;
                                                                  Gibbs M.D., Reeves R.A., Farrington G.K., Anderson P., Williams D.P., Bergquist P.L.;
Bergquist P.L.;
"Multidomain and multifunctional glycosyl hydrolases from the extreme thermophile Caldicellulosiruptor isolate Tok7B.1.";
Curr. Microbiol. 40:333-340(2000).
EMBL; AF078040; AAK06391.1; -.
Interpro; IPR001956; CBD_3.
Probon; PD001947; CBD_3: 1.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol
CGL0800.
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.0%; Score 36; DB 16; Length 273; 83.3%; Pred. No. 3.8e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 90.0%; Score 36; DB 2; Length 261; Similarity 100.0%; Pred. No. 3.6e+02; 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             261 AA; 28759 MW; 4771744A26A6AE04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
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Job time : 18.3684 secs
                         STRAIN=Tok7B.1;
MEDLINE=20171169; PubMed=10706665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.3%,
Conservative 5; Conservative
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Matches 5; Conserv
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SEQUENCE FROM N.A.
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us-09-643-260-4.rsp

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

February 18, 2004, 13:39:39; Search time 3.55263 Seconds (without alignments) 79.423 Million cell updates/sec

US-09-643-260-4 40

1 ADWSWL 6 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q92091 oncorhynchu									Q07583 influenza a			Q60680 m inhibitor	O14920 homo sapien	O88351 mus musculu		P10474 c endogluca		P79209 ovis aries	P50900 clostridium	P70313 mus musculu	P29474 homo sapien	P29473 bos taurus	Q28969 sus scrofa	Q57596 methanococc	P04395 escherichia	Q9rw68 deinococcus	P46810 mycobacteri	Q58617 methanococc	8 klebs	6	P29477 mus musculu	Q06518 rattus norv	
SUMMARIES	ID	NOS2 ONCMY	NRAM_IADBU		NRAM_IADH2	NRAM IADM2	NRAM_IADU3	NRAM IAGFN	NRAM_IAHGD	NRAM IAHJI	NRAM IAMAE	NRAM IATKL	IKKA HUMAN	IKKA MOUSE			IKKB_RAT	GUNB_CALSA	RFBC_MYXXA	NOS3_SHEEP	GUX2_CLOSR	NOS3_MOUSE	NOS3 HUMAN	NOS3_BOVIN		Y132 METJA		Y801_DEIRA		YC20 METJA				NOS2_RAT	
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dr	Query Match		90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	87.5	87.5	87.5	87.5	87.5	87.5	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	85.0	
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EMBL; X97013; CAA65736.1; -.
HSSP; P29477; 1NOS.
InterPro; IPR001094; FAD binding.
InterPro; IPR001094; Flavdoxin like.
InterPro; IPR001226; Flavodoxin.
InterPro; IPR004030; NO synthase.
Pfam; PF00667; FAD binding_1; 1.
Pfam; PF00258; flavodoxin; 1.

060591 homo sapien 054705 cavia porce p35228 homo sapien P22533 caldocellum P22534 caldocellum P22543 caldocellum P225534 caldocellum P24550 cacies 034453 bacillus su P27250 cacherichia 03383 penicillium 013911 schizosacch	
NS2D HUWAN NOS2_CAVPO NOS2_CAVPO MANB_CALSA GUNA_CALSA GUNA_CALSA GUNA_CALSA GUNA_CALSA C1B2_SHEEP NOSO_BACSU NOSO_BACSU NOSO_BACSU PGLR_PENGR POKI_SCHPO NRAM_IAQIT	
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ALIGNMENTS

RESU	RESULT 1
T C	NOSC ONCAY STANDARD: PRT: 470 AA.
	0000
占	(Rel. 39,
Ü	Last annotation update)
DΕ	Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)
DΕ	(Inducible NOS) (iNOS) (Fragment).
S	NOS2.
SO	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
ဗ	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
႘	Actinopterygii; Neopterygii; Teleostei; Euteleostei;
႘	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
ŏ	NCBI_TaxID=8022;
RN	[1]
RP.	
æ	Grabowski P.S., Laing K.J., Hardie L., Macguigan F., Ralston S.,
æ	
RT	"Detection of mRNA for a nitric oxide synthase in macrophages and
RI	gill of rainbow trout challenged with an attenuated bacterial
RT	pathogen.";
Z	(In) Moncada S., Stamler J., Gross S., Higgs E.A. (eds.);
Z.	4th International meeting on the biology of nitric oxide, Amelia
Z :	Island, Florida, Sep. 1995, pp.10:48-48, Portland Press,
Z :	Brookfield (1996).
ខ្ល	-I- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
មូខ	WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO
ဗ ဗ	MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.
) (-!- CAIALYTIC ACTIVITY: L-arginine + N NADRH + M O(2) = cicruiline +
ဗ (
ខ្ល	-!- COFACTOR: HEME, BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
3 8	TELEMENTONOBLOVIENTN (BR44) WALCH MAI SIABILIZE THE DIMEKIC FORM OF
3 6	IND BUZING (BI SUBLIMENTIL)
3 5	
88	-!- SUBLUIT: Homodimer (By similarity)
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Ü	
3 5	
ខ	This SWISS-PROT entry is copyright. It is produced through a collaboration
႘	between the Swiss Institute of Bioinformatics and the EMBL outstation -
Ü	the European Bioinformatics Institute. There are no restrictions on its
႘	use by non-profit institutions as long as its content is in no way
႘	atement is not removed. Usage by and for commerc
ខ	entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virology 193:868-876(1993).

-!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.
-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-56)-, alpha-(2-8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
                                                                                                                                                                                 Gaps
                                                                                            (PYRIMIDINE PART) (BY SIMILARITY). (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93212550; PubMed=8460490;
Saito T., Kawaoka Y., Webster R.G.;
"Phylogenetic analysis of the N8 neuraminidase gene of influenza A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION.
-i- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                 o;
                                                                     CALMODULIN-BINDING (POTENTIAL).
                                                                                                                                                         DB 1; Length 470;
                                                                                                                                                                                                                                                                                                                                                                          Influenza A virus (strain A/Duck/Burjatia/652/88).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
        PRINTS; PRO0369; FLAVODOXIN.
PROSITE; PS60902; FLAVODOXIN LIKE; 1.
PROSITE; PS60001; NOS; PARTIĀL.
Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme.
                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANCHOR (BY SIMILARITY).
HYPERVARIABLE STALK REGION.
HEAD OF NEURAMINIDASE.
BY SIMILARITY.
                                                                                                                                 40B6717EE500B64D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probom; P0000431; Glyco hydro 34; 1.
Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
88-FEB-2003 (Rel. 41, Last annotation update)
Neuraminidase (EC 3.2.1.18).
                                                                                  FLAVODOXIN-LIKE. FMN (PYRIMIDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
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Pred. No. 82;
0; Mismatches
                                                                                                                                                                                                                                                                                          470 AA
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Pfam; PF00064; neur; 1.
Pfam; PF02898; NO synthase; 1.
                                                                                                                                 53329 MW;
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Best Local Similarity 83.3%,

Best Local Similarity 63.3%,
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307
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470 AA;
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Q07570;
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-!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.

-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
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BEDLINES-29212550;
Saito T., Kawaoka Y., Webster R.G.;
"Phylogenetic analysis of the N8 neuraminidase gene of influenza A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SÜBÜNIT: Homotetramer.
-!- SÜBÜLÜLAR LOCATION: VIRAL MEMBRANE. FORMS A MÜSHROOM-SHAPED
- SÜBÜLÜLAR SÜREGEG OF THE VIRION.
-!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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HYPERVARIABLE STALK REGION.
HEAD OF NEURANINIDASE.
BY SIMILARITY.
BY SIMILARITY.
CONTRACTOR (CLONG. COTENT)
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Pred. No. 82;
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                                                                                                         (GLCNAC. . .)
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(GLCNAC. . .)
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N-LINKED (GLCNAC. .
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01-FEB-1995 (Rel. 31, Last sequence update)
20-FEB-2003 (Rel. 41, Last annotation update)
Neuraminidase (EC 3.2.1.18).
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NCBI_TaxID=38957;
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Pfam; PF00064; neur; 1.
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                                                                                                                                                                                                                                                                                  MW;
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HSSP; P06820; 2BAT.
275
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TRANSMEM 7 38
                                                                                                                                                                                                                                                                             470 AA;
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Length 470;

DB 1;

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Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                 Virology 193:868-876(1993).

-!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.
-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-56)-, alpha-(2-8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
                                                                                                                                                                                                                                                                                                                                     MEDLINE=93212520; PubMed=8460490;
Saito T., Kawaoka Y., Webster R.G.;
"Phylogenetic analysis of the N8 neuraminidase gene of influenza A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBUNIT: Homotetramer.
-1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION.
-1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                  Length 470;
                                                                                                                                                                                                                                                                            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
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                           52070 MW; 169AB89FBE8006DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ElClD3E2C650B93C CRC64;
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                                                                                                                                                                                                                                                              Influenza A virus (strain A/Duck/Hokkaido/8/80).
                                                  DB 1;
                                                                                                                                                                                                     (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 41, Last annotation update)
                                                              Pred. No. 82;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                 90.0%; Score 36;
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Hydrolase; Glycosidase; Glycoprotein
TRANSMEM 7
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Pfam; PF00064; neur; 1.
                                                    100.0%; FAC
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   293 2
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470 AA;
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470 AA;
                                                            Local Similarity
                                                                                                                      453 ADWSW 457
                                                                                                                                                                                                                                                                                                   NCBI_TaxID=11358;
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Q07572;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VITOTOGY 193:868-876(1993).

-I-FUNCTION: Removes the terminal stalic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.

-I-CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->6)-glycosidic linkages of terminal stalic residues in oligoaccharides, glycoproteins, glycolipids, colominic acid and synthetic guberrates.
                                             Gaps
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Saito T., Kawaoka Y., Webster R.G.;
"Phylogenetic analysis of the N8 neuraminidase gene of influenza A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION.
-:- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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                                               Indels
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ANCHOR (BY SIMILARITY).
HYPERVARIABLE STALK REGION.
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                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuraminidase (EC 3.2.1.18).
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Score 36;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000431; Glyco hydro 34; 1.
Hydrolase; Glycosidase; Glycoprotein
TRANSMEM 7 38 ANCHOR
  90.00,
100.0%; Pre-
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HSSP; P06820; 2BAT.
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Matches 5; Conservative
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NRAM_IADM2
ID NRAM_IADM2
AC Q07573;
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                                                                                                                                                                                                                                                                     Virology 193:868-876(1993).

-!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.
-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-56)-, alpha-(2-8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and symmetry contains.
                                                                                                                                                                                                                          MEDLINE=93212520; PubMed=8460490;
Saito T., Kawaoka Y., Webster R.G.;
"Phylogenetic analysis of the N8 neuraminidase gene of influenza A
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82;
                                                                                                                                                       Influenza A virus (strain A/Duck/Ukraine/1/61).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
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HYPERVARIABLE STALK REGION.
HEAD OF NEURAMINIDASE.
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Bran; PF00064; neur; 1.
ProDom; PD000431; Glyco hydro 34; 1.
Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
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N-LINKED (GLCNAC. . .)
                                                                                                  01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuraminidase (EC 3.2.1.18).
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100.0%; Pred
0; N
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                                                                             STANDARD;
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470 AA;
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Best Local Similarity
                     453 ADWSW 457
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                          NCBI_TaxID=11374;
Ŋ
                                                                             NRAM IADU3
Q07599;
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NRAM_IADU3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chains of the host cell surface proteins and from the viral chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.

-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alpha-(2-b)-, alph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saito T., Kawaoka Y., Webster R.G.; "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SÜBÜNIT: Homotetramer.
-!- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MÜSHROOM-SHAPED SPIKE ON THE SÜRFACE OF THE VIRION.
-!- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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                                                                                                                                                                                                                                                                 Influenza A virus (strain A/Guinea fowl/New York/4-3587/84).
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Pred. No. 82;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                    Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
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Hydrolase; Glycosidase; Glycoprotein; Transmembrane.

TRANSMEM 7 38 ANCHOR (BY STMILADITY)
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                                                                                                              Last sequence update)
Last annotation update)
470 AA
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MEDLINE=93212520; PubMed=8460490;
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100.0%; Pre
                                                                       (Rel. 31, Created)
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HSSP; P06820; 2BAT.
                                                                                                                                                                                         Neuraminidase (EC 3.2.1.18)
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                                                                       01-FEB-1995
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28-FEB-2003
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                                                                                                                                                                                                                                                                                  ology 193:868-876(1993).

FUNCTION: Removes the terminal stalic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.

CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal stalic residues in eligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION. SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                      SEQUENCE FROM N.A.

BEDLINE-23112520, PubMed=8460490;
Saito T., Kawaoka Y., Webster R.G.;
"Phylogenetic analysis of the N8 neuraminidase gene of influenza."
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HYPERVALIALE STALK REGION.
HEAD OF NEURAMINIDASE.
BY SIMILARITY.
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                                                                                         Influenza A virus (strain A/Herring gull/DE/677/88).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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Fam, PF00064; neur; 1.
ProDom; PD000431; Glyco_hydro_34; 1.
Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
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82;
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                   Last sequence update)
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28-FEB-2003 (Rel. 41, Last 8
Neuraminidase (EC 3.2.1.18)
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                                                                                                                                                                                                                                                                                   -i. FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.
-i. CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
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                                                                                                                             SEQUENCE FROM N.A.
BIRDLINES-2212520; Pubmed-8460490;
Saito T., Kawaoka Y., Webster R.G.;
"Phylogenetic analysis of the N8 neuraminidase gene of influenza A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SÜBUNIT: Homotetramer.
SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
SPIKE ON THE SURFACE OF THE VIRION.
SIMILARITY: BELONGS TO PAMILY 34 OF GLYCOSYL HYDROLASES.
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82;
                      Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses; Influenzavirus A.
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Influenza A virus (strain A/Equine/Jillin/1/89)
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01-FRB-1995 (Rel. 31, Last sequence update)
228-FEB-2003 (Rel. 41, Last annotation update)
Neuraminidase (EC 3.2.1.18).
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ANCHOR (BY
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                                                                                                                                                                                                                                       viruses.";
Virology 193:868-876(1993).
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293
398
470 AA;
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                                                          VIOLOGY 193:868-876(1993).

-!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.

-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->6)-, oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
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O1511; O14666; Q13132; Q92467;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2003 (Rel. 42, Last sequence update)

16-OCT-2003 (Rel. 42, Last sequence update)

17-SEP-2003 (Rel. 42, Last sequence update)

Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)

(I kappa-B kinase alpha) (IRBKA) (IKK-alpha) (IKK-A) (IkappaB kinase)

(I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKBIKA).
Saito T., Kawaoka Y., Webster R.G.; "Phylogenetic analysis of the .N8 neuraminidase gene of influenza A
                                                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION.
-i- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 82;
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Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
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TISSUE=T-cell;
MEDLINE=97386461; PubMed=9244310;
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                                                                                                                                           Virology 193:868-876(1993).

-!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.

-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->6)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoptoteins, glycolipids, colominic acid and synthetic substrates.
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                                                               MEDLINE=93212520; PubMed=8460490;
Saito T., Kawaoka Y., Webster R.G.;
"Phylogenetic analysis of the N8 neuraminidase gene of influenza
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HYPERVARIABLE STALK REGION.
HEAD OF NEURAMINIDASE.
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BY SIMILARITY.
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Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
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01-FEB-1995 (Rel. 31, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
Neuraminidase (EC 3.2.1.18).
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Influenza A viruses; Influenzavirus A.
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Pfam; PF00064; neur; 1.
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MEDLINE=93212520; PubMed=8460490;
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HSSP; P06820; 2BAT.
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470 AA;
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Matches 5; Conserv
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  NCBI_TaxID=38965;
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R GO; GO:0005737; C:Cytoplasm; TAS.

GO; GO:0007349; F:RappaB Kinase activity; TAS.

R GO; GO:0007349; F:RappaB Kinase activity; TAS.

R GO; GO:0007352; P:I-KappaB phosphorylation; TAS.

GO; GO:0007252; P:I-KappaB phosphorylation; TAS.

GO; GO:00007252; P:I-KappaB phosphorylation; TAS.

GO; GO:00007252; P:I-KappaB phosphorylation; TAS.

R GO; GO:00007252; P:I-KappaB phosphorylation; TAS.

R InterPro; IPR001249; Prot Kinase.

R InterPro; IPR001245; Tyr_Dkinase.

R PRUNTS; PR00109; TYRKINASE.

R PRODOM; PROOIDOU; PROC Linase; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS001109; PROTEIN KINASE ATP; 1.

R PROSITE; PS001109; PROTEIN KINASE DOM; 1.

R TRANSFERSE: SES0011; PROTEIN KINASE DOM; 1.
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EMBL; AF009225; AAC51671.1; -.
EMBL; AF080157; AAD08996.1; -.
EMBL; U2251.3 AAC50713.1; -.
HSSP; Q63450; 1A06.
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DOMAIN 15
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    Nemoto S., Dibonato J.A., Lin A.; "Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase 1 and NP-kappaB-inducing kinase."; Mol. Cell. Biol. 18:7336-7343(1998).
                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLLINE=97394468; PUDNed=9252186;
DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
"A cytokine-responsive IkappaB kinase that activates the transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 32-745 FROM N.A.
TISSUB=Cervical carcinoma;
MEDLINE=96258427; PubMed=8777433;
Connelly M.A., Marcu K.b.;
"CHUK, a new member of the hellx-loop-helix and leucine zipper families of interacting proteins, contains a serine-threonine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Delhase M., Hayakawa M., Chen Y., Karin M.;
"Poolstive and negative regulation of IkappaB kinase activity through
IKKDeta subunit phosphorylation.";
Science 284:309-313(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98188283; PubMed-9520446;
Ling L., Cao Z., Goeddel D.V.;
"NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
                                                                                                                                                                                                                                      SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179
                                                                                                                                                                                                                                                                     TISSUB-Cervical carcinoma;
MEDLINE-98008813; PubMed-9346484;
Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
Mi J. W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
IIK-1 and IKK-2: cytokine-activated IkappaB kinases essential for NF-kappaB activation.'
Science 278:860-866(1997).
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Hu M.C.-T., Wang Y.-P.;
"IkappaB Kinase-alpha and -beta genes are coexpressed in adult and
embryonic tissues but localized to different human chromosomes.";
Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.; "Identification and characterization of an IkappaB kinase."; Cell 90:373-383(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "NF-kappaB activation by tumour necrosis factor requires the Akt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jobin C., Sartor R.B.;
"The I kappa B/NF-kappa B system: a key determinant of mucosal
Inflammation and protection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99413720; Pubmed=10485710;
Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             catalytic domain.";
Cell. Mol. Biol. Res. 41:537-549(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99212141; PubMed=10195894;
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MEDLINE-99038238; PubMed=9819420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             serine-threonine kinase.";
Nature 401:82-85(1999).
                                                                                                                                                                                           Nature 388:548-554(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 222:31-40(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                       factor NF-kappaB
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BY SIMILARITY.

PHOSPHORYLATION (BY PKB/AKT1).

PHOSPHORYLATION (BY MAP3K14).

T->A: LOSS OF PHOSPHORYLATION AND

DECREASE OF KINASE ACTIVITY.

K->A: LOSS OF KINASE ACTIVITY.

K->A: LOSS OF WINASE ACTIVITY.

K->A: LOSS OF PHOSPHORYLATION.

44 44 176

PROTEIN KINASE. LEUCINE-ZIPPER (POTENTIAL)

NEMO-BINDING. ATP (BY SIMILARITY). ATP (BY SIMILARITY).

302 476 743 29 44 144 176 23

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 when dephosphorylated.
-!-SUBUNIT: Preferentially found as a heterodimer with IKK-beta but also as an homodimer. Directly interacts with IKK-beta but also as an homodimer. Directly interacts with IKK-GAMMA/NEMO.
Heterodimers form the active complex. The tripartite complex can also bind to MAP3K14/NIK, MEKK1, IKAP and IKB-alpha-P65-P50 complex. A weak interaction with TRAF2 cannot be excluded. Part of a complex composed of NCOA2, NCOA3, IKKB, IKBKG and CREBBP.
-!-SUBCELLULAR LOCATION: Cytoplasmic.
-!-TISSUE SPECIFICITY: Widely expressed.
-!-PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by MEKK1, and dephosphorylated by PP2A. Autophosphorylated.
-!-SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
IKAPPAB KINASE SUBFAMILY.
 "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator activity by I kappa B kinase.";
Mol. Cell. Biol. 22:3549-3561(2002).
-I- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NR-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates
 [11]
SUBINIT OF A COMPLEX CONTAINING CREBBP, NCOA2; NCOA3; IKKB AND IKBKG.
MEDLINE=21968797; Pubmed=11971985;
Wu R.C., Oin J., Habhimoto Y., Wong J., Xu J., Teai S.Y., Teai M.J.,
O'Malley B.W.;
 NCOA3. ENZYME REGULATION: Activated when phosphorylated and inactivated
Physiol. 278:C451-C462(2000)
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 STRAIN-CSTREAGO, PubMed=1117851,

MEDLINE=21085660, PubMed=1117851,

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Shinagawa A., Shibata K., Kiyosawa H., Adachi J., Pukuda S.,

A Azawa T., Hara A., Nishi K., Kiyosawa H., Kando S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Relischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Kachim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Carninci P., de Bonado M.F.,

Blawe J., Boffelli D., Bojunga N., Carninci P., de Bonado M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 JANATONE (1902X3); (2002X3); (2002X3); (2002X3); (2002X2); (2001 (Rel. 40, Created)); (2002X-2001 (Rel. 40, Last sequence update); (2002X-2003 (Rel. 42, Last annotation update); (2002X-2003 (Rel. 42, Last annotation update); (2002X-2003 (Rel. 42, Last annotation); (2002X-2003 (IKK-A) (IKM-A); (2002X-2003 (IKK-A) (IKM-A); (2002X-2003X-
 STRAIN=BALB/c;
MEDILIE=56044444; PubMed=7558004;
MCK B.A., Connelly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
"CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human
 Gaps
 Connelly M.A., Marcu K.B., "Chur, a new member of the helix-loop-helix and leucine zipper families of interacting proteins, contains a serine-threonine kinase
 S-SE: FULL ACTIVATION.
T-A: NO CHANGE IN PHOSPHORYLATION.
S->A: NO CHANGE IN PHOSPHORYLATION.
E -> G (IN REF. 2).
L -> R (IN REF. 5).
TS -> AY (IN REF. 5).
TS -> D. (IN REF. 5).
TS -> D. (IN REF. 5).
TG -> D. (IN REF. 5).
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 ..
 90.0%; Score 36; DB 1; Length 745; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
 745 AA
 chromosome 10 and mouse chromosome 19."; Genomics 27:348-351(1995).
 Cell. Mol. Biol. Res. 41:537-549(1996).
 PRT;
 STRAIN=BALB/C;
MEDLINE=96258427; Pubmed=8777433;
 SEQUENCE FROM N.A. (ISOFORM 1).
 SEQUENCE FROM N.A. (ISOFORM 1).
 SEQUENCE FROM N.A. (ISOFORM 3).
 84653 MW;
 Conservative
 STANDARD;
 176
179
180
543
604
680
684
 Mus musculus (Mouse)
 180
543
604
679
684
686
 Query Match
Best Local Similarity
 739 DWSWL 743
 catalytic domain."
 NCBI_TaxID=10090;
 2 DWSWL 6
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2
 IKKA MOUSE
 MUTAGEN
MUTAGEN
CONFLICT
CONFLICT
CONFLICT
 CONFLICT
 MUTAGEN
 IKKA_MOUSE
 Matches
SPTFFFFFF
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MEDLINE=99038238; PubMed=9819420; Nemoto S., Dibonato J.A., Lin A.; Nemoto S., Dibonato J.A., Lin A.; Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase l and MP-kappaB-inducing kinase."; Mol. Cell. Biol. 18:7336-7343(1998).
 when dephosphorylated.
SUBUNIT: Preferentially found as a heterodimer with IKK-beta but also as an homodimer. Directly interacts with IKK-gamma/NEMO. Heterodimers form the active complex. The tripartite complex can also bind to MapSXI4/NIK, MEKKI, IKAP and IKR-alpha-P65-P50 complex. A weak interaction with TRAP2 cannot be excluded. Part of a complex composed of NCOA2, NCOA3, IKKB, IKBKG and CREBBP (By
 Name=2; Synonymar=Delta H;
IsoId=Q60680-2; Sequence=VSP_004866, VSP_004867;
Name=3; Synonymas=Delta H;
Name=3; Synonymas=Delta H;
IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;
TISSUE SPECIFICITY: Ubiquitous only for isoform 1, isoforms 2 and 3 are expressed predominantly in brain and T-lymphocytes.
DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by E11, E15 and E17 days. In the limb development, its expression predominates in the limb buds at E12.5 day.
PTHY: PROSPORYJAted by MASTAL4/NIK, ART and to a lesser extent by MEKKI, and dephosphorylated by PP2A. Autophosphorylated.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 MEDILINE=20178139; PubMed=10712233;
Jobin C., Sartor R.B.;
"The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";
Am. J. Physiol. 278:C451-C462(2000).
-!- FUNCTION: Phosphorylates inhibitor/NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor.
 MEDLINE=20198447; PubMed=10733566;
McKenzie F.R., Connelly M.A., Balzarano D., Mueller J.R.,
Geleziunas R., Marcu K.B.;
"Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking
leucine zipper and helix-loop-helix domains reveal that IKKalpha and
IKKbeta have different activation requirements.";
Mol. Cell. Biol. 20:2635-2649(2000).
 MEDLINE-99212141; Pubmed-10195894;
Delhase M., Hayakawa M., Chen Y., Karin M.;
"Positive and negative regulation of IkappaB kinase activity through
 ENZYME REGULATION: Activated when phosphorylated and inactivated
 PHOSPHORYLATION BY MAP3K14/NIK.
MEDLINE=98188238; PubMed=9520401;
Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 S.
 Okumura K.;
"Differential regulation of IkappaB kinase alpha and beta by two
upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 "Functional annotation of a full-length mouse cDNA collection.";
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki
Hayashizaki Y.;
 protein kinase/ERK kinašė kinase-1.";
Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 Event=Alternative splicing; Named isoforms=3;
 Isold=Q60680-1; Sequence=Displayed;
 similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS:
 IKKbeta subunit phosphorylation."; Science 284:309-313(1999).
 Nature 409:685-690(2001).
 ALTERNATIVE SPLICING.
 PHOSPHORYLATION
 IKKA-IKKB BINDING.
 REVIEW
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TISSUE=Heart
 TISSUE=Lung
 SEOUENCE
 REVIEW.
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 MISLLRYNANLTRWKNTLIS -> IFRKNVKSMERNGRKGH
SLF (in isoform 2).
/FTIdavSp 004866.
/FTIdavSp (in isoform 2).
/FTIdavSp 004867.
DHLXSDST -> GKTLQSQY (in isoform 3).
 014920; 075327;
116-0CT-2001 (Rel. 40, Created)
116-0CT-2001 (Rel. 40, Last sequence update)
115-SEP-2003 (Rel. 42, Last annotation update)
115-SEP-2003 (Rel. 42, Last annotation update)
115-SEP-2003 (Rel. 42, Last annotation update)
116-SEP-2003 (Rel. 42, Last annotation update)
117-SEP-2003 (Rel. 40, Last annotation update)
117-SEP-2003 (Rel. 40, Last annotation update)
117-SEP-2003 (Rel. 40, Last annotation update)
117-SEP-2003 (Rel. 40, Last annotation update)
117-SEP-2003 (Rel. 40, Last annotation update)
117-SEP-2003 (Rel. 40, Last annotation update)
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117-SEP-2003 (Rel. 40, Last annotation update)
117-SEP-2003 (Rel. 40, Last annotation update)
117-SEP-2003 (Rel. 40, Las
 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 ö
 InterPro; IPR001245; Tyr_bkinase.
Pfam; PF00069; pkinase; 1.
Prinas; PR00109; TYRINASE.
Probom: PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
 ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (BY PKB/AKT1)
 DB 1; Length 745;
 PHOSPHORYLATION (BY MAP3K14) (BY SIMILARITY).
 0; Indels
 LEUCINE-ZIPPER (POTENTIAL).
 3FEF5582AFF92233 CRC64;
 Missing (in isoform 3).
/FIId=VSP_004869.
 (BY SIMILARITY).
 -> E (IN REF. 3).
 Pred. No. 1.2e+02
 FTId=VSP_004868.
 (BY SIMILARITY).
 PROTEIN KINASE.
 756 AA.
 0; Mismatches
 NEMO-BINDING
 90.0%; Score 36;
 Phosphorylation; Alternative splicing.
 HSSF; WGT:99484; Chuk.
InterPro; 1PR000719; Prot kinase.
InterPro; 1PR002290; Ser_thr_pkinase.
InterPro; 1PR001245; Tyr_pkinase.
 PRT;
 84728 MW;
 100.08;
 IKAPPAB KINASE SUBFAMILY
 EMBL; U12473; AAC52589.1; -.
 EMBL; AK018671; BAB31335.1;
 Local Similarity 100.
 STANDARD;
 745
 176
 745
 584
 471
 PIR; 149101; 149101.
HSSP; Q63450; 1A06.
 Homo sapiens (Human)
 236 2
400 4
745 AA;
 DWSWL 743
 2 DWSWL 6
 15
738
738
144
144
23
 176
 452
 472
 585
 IKKB HUMAN
 CONFLICT
CONFLICT
SEQUENCE
 ACT_SITE
MOD_RES
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NP_BIND
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IKKB HUMAN
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Matches
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IKK PHOSPHORYLATION.
MEDLINE=99038218; PubMed=9819420;
MEDLINE=99038218; PubMed=9819420;
Nemoto S., Dibonato J.A., Lin A.;
"Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase i and MP-kappaB-inducing kinase.";
Mol. Cell. Biol. 18:7336-7343(1998).
 IDENTIFICATION IN A COMPLEX WITH CREBBP; NCOA2; NCOA3; IKKA AND IKBKG. MEDLINE=21968797; PubMed=11971985; Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
 Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.; "IkappaB kinase-beta: NF-kappaB activation and complex formation with IkappaB kinase-alpha and NIK."; Science 278:866-869(1997).
 Mihara M., Okumura K.;
to human chromosome band
SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181. ISSUB-Ceverical carcinoma, MESURE-98009813; Pubmed-9346484; Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L., Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L., I.J. W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.; IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for NF-kappaB activation.";
 Hu M.C.-T., Wang Y.-P.;
TrappaB Kinase-alpha and -beta genes are coexpressed in adult and
"TrappaB Kinase-alpha and localized to different human chromosomes.";
Gene 222:31-40(1998).
 "The I kappa B/NF-kappa B system: a key determinant of mucosal
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 AND MUTAGENESIS OF LYS-44.
 SEQUENCE FROM N.A., AND GENE MAPPING.
MEDLINE=98438415; PubMed=9763654;
Shindo M., Nakano H., Sakon S., Yagita H.,
"Assignment of IkappaB kinase beta (IKBKB)
Bp12-->p11 by in situ hybridization.";
Cytogenet. Cell Genet. 82:32-33(1998).
 inflammation and protection.";
Am. J. Physiol. 278:C451-C462(2000).
 MEDLINE=20178139; PubMed=10712233;
 MEDLINE=98008814; PubMed=9346485;
 MEDLINE=99032998; PubMed=9813230;
 human and mouse cDNA sequences.
 SEQUENCE OF 1-256 FROM N.A.
 Science 278:860-866(1997).
 Jobin C., Sartor R.B.;
 SEQUENCE FROM N.A.,
 FROM N.A.
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 WHSKVRQKSEVDIVVSEDLNGTVKF -> CVRMWPGTVAHS
CNPSTLGGRGRWI (IN REF. 5).
 also as a homodimer. Directly interacts with IKK-gamma/NEMO. Heterodimers form the active complex. The tripartite complex also bind to MEKKI, MAPNIAIVIK, IKAP and IKB-alpha-P65-P50 complex. Phosphorylated IKB-alpha is further released from the complex. Pound in a complex composed of NCOA2, NCOA3, IKKA, IKBKG
O'Malley B.W.;
"Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
"activity by I kappa B kinase.";
activity by I kappa B kinase.";
Mol. Cell. Biol. 22:3549-3561(2002).
-!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates
 NCOA3 (By similarity).
SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
 TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal
 muscle, kidney, pancreas, spleen, thymus, prostate, testis and peripheral blood.
 PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK. Weakly autophosphorylated.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
IKAPPAB KINASE SUBFAMILY.
 K->A: LOSS OF KINASE ACTIVITY AND NO EFFECT ON BINDING TO NIK.
S->A: DECREASE OF ACTIVITY.
 MIM) 603258; —.

MIM) 603258; —.

GO, GO:0005737; C:cytoplasm; NAS.

GO, GO:0004524; F:ATP binding activity; NAS.

GO, GO:0004654; F:Protein serine/threonine kinase activity; NAS.

GO; GO:000468; F:protein amino acid phosphorylation; NAS.

InterPro; IPR002290; Ser thr pkinase.

Pfam; PP00069; ubiquitin; 1.

Pfam; PF00240; ubiquitin; 1.
 PHOSPHORYLATION (BY SIMILARITY) PHOSPHORYLATION.
 Transferase; Serine/threonine-protein kinase; ATP-binding;
 S->E: FULL ACTIVATION.
S->A: DECREASE OF ACTIVITY.
S->E: FULL ACTIVATION.
 LEUCINE-ZIPPER (POTENTIAL) NEMO-BINDING.
 -> H (IN REF. 1).
F9CADF671AE9E14E CRC64;
 FULL ACTIVATION
 (BY SIMILARITY)
(BY SIMILARITY)
 Prodom; PD000001; Frot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 PHOSPHORYLATION
 PROTEIN KINASE
 SIMILARITY
 SUBCELLULAR LOCATION: Cytoplasmic.
 ATP
BY S
 EMBL; AF029684; AAC51860.1; -. EMBL; AF080158; AAD08997.1; -. EMBL; AF031416; AAC64675.1; -.
 EMBL; BC006231; AAH06231.1; -. HSSP; Q63450; 1A06.
 86563 MW;
 Genew; HGNC:5960; IKBKB.
 29
44
145
23
177
181
 177
177
181
181
255
 425
756 AA;
 Phosphorylation
DOMAIN 15
 15
458
737
21
44
 181
 CREBBP
 ACT_SITE
MOD_RES
MOD_RES
MOD_RES
 CONFLICT
 DOMAIN
DOMAIN
NP_BIND
 MUTAGEN
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MUTAGEN
 CONFLICT
 BINDING
 MUTAGEN
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 Nemoto S., DiDonato J.A., Lin A.; "Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase 1 and NF-kappaB-inducing kinase."; Mol. Cell. Biol. 18:7336-7343 (1998).
 Jobin C., Sartor R.B.;
"The I kappa B/NP-kappa B system: a key determinant of mucosal inflammation and profection.";
Am. J. Physiol. 278:0451-0462(2000)
-!- FUNCTION: Phosphorylates inhibitors of NP-kappa-B thus leading to the dissociation of the inhibitor/NP-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates NCOA3.
 SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but also as a homodimer. Directly interacts with IKK-gamma/NEMO. Heterodimers form the active complex. The tripartite complex can also bind to MEKKI, MAPNIAIVNIK, IKAP and IKB-ALPHA-F65-F50 complex. Phosphorylated IKB-alpha is further released from the complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKBKG
 088351; Q9R1J6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
(I-kappa-B-kinase beta) (IKBKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta)
 Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
"Murine IKB kinase-B, a developmentally regulated protein kinase that
constitutively phosphorylates serine residues of IkB.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
 Gaps
 DEVELOPMENTAL STAGE.
MEDLINE=9945228; PubMed=10523828;
MEDLINE=9945228; PubMed=10523828;
MEDLINE=9945228; PubMed=10523828;
MHU M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
"Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
pathway activates IkappaB kinases (IKK-alpha/beta) and IKK-beta is a
developmentally regulated protein kinase.";
Oncogene 18:5514-5524(1999).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 "Differential regulation of IkappaB kinase alpha and beta by two upstream kinases, NF-kappaB-inducing kinase and mitogen-activated protein kinase/ERK kinase kinase-1.";
 [1] SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEKKI. SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEKKI. STRAIN=CS7BL/6; TISSUE=Spleen; MEDLINE=98188238; Pubmed=9520401; MEDLINE=98188238; Pubmed=9520401; Makano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita I
 .
90.0%; Score 36; DB 1; Length 756; 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels
 Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 757 AA
 MEDLINE=20178139; PubMed=10712233;
 MEDLINE=99038238; PubMed=9819420;
 5; Conservative
 STANDARD;
 Mus musculus (Mouse)
 PHOSPHORYLATION
 Query Match
Best Local Similarity
Matches 5; Conserv
 738 DWSWL 742
 SEQUENCE FROM N.A.
 NCBI TaxID=10090;
 9
 2 DWSWL
 KBKB OR IKKB
 IKKB MOUSE
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 -I- SUBCELLULAR LOCATION: Cytoplasmic.
-I- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
-I- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
-I- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout the mouse embryo, at E9:5 day its expression begins to be localized to the brain, neural ganglia, neural tube, and in liver at E12:5 day. At E15:5 day, the expression is further restricted to specific tissues of the embryo.
-I- PTM: Phosphorylated by MEKKI and probably also by MAP3K14/NIK.
-Weakly autophosphorylated.
-I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 Gaps
 K -> R (IN REF. 2).
TLDWSWLQMEDEERCSLEQACD -> VTA (IN REF
 LEUCINE-ZIPPER (POTENTIAL).
NEMO-BINDING.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
 ô
 90.0%; Score 36; DB 1; Length 757; 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Indels
 Pfam, PF00069; pkinase; 1.
PRINTS; PR00109; TYKKINASE.
PRODOM; PD000001; Proc kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
PROSITE; PSS0011; PROTEIN KINASE DM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
 FED962F095449C5E CRC64;
 N -> D (IN REF. 2).

K -> B (IN REF. 2).

L -> F (IN REF. 2).

P -> Q (IN REF. 2).
 PROTEIN KINASE
 EMBL; AF026524; AAC23557.1; -.
EMBL; AF088910; AAD52095.1; -.
HSSP; G03450; 1A06.
MGD; MG1:1338071; Ikbkb.
InterPro; IPR000719; Proc kinase.
InterPro; IPR000290; Ser Thr Dkinase.
InterPro; IPR001249; Tyr Dkinase.
Pfam: DF00069. https://prinase.
CREBBP (By similarity)
 86690 MW;
 Query Match
Best Local Similarity 100.
Matches 5; Conservative
 757 AA;
 2 DWSWL 6
 hosphorylation
 DOMAIN
NP BIND
BINDING
ACT SITE
MOD_RES
MOD_RES
CONFLICT
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|                                       | •                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    |                                              |     |                                       |   |                                         |
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|                                       |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    |                                              |     |                                       |   |                                         |
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| e e e e e e e e e e e e e e e e e e e |                                           | .*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |    |                                              |     |                                       |   |                                         |
|                                       |                                           | *.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |    |                                              |     |                                       |   |                                         |
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|                                       |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    |                                              |     |                                       |   |                                         |
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| e e e e e e e e e e e e e e e e e e e |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    |                                              |     |                                       | • |                                         |
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| and the second                        |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    | •                                            |     | 4                                     |   |                                         |
|                                       |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    |                                              |     |                                       |   |                                         |
| Section 1                             |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    |                                              |     |                                       |   |                                         |
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|                                       |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    | •                                            |     |                                       |   |                                         |
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|                                       | ş.                                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    |                                              |     |                                       |   |                                         |
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|                                       |                                           | •                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |    |                                              |     |                                       |   |                                         |
| e e e e e e e e e e e e e e e e e e e |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    |                                              |     |                                       |   |                                         |
|                                       |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    |                                              |     |                                       |   |                                         |
|                                       |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    |                                              |     |                                       |   |                                         |
|                                       |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | •  |                                              |     |                                       | * |                                         |
| •                                     |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    | <i>h</i>                                     |     |                                       |   |                                         |
|                                       |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    |                                              |     |                                       |   |                                         |
|                                       |                                           | · ·                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |    |                                              |     |                                       |   |                                         |
|                                       |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    |                                              |     | •                                     |   |                                         |
|                                       |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    |                                              |     |                                       |   |                                         |
|                                       |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    |                                              | •   | •                                     |   |                                         |
|                                       |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    |                                              |     |                                       |   |                                         |
|                                       |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    |                                              |     |                                       |   | i                                       |
|                                       |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    | •                                            |     |                                       |   |                                         |
|                                       |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    |                                              | *   |                                       |   |                                         |
|                                       |                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |    |                                              | A S |                                       |   |                                         |

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

February 18, 2004, 14:12:09; Search time 6.5921 Seconds (without alignments) 87.531 Million cell updates/sec Run on:

US-09-643-260-4 40

1 ADWSWL 6 Perfect score: Seguence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|            | Description           |    | mel-13a protein - | conserved hypothet | Ig V-D-J region ( | conserved helix-lo | hypothetical prote |        | TonB-dependent rec | cellulase (EC 3.2 | cellulase (EC 3.2 | probable potassium | O-antigen blosynth | type I restriction | nitric-oxide synth | nitric-oxide synth | nitric-oxide synth | alkaline phosphata | extracellular nucl | hypothetical prote |        | 3-oxoacy1-[acy1-ca | hypothetical prote | DNA-3-methyladenin | 3-methyl-adenine | 3-methyl-adenine | probable glycosyl | hypothetical prote | DNA-3-methyladenin | probable rfbE prot | 4 |
|------------|-----------------------|----|-------------------|--------------------|-------------------|--------------------|--------------------|--------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|------------------|------------------|-------------------|--------------------|--------------------|--------------------|---|
| SOUTHERIES | ΙD                    |    | 865785            | D87226             | 606698            | 149101             | D70802             | F90485 | E87304             | A43802            | \$02711           | A10379             | T18556             | C69226             | S71424             | A47501             | A38943             | 874916             | 874915             | G83692             | D64316 | T44932             | B75337             | DGECMA             | E90988           | G85833           | A86923            | C90290             | AI0770             | B70696             |   |
|            | 08                    |    | N                 | ~                  | N                 | н                  | ~                  | 7      | ~                  | ~                 | 7                 | ~                  | ~                  | N                  | ~                  | -                  | Н                  | ~                  | ~                  | ~                  | ~      | ~                  | ~                  | -                  | ~                | 7                | 7                 | 7                  | 7                  | ٦                  |   |
|            | Query<br>Match Length |    | 132               | 1329               | 122               | 745                | 747                | 803    | 889                | 915               | 1039              | 1139               | 1275               | 919                | 1202               | 1203               | 1205               | 1409               | 1879               | 214                | 220    | 248                | 276                | 282                | 282              | 282              | 283               | 287                | 289                | 304                |   |
| de         | Query<br>Match        | ١, | 92.5              | 92.5               | 90.0              | 0.06               | 0.06               | 90.0   | 90.0               | 90.0              | 0.06              | 90.0               | 90.0               | 87.5               | 87.5               | 87.5               | 87.5               | 87.5               | 87.5               | 85.0               | 85.0   | 85.0               | 85.0               | 85.0               | 85.0             | 85.0             | 85.0              | 85.0               | 85.0               | 85.0               |   |
|            | Score                 |    | 3.7               | 37                 | 36                | 36                 | 36                 | 36     | 36                 | 36                | 36                |                    |                    |                    | 35                 | 35                 | 35                 | 35                 | 35                 | 34                 | 34     | 34                 | 34                 | 34                 | 34               | 34               | 34                | 34                 | 34                 | 34                 |   |
|            | Result<br>No.         |    | -1                | ~                  | m                 | 4                  | S                  | 9      | 7                  | 80                | 6                 | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19     | 20                 | 21                 | 22                 | 23               | 24               | 25                | 56                 | 27                 | 28                 | • |

| AA3-600 quinol oxi | lycopene cyclase - | probable GMP synth | hypothetical prote | restriction modifi | GMP synthase (glut | type I restriction | nitric-oxide synth | nitric-oxide synth | nitric-oxide synth | nitric-oxide synth | nitric-oxide synth | nitric-oxide synth | nitric-oxide synth | nitric-oxide synth | nitric-oxide synth |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| AF1806             | D75475             | C86958             | A87347             | C64452             | S72813             | E75221             | A43271             | S47647             | 156575             | 538253             | 153165             | JC5027             | JC5028             | JC5029             | S65440             |
| ~                  | ~                  | ~                  | 7                  | 7                  | 7                  | 7                  |                    | Н                  | Н                  | Н                  | н                  | 7                  | 7                  | ~                  | ~                  |
| œ                  | 410                | 529                | 549                | 578                | 590                | 623                | 1144               | 1147               | 1147               | 1147               | 1147               | 1147               | 1147               | 1147               | 1147               |
| 36                 |                    |                    |                    |                    |                    |                    |                    | _                  |                    |                    | _                  |                    | _                  | 0                  | 0                  |
| 85.0 36            | 85.0               | 85.0               | 85.0               | 85.0               | 85.0               | 85.0               | 85.0               | 85.0               | 85.0               | 85.0               | 85.0               | 85.0               | 85.0               | 85.                | 85.0               |
| 34 85.0 36         | 34 85.0            | 34 85.0            | 34 85.0            | 34 85.0            | 34 85.0            | 34 85.0            | 34 85.0            | 34 85.0            | 34 85.0            | 34 85.0            | 34 85.0            | 34 85.0            | 34 85.(            | 34 85.             | 34 85.             |

### ALIGNMENTS

```
RESULT 1
S65785
mel-13a protein - mouse
C;Species: Mus musculus (house mouse)
C;Accession: S65785
C;Accession: S65785
C;Accession: S65785
C;Accession: S65785
C;Accession: S65785
C;Accession: S65785
C;Accession: S65785
C;Accession: S65785
C;Accession: S65785
A;Title: Cloning and characterization of two transcripts generated from the mel-13 gene A;Title: Cloning and characterization of two transcripts generated from the mel-13 gene A;Accession: S65785
A;Accession: S65785
A;Accession: S65785
A;Accession: S65785
A;Cross-references: EMBL:U35309
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Keywords: alternative splicing
 ö
 Gaps
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 Length 132;
 0; Indels
 Query Match 92.5%; Score 37; DB 2; Best Local Similarity 83.3%; Pred. No. 28; Matches 5; Conservative 1; Mismatches
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### 1 ADWSWL 6 ò g

Conserved hypothetical protein ML2535 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Accession: D87226
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ham.
R;Cole, S.T.; Eiglmeier, K.; Dathoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd
eam, M.A.; Devlier, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A;Ttle: Massive gene decay in the leprosy bacillus
A;Reference number: A86909; MUID:21128732; PMID:111234002
A;Residues: Drelliminary
A;Residues: 1-1329
A;Residues: 1-1329
A;Residues: 1-1329
A;Residues: 1-1329
A;Cross-references: GB:AL450380; NID:g13093796; PIDN:CAC32066.1; GSPDB:GN00147
C;Genetics:
A;Gene: ML2535

Score 37; DB 2; Length 1329; Pred. No. 2.8e+02; 92.5%; 83.3%; Query Match Best Local Similarity

2

genome

ö

Gaps

;

0; Indels

Length 747;

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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1.747 <COL>
A;Cross-references: GB:AL022120; GB:AL123456; NID:g3261558; PIDN:CAA17962.1; PID:g296022
A;Experimental source: strain H37Rv
C;Genetics:
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70802
 Cross-references: GB:AE006641; NID:g13816440; PIDN:AAK43141.1; GSPDB:GN00155; Genetics:
 DB 2; Le
 DB 2;
 90.0%; Score 36; DB 100.0%; Pred. No. 2.3 tive 0; Mismatches
 90.0%; Score 36;
 E87304
TonB-dependent receptor [imported]
 Query Match
Best Local Similarity 100.00
Thes 5; Conservative
 Query Match
Best Local Similarity 100.
Matches 5, Conservative
 DWSWL 271
 DWSWL 544
 A, Residues: 1-889 <STO>
 9
 DWSWL 6
 A;Status: preliminary
A;Molecule type: DNA
 2 DWSWL
 A; Accession: E87304
 A; Gene: 5S03039
 C;Genetics:
A;Gene: Rv3870
 A;Gene: CC0446
 267
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 540
 Query Match
 C; Genetics:
 RESULT 7
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B
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 A, Cross-references: EMBL: 233399, NID: 9871348; PIDN: CAAB3850.1; PID: 9871349
A, Note: the sequence of residues 112-122 and the corresponding nucleic acid sequence are C; Superfamily: immunoglobulin V region; immunoglobulin homology
P;15-97/Domain: immunoglobulin homology < IMM>
 C;Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homold C;Keywords: ATP; phosphotransferase F;13-283/Domain: protein kinase homology <KIN>
 D70802
hypothetical protein Rv3870 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Ny-Ju1-1998 #sequence_revision 17-Ju1-1998 #text_change 20-Jun-2000
C;Accession: D70802
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
 in the pathogenesis of multi
 C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: 149101
R;Mock, B.A.; Connelly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.
R;Mock, B.A.; Connelly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.
A;Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome
A;Reference number: 149101; MUID:96044444; PMID:7558004
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 A;Cross-references: EMBL:U12473; NID:g1079492; PIDN:AAC52589.1; PID:g1079493 C;Genetics:
 C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
 Gaps
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0
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0
 90.0%; Score 36; DB 1; Length 745; 100.0%; Pred. No. 2.3e+02; ive 0; Mismatches 0; Indels
 conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.-) CHUK
 Length 122;
 Indels
 Indels
 Richards, S. Hamblin, T.; Oscier, D.G.; Stevenson, F.K.
Leukemia 8, 1285-1289, 1994 and A.; Title: Assessment of the role of clonogenic B lymphocytes A; Reference number: S69909; MUID:94335115; PMID:8057663 A; Status: preliminary; nucleic acid sequence not shown A; Molecule type: mRNA
 ö
 DB 2;
37;
 A, Accession: 149101
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100.0%; Pred. No.
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 Conservative
 Ig V-D-J region (MS) - human
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SDWSWL 265
 Query Match
Best Local Similarity
 A; Residues: 1-122 <SAH>
 DWSWL 743
 1 ADWSWL 6
 DWSWL 37
 2 DWSWL 6
 2 DWSWL 6
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 739
 33
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 Matches
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C; Accession: E87304
R; Nierman, W.C; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
R; Nierman, W.C; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Haft, D.H.; Kolon
n, J.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A; Erc., Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Reference number: A87249; MUID:21173698; PMID:11259647
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 A;Cross-references: GB:AE005673; NID:g13421615; PIDN:AAK22433.1; GSPDB:GN00148
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
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90.0%; Score 36; DB 2; Length 803; 100.0%; Pred. No. 2.4e+02; ive 0; Mismatches 0; Indels
 - Caulobacter crescentus
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Length 889

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probable potassium efflux system YPO3129 [imported] - Yersinia pestis (strain CO92) C;Species: Yersinia pestis C;Species: Yersinia pestis C;Species: Yersinia pestis C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001 C;Accession: A0379 R;Accession: A0379 R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; IL, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: A10379
A;Kesidues: DNA
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A;Molecule type: DNA
A;Residues: 1-1139 cKUR>
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C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Actor, D: Bowden, M.G.; Pershad, R.; Kaplan, H.B.
J. Bacteriol. 178, 1631-1639, 1996
A; Title: The Myxococcus xanthus rfbABC operon encodes an ATP-binding cassette transport: A; Reference number: Z18970; MUID:96198166; PMID:8626291
A; Reference number: Z18970; MUID:96198166; PMID:8626291
A; Reference number: Z18970; MUID:96198166; PMID:8626291
A; Status: preliminary; translated from GB/EMBL/DDBJ
 Cype I restriction modification enzyme, subunit M - Methanobacterium thermoautotrophicu. Cispecies: Methanobacterium thermoautotrophicum Cispecies: Methanobacterium thermoautotrophicum Cispecies: Methanobacterium thermoautotrophicum Cispecies: Methanobacterium thermoautotrophicum Cispace: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999 Ciscession: C69226

R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Olu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func A;Reference number: A69000; MUID: 98037514; PMID: 9371463
A;Accession: C69226
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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 Length 1139;
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83.3%; Pred. No. 3.9e+02;
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100.0%; Pred. No. 3.5e+02;
ive 0; Mismatches 0;
 Conservative
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 348 ADWEWL 353
 Local Similarity
nes 5; Conserv
 Best Local Similarity
Matches 5; Conserv
 481 DWSWL 485
 1 ADWSWL 6
 9
 2 DWSWL
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 C; Date: 30-Jan-1993 #sequence_revision 30-Sep-1993 #text_change 10-Jul-1998
C; Accession: A43802
R; Saul, D.J.; Williams, L.C.; Grayling 1. Chamley, L.W.; Love, D.R.; Bergquist, P.L.
Appl. Environ. Microbiol. 56, 3117-3124, 1990
A; Title: celB, a gene coding for a bifunctional cellulase from the extreme thermophile "A; Reterence number: A43802, MUID:91136262; PMID:2126700
A; Accession: A43802
A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
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C; Keywords: glycosidase; hydrolase; polysaccharide degradation
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C; Keywords: glycosidase; hydrolase; polysaccharide degradation
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A;Molecule type: DNA
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A;Molecule type: DNA
A;Molecule type: DNA
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A;Gene: celB
C;Function: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as ce
A;Pathway: cellulose degradation
C;Superfemily: Streptomyces endo-1,4-beta-xylanase A homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
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 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Accession: S02711
F;Saul, D.J.; Williams, L.C.; Love, D.R.; Chamley, L.W.; Bergquist, P.L.
Nucleic Acids Res. 17, 439, 1989
A;Title: Nucleotide sequence of a gene from Caldocellum saccharolyticum encoding for A;Reference number: S02711; MUID:89098398; PMID:2789517
 Alternate names: endo-1,4-beta-glucanase
Contains: cellulase (EC 3.2.14); cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91)
:Species: Caldocellum saccharclyticum
:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
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 cellulase (EC 3.2.1.4) / cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) - (N)Alternate names: endo-1,4-beta-glucanase
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C. Species: 30-Jan-1993 #sequence_revision 30-Sep-1993 #text_change 10-Jul-1998
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 - Caldocellum saccharolyticum
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: Mismatches 0;
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 100.08;
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 5; Conservative
 Best Local Similarity
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 1 ADWSW 5
 2 DWSWL 6
 DWSWL 6
 469
 Matches
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 A; Accession: A38948
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 A;Accession: A49813
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C:Date: 02-Jun-1995 #rext_change 03-Mar-2000
C:Date: 02-Jun-1995 #sequence revision 21-Jul-1995 #rext_change 03-Mar-2000
C:Accession: A47501; S24052; Ā38948; A49813; A42867; S45691; I37361
C:Accession: A47501; S24052; Ā38948; A49813; A2887; S45691; I37361
J. Biol. Chem. 268, 17478-17488, 1993
A;Title: Structure and chromosomal localization of the human constitutive endothelial ni A;Reference number: A47501; MUID:93352539; PMID:7688726
A;Accession: A47501
A;Molecule type: DNA
A;Residues: 1-1203 <AMAR1>
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0698; NID:g348224; GB:L10709; NID:g348225; GB:L10700; NID:g348226; GB:L10701; NID:g34822
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F; 790-803/Region: FAD-isoalloxazine binding #status predicted
F; 1009-1027/Region: NADP-ribose binding #status predicted
F; 1009-1027/Region: NADP-adenine binding #status predicted
F; 1009-1021/Region: App-adenine binding #status predicted
F; 1009-1037/Region: NADP-adenine binding #status predicted
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A;Experimental source: strain Delta H
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A;Genetics:
A;Start codon: GTG
C;Superfamily: type I site-specific deoxyribonuclease chain hsdM
 g
 C;Accession: S71424
R;Gnanapandithen, K.; Chen, Z.; Kau, C.L.; Gorczynski, R.M.; Marsden, P.A.
Bjochim. Biophys. Acta 1308, 103-106, 1996
A;Title: Cloning and characterization of murine endothelial constitutive nitric oxide A;Reference number: S71424; MUID:96350460; PMID:8764825
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 A;Reference number: S71424; MUID:96350460; PMID:8764825
A;Accession: S71424
A;Molecule type: MUID:96350460; PMID:8764825
A;Residues: 1-1202 cgNA>
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Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 04-Mar-2000
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 87.5%; Score 35; DB 2; Length 120
66.7%; Pred. No. 5.2e+02;
ive 2; Mismatches 0; Indels
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 tric-oxide synthase (EC 1.14.13.39), endothelial - human
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4; Conservative
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Matches 4; Conserv
 1-616 <MTH>
 1 ADWSWL 6
 1 ADWSWL 6
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A;Residues: 1-616 <M
 Query Match
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R; Marsden, P.A.; Schappert, K.T.; Chen, H.S.; Flowers, M.; Sundell, C.L.; Wilcox, J.N.; FEBS Lett. 307, 287-293, 1992
A;Title: Molecular cloning and characterization of human endothelial nitric oxide synthman
 A; Molecule type: mRNA
A; Residues: 1-82,'S', 84-179,'F',181-566,'W',568-647,'Q',649-854,'V',856-1008,'G',1010-11
A; Residues: 1-82,'S', 84-179,'E', 181-566,'W',568-647,'Q',649-854,'V',856-1008,'G',1010-11
A; Cross-references: GB:M93718; NID:g189211
A; Note: this sequence has been revised in reference A49813
A; Note: this sequence has been revised in reference A49813
A; Note: Tuttle, J.V.; Covington, K.; Merrill, B.M.; Wood, E.R.; Baylis, S.A.; Ch
Arch. Biochem. Biophys. 311, 235-241, 1994
A; Title: Purification and characterization of the constitutive nitric oxide synthase fro
 A;Map position: 7q36-7q36
A;Introns: 53/2; 90/3; 140/2; 194/3; 225/2; 272/3; 319/2; 377/3; 411/3; 476/3; 501/2; 54
 A, Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH C; Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct C; Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct C; Keywords: blocked amino end; calmodulin binding predicted P; 520-1159/Domain: RADPH-ferrihemoprotein reductase homology <FEH> F; 520-105/Domain: NADPH-ferrihemoprotein reductase homology <FEH> F; 522-703/Domain: flavodoxin homology <FIX> F; 648-680/N Region: FMD-pyrophosphate binding #status predicted F; 791-804/Region: FAD-pyrophosphate binding #status predicted
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A;Residues: 'XX',169-175,531-536,'X',538-540;835,'X',837-843,'X',845;876-877,'X',879-881
 A; Experimental source: placenta
R; Nadaud, S.; Bonnardeaux, A.; Lathrop, M.; Soubrier, F.
Bocchem, Biophys. Res. Commun. 198, 1027-1033, 1994
A; Title: Gene structure, polymorphism and mapping of the human endothelial nitric oxide
A; Reference number: 137361; MUID: 94161710; PMID: 7509596
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C
 A; Molecule type: mRNA
A; Residues: 1191-1203 < JAN2>
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A; Notes: sequence extracted from NCB1 backbone (NCBIP:117314)
B; Janssens, S.P.; Shimouchi, A.; Quertermous, T.; Bloch, D.B.; Bloch, K.D.
J. Biol. Chem. 267, 14519-14522, 1992
A; Title: Cloning and expression of a cDNA encoding human endothelium-derived relaxing A; Reference number: A42867; MUID: 92340475; PMID: 1378832
 A; Molecule type: mRNA
A; Roseidues: 1-1203 - 43AN1>
A; Cross-references: GB: M93718; NID: 9189211; PIDN: AAA36364.1; PID: 9189212
A; Cross-reference in GenBank entry HUMNIOXSYN, release 111.0, has been corrected: R; Janssens, S. P.; Simouchi, A.; Quertermous, T.; Bloch, D.B.; Bloch, K.D.
A; Reicerence number: A49813; MUID: 93054573; PMID: 1385404
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F;3/Modified site: aspartic acid (Asn) #status predicted
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A;Residues: 1-1203 <MBR2>
A;Cross-references: GB:M95296; NID:9189259; PIDN:AAA36372.1; PID:9189260
R;Janssens, S.P.; Shimouchi, A.; Quertermous, T.; Bloch, D.B.; Bloch, K.D. submitted to GenBank, September 1992
 A;Accession: 137361
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 A;Cross-references: GDB:209976; OMIM:163729
 A;Status: nucleic acid sequence not shown
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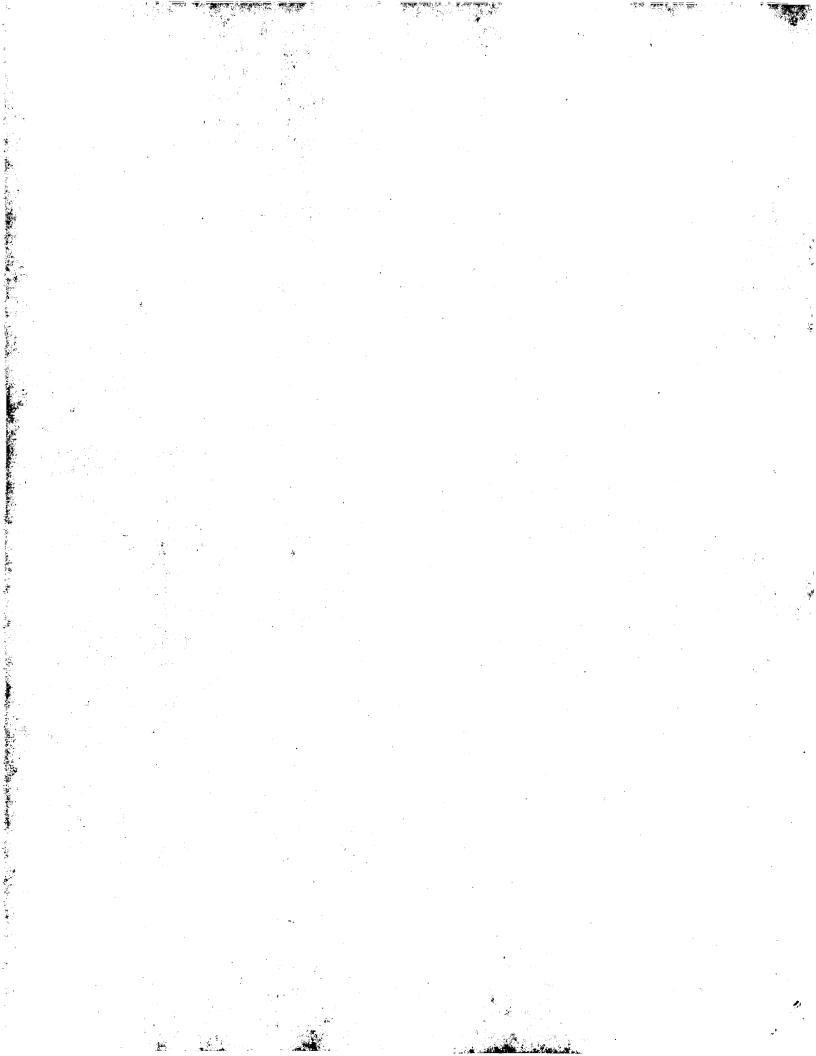
Gaps

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Length 1205; 0; Indels

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Matches 4; Conservative
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 MOLECULE 17-2. MIS>
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S8888, W.C.; Harrison, J.K.; Barber, C.M.; Zeng, D.; Durieux, M.E.; D'Angelo, D.D.; Ly
S8888, W.C.; Harrison, J.K.; Barber, C.M.; Zeng, D.; Durieux, M.E.; D'Angelo, D.D.; Ly
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(Note: sequence extracted from NCBI backbone (NCBIP:108720)
(Nishida, K.; Harrison, D.G.; Navas, J.P.; Fisher, A.A.; Dockery, S.P.; Nerem, R.M.; Al. Clin. Invest. 90, 2092-2096, 1992
(Sin. Invest. 90, 2092-2096, 1992)
(Sin. Invest. Note and Characterization of the constitutive bovine aortic Endoth Reference number: 145945; MUID:93055452; PMID:1385480
 | Residues: 1-51, N',53-99,'R',101-147,'M',149-164,'I',166-317,'GA',320,'HTGVVRGP',329-3 | R',517-692,'G',694-740,'A',742-753,'N',755-799,'N',801-803,'SA',806-856,'V',858-906,'LV | Experimental source: aortic endothelial cells | Sequence extracted from NCBI backbone (NCBIP:109564); contains a number of typog | Accession: 145946
 A Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH C; Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct C; Keywords: blocked amino end; calmodulin binding; chromoprotein; FAD; flavoprotein; FMN F; 422-1167, Region: calmodulin binding #status predicted
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F; 524-705, Domain: flavodoxin homology <FEX>
F; 2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 Sessa, W.C.; Harrison, J.K.; Barber, C.M.; Zeng, D.; Durieux, M.E.; D'Angelo, D.D.; Ly. Biol. Chem. 267, 15274-15276, 1992
Title: Molecular cloning and expression of a cDNA encoding endothelial cell nitric oxi, Reference number: A42841; MUID:92348367; PMID:1379225
 Residues: 1799, W. 101-164, I', 166-317, 'GA', 320,'HTGVVRGP', 329-454,'Y', 456-458,'P', 460 (Cross-references: GB:M95674; NID:9163426; PIDN:AAA30669.1; PID:9163427 (Cross-references: GB:M95674; NID:9163426; PIDN:AAA30669.1; PID:9163427 (Cross-references: GB:M95674; NID:9163427 (GB: submitted to GenBank, August 1992 (GB:M9625) (Mote: GenBank entry BOVNOS, release 103.0, has a typographical error in the reference
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A;Reafdues: 1-1205 < GLMM1>
A;Experimental source: aortic endothalial cells
A;Experimental source: aortic endothalial cells
R;Lamas, S.; Marsden, P.A.; Li, G.K.; Tempst, P.; Michel, T.
Proc. Natl. Acad. Sci. U.S.A. 89, 6318-6352, 1992
A;Title: Endothalial nitric oxide synthase: molecular cloning and characterization of A;Reference number: A46033; MUID:92335295; PMID:1378626
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A;Reference number: A38943
 Gaps
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Best Local Similarity
Matches 4; Conserv
 1 ADWSWL 6
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 Molecule type: mRNA
 Accession: A46033
 Accession: I45945
 Accession: A42841
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Sequence Sequence Sequence

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Sequence Sequence

Sequence Sequence Sequence

Minimum DB Maximum DB

Database

Searched:

Sequence:

Run on:

Sequence 1 Sequence 1 Sequence 1

Sequence

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OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
 APPLICANT: May, Michael J.
APPLICANT: May, Michael J.
APPLICANT: Ghosh, Sankar
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFREENCE: PPI-117CP
CURRENT APPLICATION NUMBER: US/09/847,940B
CURRENT APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR PILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 6
 Similarity 100.0%; Score 40; DB 10; Length Similarity 100.0%; Pred. No. 7e+05; 6; Conservative 0; Mismatches 0; Indels
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US-09-847-946A-3
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 -09-847-946A-132
 US-09-847-946A-68
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 ; Sequence 4, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
 Sequence 4, Application US/09847946A, Publication No. US20330054999A1, GENERAL INFORMATION: APPLICANT: May, Michael J
 LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
 Best Local Similarity
Matches 6; Conserv
ADWSWL
 1 ADWSWL
 US-09-847-940B-4
 US-09-847-940B-4
 RESULT 2
US-09-847-946A-4
Query Match
 FEATURE:
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 February 18, 2004, 14:36:10; Search time 16.6974 Seconds (without alignments) 75.239 Million cell updates/sec
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 Description
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 Published Applications AA:*

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14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
 Pred. No. is the number of results predicted by chance to he score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 US-09-847-9468-4
US-09-847-9468-3
US-09-847-9468-39
US-09-847-9468-55
US-09-847-9468-48
US-09-847-9468-48
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US-09-847-9468-47
US-09-847-9468-50
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US-09-847-9468-53
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US-09-847-9468-53
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US-09-847-9468-53
US-09-847-9468-53
 fotal number of hits satisfying chosen parameters:
 801455 segs, 209382283 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
 seq length: 0
seq length: 200000000
 DB
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 Query
Match Length
 1 ADWSWL 6
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 Title:
Perfect score:
 Scoring table:
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Result

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TYPE: PRT
ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
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 Query Match
Best Local Similarity
Laca 6; Conserve
 1 ADWSWL 6
 RESULT
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APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips Kathryn
APPLICANT: Phillips Kathryn
APPLICANT: Hanlips Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT APPLICATION NUMBER: US/0201,261
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR PILING DATE: 2000-08-22
PRIOR PILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PATENTIN Ver. 2.0
 GENERAL INCHMENT: May, Michael J
APPLICANT: May, Michael J
APPLICANT: Glosh, Sankar
APPLICANT: Findeis, Mark
APPLICANT: Findeis, Mark
APPLICANT: Findeis, Mark
APPLICANT: Findeis, Mark
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
CURRENT APPLICATION NUMBER: 050-02
PRIOR APPLICATION NUMBER: 60/201, 261
PRIOR APPLICATION NUMBER: 60/201, 261
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SEQ ID NOS: 160
SEQ ID NO 39
LENGTH: 6
 OTHER INFORMATION: Description of Artificial Sequence:NEMO binding OTHER INFORMATION: sequence US-09-847-946A-39
 ; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide US-09-847-946A-4
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 Query Match
100.0%; Score 40; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels
 100.0%; Score 40; DB 11; Length 6; ilarity 100.0%; Pred. No. 7e+05; Conservative 0; Mismatches 0; Indels
 US-09-847-946A-51; Sequence 51, Application US/09847946A; Publication No. US20030054999A1
 Sequence 39, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity
Matches 6; Conserv
 1 ADWSWL 6
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1 ADWSWL 6
 1 ADWSWL
 US-09-847-946A-39
 RESULT 4
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APPLICANT: Ghodis, Sankar A APPLICANT: Ghodis, Sankar A APPLICANT: Ghodis, Sankar A APPLICANT: Philips, Kath. The APPLICANT: Philips, Kath. The APPLICANT: Philips, Kath. The APPLICANT: Philips, Kath. The APPLICANT: Philips, Kath. The APPLICANT: Philips, Kath. The APPLICANT: Philips, Kath. The APPLICANT: Philips, Kath. The APPLICANT: Philips, Kath. The APPLICANT: Philips, Mark A PRICA PHILIPS DAYS 0.6021.261

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PHILIS OF THING DAYS: 2000-09.2621.261

PHILIS OF SEAD IN NOS: 100

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SECONDARY ATTHERS OF SEAD IN NOS: 100

SECONDARY ATTHERS OF SEAD IN NOS: 100

OWNERS OF SEAD IN NOS: 100

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ON THE REPORT OF SEAD IN NOS: 100

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 US-09-847-946A-56

Sequence 56, Application US/09847946A

Publication No. US20030054999A1

GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: FILIDIS, Kachryn
APPLICANT: FILING BATE: 2000-05-02
PRIOR PILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 160
SEQ ID NO 56
LENGTH: 8
LENGTH: 8
 APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Ghosh, Sankar
APPLICANT: Pindeish Mark A
APPLICANT: Pindeish Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
ITLE BEPERBUEL: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR PILING DATE: 2000-06-05
PRIOR PILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
 OTHER INFORMATION: Description of Artificial Sequence:NEMO binding OTHER INFORMATION: sequence
 OTHER INFORMATION: Description of Artificial Sequence: NEMO binding OTHER INFORMATION: sequence
 ö
 100.0%; Score 40; DB 11; Length 8; 100.0%; Pred. No. 7e+05; tive 0; Mismatches 0; Indels
 Query Match 100.0%; Score 40; DB 11; Length 8; Best Local Similarity 100.0%; Pred. No. 7e+05; Matches 6; Conservative 0; Mismatches 0; Indels
Sequence 48, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION:
 ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 Ouery Match
Best Local Similarity 100.
 ADWSWL 8
 1 ADWSWL 6
 US-09-847-946A-48
 US-09-847-946A-56
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ADWSWL 6

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Gaps

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Wed Feb 18 17:21:31 2004

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APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeas, Mark A
APPLICANT: Findeas, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence:NEMO binding OTHER INFORMATION: sequence
 OTHER INFORMATION: Description of Artificial Sequence: NEMO binding OTHER INFORMATION: sequence
 Sequence 52, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Pindeis, Mark A
APPLICANT: Pindeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
APPLICANT: Hannig, Gerhard
TILLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REPERENCE: PPI-119
 Length 10;
 0; Indels
 Indels
 100.0%; Score 40; DB 11;
100.0%; Pred. No. 15;
tive 0; Mismatches 0;
 CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR PRILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SEQ ID NO 52
 Mismatches
 Sequence 49, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION:
100.001
100.001
 TYPE: PRT ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 49
LENGTH: 10
 6; Conservative
 6; Conservative
 Query Match
Best Local Similarity
Matches 6; Conserv
 Best Local Similarity
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2 ADWSWL 7
 ADWSWL 7
 US-09-847-946A-49
 US-09-847-946A-49
 US-09-847-946A-52
 TYPE: PRT
 Matches
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 Gaps
 GENERAL INCOMPATION;
GENERAL INCOMPATION;
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
SOFTWARE: PALENTIN VET: 2.0
SOFTWARE: PALENTIN VET: 2.0
 APPLICANT: May, Michael J
APPLICANT: May, Michael J
APPLICANT: Glosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Kathryn
CURRENT ENEWENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 160
SEQ ID NOS: 160
SEQ ID NOS: 160
SEQ ID NOS 54
LENGTH: 9
) OTHER INFORMATION: Description of Artificial Sequence:NEWO binding ; OTHER INFORMATION: sequence US-09-847-946A-53
 OTHER INFORMATION: Description of Artificial Sequence:NEWO binding; OTHER INFORMATION: sequence
US-09-847-946A-54
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 100.0%; Score 40; DB 11; Length 9; 100.0%; Pred. No. 7e+05; ive 0; Mismatches 0; Indels
 100.0%; Score 40; DB 11; Length 9;
 Sequence 54, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION:
 Sequence 53, Application US/09847946A
Publication No. US20030054999A1
 TYPE: PRT
ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
 3 ADWSWL 8
 GENERAL INFORMATION
 ADWSWL
 US-09-847-946A-54
 Query Match
 FEATURE:
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Gaps

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 APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Rametkar, Sumban
APPLICANT: Rametkar, Shubhangi
APPLICANT: Glatt, Karen
APPLICANT: Glatt, Karen
APPLICANT: Glatt, Karen
APPLICANT: Glatt, Karen
APPLICANT: Glatv, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: DEPETIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US 60/299,159
PRIOR APPLICATION NUMBER: US 60/299,155
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
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 Gaps
 Sequence 46, Application US/09847946A
; Sequence 46, Application US/09847946A
; Sequence 46, Application US/09847946A
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Pinlais, Mark A
; APPLICANT: Pinlais, Mark A
; APPLICANT: Pinlais, Mark A
; APPLICANT: Pinlais, Mark A
; APPLICANT: Pinlais, Mark A
; APPLICANT: Hannig, Gerhard
; TITLE OF TINVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: P11-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR PILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SEQ ID NO 46
; LENGTH: 11
TYPE: PRT
; ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence:NEMO binding; OTHER INFORMATION: sequence
US-09-847-946A-46
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 100.0%; Score 40; DB 11; Length 11; 100.0%; Pred. No. 17; tive 0; Mismatches 0; Indels
 100.0%; Score 40; DB 11; Length 10; 100.0%; Pred. No. 15;
 Indels
 0; Mismatches
 Sequence 234, Application US/10171311
Publication No. US20030087270A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Zhao, Xumei
 Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
 Query Match
Best Local Similarity 100.
Matches 6; Conservative
 1 ADWSWL 6
 3 ADWSWL 8
 3 ADWSWL 8
US-09-847-946A-52
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|------------------------------------------|-----------------------------------------|-----------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------|
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|                                          |                                         |           | w <sup>1</sup>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                       |
| <b>.</b>                                 |                                         |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
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|                                          |                                         |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
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| <b>(</b>                                 |                                         |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
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|                                          | •                                       |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
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|                                          |                                         |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
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|                                          | •                                       |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
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| Je                                       |                                         |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
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|                                          |                                         |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
|                                          |                                         |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
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|                                          |                                         |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
|                                          |                                         |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
|                                          |                                         |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
|                                          |                                         |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
|                                          |                                         | •         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
| •                                        |                                         |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
|                                          |                                         |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
|                                          | e e e e e e e e e e e e e e e e e e e   |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
|                                          |                                         |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
|                                          |                                         |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
|                                          |                                         |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
|                                          |                                         |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
|                                          |                                         |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
|                                          |                                         | <b>V.</b> |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
| •                                        |                                         |           | · ***                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                       |
| w.                                       |                                         |           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                       |
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Sequence 163, Application US/09325932A
; Sequence 163, Application US/09325932A
; Patent No. 6451604
; GENERAL INPORMATION:
 APPLICANT: Film, Barry
; APPLICANT: Labham, Annette
; TITLE OF INVENTION: Compositions affecting pro
; TITLE OF INVENTION: death and their use in the
; FILE REPERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOUTHARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 163
; LENGTH: 174
; ORGANISM: Eucalyptus grandis
US-09-325-932A-163
 Local Similarity 100.
les 5; Conservative
 94 ADWSW 98
 ADWSW 5
 US-09-252-991A-31533
 US-09-325-932A-163
 Query Match
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 Sequence 163, App
Sequence 162, App
Sequence 158, App
Sequence 47, Appl
Sequence 3, Appli
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 Sequence 31533,
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 February 18, 2004, 14:16:39; Search time 7.06579 Seconds (without alignments) 35.929 Million cell updates/sec
 Description
 Sequence Seq
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 US-09-225-991A-31533
US-09-325-932A-162
US-09-325-932A-162
US-09-325-932A-158
US-09-136-574A-47
US-09-023-31-3
US-08-897-518-3
US-09-023-31-3
US-09-032-475-3
US-09-032-475-3
US-09-032-475-3
US-09-032-476-4
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US-09-032-476-4
US-09-131AA-2
US-09-168-629-2
US-09-109-986-4
US-09-109-986-4
US-09-109-986-4
US-09-109-986-4
US-09-109-986-4
US-09-109-986-3
US-09-109-986-3
US-09-023-321-4
 Total number of hits satisfying chosen parameters:
 US-09-032-475-4
US-09-099-125A-2
US-09-099-124A-2
US-09-032-476-2
 328717 segs, 42310858 residues
 SUMMARIES
 Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
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 Issued Patents AA:*
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 US-09-643-260-4
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Match Length
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 Perfect score:
 Sequence:
 Searched:
 Database
 Result
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programmed cell the modification of forestry plant devel

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Gaps

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Mismatches

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APPLICANT: Marc 7. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 10.7146-136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31533
 Sequence 2, Appli
Sequence 9, Appli
Sequence 123, App
Sequence 121, App
Sequence 43, Appl
Sequence 44, Appl
Sequence 2, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
 10, Appl
6, Appli
6, Appli
339, App
27, Appl
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 Sequence 2
Sequence 1
Sequence 9
 Sequence 3
Sequence 2
Sequence 1
 DB 4; Length 142;
87;
US-08-890-854-2
US-09-023-324-2
US-09-168-629-15
US-09-109-986-2
US-09-844-908-9
US-09-844-908-9
US-09-417-197-123
US-09-417-197-123
US-09-136-574A-43
US-09-136-574A-44
US-09-123-708-6
US-09-123-708-6
US-09-123-708-6
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US-09-123-708-6
US-09-123-708-6
US-09-123-708-6
US-09-123-708-6
 US-09-655-270A-11
 ALIGNMENTS
 Score 36;
Pred. No.
 Sequence 31533, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
 90.0%; Sc.__
100.0%; Pre
 ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31533
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Treating Cellulose Containing Fabrics Using Truncated Cellulase Enzyme Compositions
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 Gaps
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 GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: 4
CORRESPONDENCE ADDRESSER: STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
 STREET: Spring House Corporate Center, P.O. Box 457 CITY: Spring House STATE: PA
 Query Match 90.0%; Score 36; DB 3; Length 616; Best Local Similarity 100.0%; Pred. No. 3.4e+02; Matches 5; Conservative 0; Mismatches 0; Indels
 REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: 1997US001/CIP
TELECOMMUNICATION INFORMATION:
 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,574A
FILING DATE: 19-Aug-1998
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/932,571
FILING DATE: September 19, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
 NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
 Williams, Diane P. TITLE OF INVENTION: Compositions
 INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 616 amino acids
 RESULT 6
US-08-887-518-3
'Sequence 3, Application US/08887518
'Patent No. 5843721
 TELEPHONE: 215-540-9200
Farrington, Graha
Anderson, Paige
Gibbs, Moreland
 Bergquist, Peter
Daniels, Roy
Morgan, Hugh W.
 MEDIUM TYPE: Diskette
 TELEFAX: 215-540-5818
 TYPE: amino acid
STRANDEDNESS: single
 ZIP: 19477
COMPUTER READABLE FORM:
 COMPUTER READABLE FORM
 COUNTRY: USA
 123 DWSWL 127
 2 DWSWL 6
 APPLICANT:
 US-09-136-574A-47
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 US-09-325-932A-158

Sequence 158, Application US/09325932A

Sequence 158, Application US/09325932A

Sequence 158, Application US/09325932A

Sequence 158, Application US/09325932A

GENERAL INFORMATION:
APPLICANT: Lasham, Annette

TITLE OF INVENTION: Compositions affecting programmed cell

TITLE OF INVENTION: Compositions affecting programmed cell

TITLE OF INVENTION: Compositions affecting programmed cell

TITLE OF INVENTION: Lasham, Annette

CURRENT APPLICATION NUMBER: US/09/325,932A

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 206

SOPTWARE: FastSEQ for Windows Version 3.0
 RESULT 3
US-09-325-912A-162
US-09-325-912A-162

Sequence 162, Application US/09325932A

Patent No. 6451604
GENERAL INFORMATION:
APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant develc
FILE REFERENCE: 1022
CURRENT APPLICATION WHORE: US/09/325,932A

CURRENT APPLICATION WHORE: 1999-06-04

NUMBER OF SEQ ID NOS: 206

SOFTWARE: FastSEQ for Windows Version 3.0
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 DB 4; Length 174; 1e+02;
 90.0%; Score 36; DB 4; Length 225; illarity 100.0%; Pred. No. 1.3e+02; Conservative 0; Mismatches n. Thanh
 Length 378;
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 DB 4; Le...
7 2.2e+02;
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 0; Mismatches
 90.0%; Score 36; 100.0%; Pred. No.
 90.0%; Score 36; 100.0%; Pred. No.
 Sequence 47, Application US/09136574A Parent No. 6294366 GENERAL INFORMATION:
 ; ORGANISM: Eucalyptus grandis
US-09-325-932A-158
 ORGANISM: Eucalyptus grandis
 Query Match
Best Local Similarity 100...
Thes 5; Conservative
 Query Match
Best Local Similarity 100.
 Best Local Similarity
Matches 5; Conserv
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 128 ADWSW 132
 100 ADWSW 104
 1 ADWSW 5
 1 ADWSW 5
 US-09-325-932A-162
 RESULT 5
US-09-136-574A-47
 SEQ ID NO 158
LENGTH: 378
 SEQ ID NO 162
LENGTH: 225
 Query Match
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| Sequence 4, Application US/08890853
| Patent No: 5851812
| GENERAL INFORMATION:
| APPLICANT: Goeddel, David V.
| APPLICANT: Woronicz, John
| TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
| NUMBER OF EQUENCES: 4
| CORRESPONDENCE ADDRESS:
| STREET: 268 BUSH STREET, SUITE 3200
| STREET: CALIFORNIA
| COUNTRY: USA
 Sequence 3, Application US/09032475

Patent No. 565403

GENERAL INFORMATION:

APPLICANT: Roche, Mike

APPLICANT: Wu, Lin

TITLE OF INFORMATION:

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
 Length 745;
 Length 745;
 SOFTWARE: Patentin Feleage #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
 90.0%; Score 36; DB 2; Le 100.0%; Pred. No. 4.1e+02;
 90.0%; Score 36; DB 2; I 100.0%; Pred. No. 4.1e+02;
 100.0%; Prec. ... 0; Mismatches
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 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 797-(
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 343-4341
TELEFAX: (415) 343-4341
TELEFAX: (415) 343-4341
TELEFAX: (515) 343-4341
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TELEFAX: (515) 343-4341
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TELEFAX: (515) 343-4341
 LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
 Query Match
Best Local Similarity 100.
Matches 5; Conservative
 Best Local Similarity 100.
Matches 5; Conservative
 MOLECULE TYPE: peptide
 MOLECULE TYPE: peptide
 TOPOLOGY: linear
 739 DWSWL 743
 739 DWSWL 743
 2 DWSWL 6
 2 DWSWL 6
 FILING DATE:
 COUNTRY: U
 US-08-890-853-4
 RESULT 9
US-09-032-475-3
 US-09-023-321-3
 Query Match
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 Gaps
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 GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAM FRANCISCO
STATE: USA
COUNTRY: USA
 Query Match 90.0%; Score 36; DB 2; Length 745; Best Local Similarity 100.0%; Pred. No. 4.1e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/887,518
 CLASSIFICATION: 435
CLASSIFICATION: 435
NAME: OGMAN, RICHARD A
REGISTRATION NUMBER: 35,627
REFERENCE/DOCKET NUMBER: 197-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNES: single
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
 ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A,
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 197-008
TELECOMMUNICATION INFORMATION:
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 US-09-023-321-3
; Sequence 3, Application US/09023321
; Patent No. 5844073
 (415) 343-4341
 Floppy disk
 TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO:
 LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
 SEQUENCE CHARACTERISTICS:
 MOLECULE TYPE: peptide
 TOPOLOGY: linear
 739 DWSWL 743
MEDIUM TYPE:
 US-08-887-518-3
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SEQUENCE CHARACTERISTICS
LENGTH: 745 amino acid
 TOPOLOGY: linear
MOLECULE TYPE: peptide
 TOPOLOGY: linear MOLECULE TYPE: peptide
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 739 DWSWL 743
 2 DWSWL 6
 DWSWL 6
 STRANDEDNESS:
 TELEPHONE:
 US-09-099-125A-4
 US-09-099-124A-4
 STATE: CA
 US-09-099-124A-4
 RESULT 11
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 Gáps
 Sequence 4, Application US/09099125A

Sequence 4, Application US/09099125A

Better No. 591676

GENERAL INFORMATION:

APPLICANT: Geoddel, David V.

APPLICANT: Woronicz, John

TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALLFORNIA
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 90.0%; Score 36; DB 2; Length 745; 100.0%; Pred. No. 4.1e+02; tive 0; Mismatches 0; Indels
 ZIP: 94104

COMPUTER READABLE FORM:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,125A
 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,475
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: USA
 100.0%; Pred. ...
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
 ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
 TELEPHONE: (415) 343-4341
TELEPAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 745 amino acids
 ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
 Query Match
Best Local Similarity 100.0
Matches 5; Conservative
 TOPOLOGY: linear
MOLECULE TYPE: peptide
 TYPE: amino acid
STRANDEDNESS: si
 739 DWSWL 743
 2 DWSWL 6
 FILING DATE:
 FILING DATE:
 US-09-099-125A-4
 US-09-032-475-3
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 Sequence 4, Application US/09099124A
Patent No. 5939302
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: IKK-
NUMBER OF SEQUENCE: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
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 Length 745;
 90.0%; Score 36; DB 2; Length 745; 100.0%; Pred. No. 4.1e+02; tive 0; Mismatches 0; Indels
 COMPUTER READABLE FORM:
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COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/099,124A
 Query Match 90.0%; Score 36; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0;
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMUNICATION INFORMATION:
TELEPAN: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T9
 TELECOMMUNICATION INFORMATION:
 (415) 343-4341
 TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
 Query Match
Best Local Similarity 100.vv
-hes 5; Conservative
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Sequence 4, Application US/09023324
Patent No. 6235513
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
APPLICANT: R gnier, Catherine
TITLE OF INVENTION: IKA' Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 90.0%; Score 36; DB 3; Length 745; 100.0%; Pred. No. 4.1e+02; Live 0; Mismatches 0; Indels
 O'PERMITING SYSTEM: EL-LOSPINS-LOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,854
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN: RICHARD A
REGISTRATION NUMBER: T97-006-1
TELEROMUNICATION SA3-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: A45 amino acide
TYPE: amino acid
STRANDEDNESS: single
 ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/023,324
FILING DATE:
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FILING DATE:
ATTORNAY AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
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 268 BUSH STREET, SUITE 3200
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
 Query Match
Best Local Similarity 100.
 TOPOLOGY: linear MOLECULE TYPE: peptide
 CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
 739 DWSWL 743
 2 DWSWL 6
 US-08-890-854-4
 US-09-023-324-4
 STREET:
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 | Sequence 4, Application US/08890854
| Patent No. 623512
| GENERAL INFORMATION:
| APPLICANT: Rothe, Mike
| APPLICANT: Rothe, Mike
| APPLICANT: Rothe, Mike
| TITLE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods
| TITLE OF SEQUENCES: 5
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
| STREET: 268 BUSH STREET, SUITE 3200
| CITY: SAN FRANCISCO
| STATE: CALIFORNIA
| COUNTRY: USA
 APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
APPLICANT: Rothe, Catherine
TITLE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAM FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
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 90.0%; Score 36; DB 3; Length 745; 100.0%; Pred. No. 4.1e+02; tive 0; Mismatches 0; Indels
 ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PILING DATE: US/09/032,476
 ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMUNICATION INFORMATION:
TELEPONE: (415) 343-441
TELEPX: (415) 343-441
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
 Sequence 4, Application US/09032476
Patent No. 6235492
GENERAL INFORMATION:
 LENGTH: 745 amino acida
TYPE: amino acid
STRANDEDNESS: single
 Query Match 90.0
Best Local Similarity 100.
Matches 5; Conservative
 SEQUENCE CHARACTERISTICS:
 TOPOLOGY: linear
MOLECULE TYPE: peptide
 739 DWSWL 743
739 DWSWL 743
 2 DWSWL 6
 FILING DATE:
 US-09-032-476-4
 US-09-032-476-4
 US-08-890-854-4
 RESULT 13
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Gaps

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TENGTH: 745 amino acids
TTENGTH: 745 amino acids
TTENGTH: amino acid
STRANDEDERS: anino acid
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STRANDEDERS: anino
TOPCLOCAT: linear
WOLGCULE TYPE: peptide
US-0-033-324-4

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Search completed: February 18, 2004, 14:41:46 Job time : 8.06579 secs

739 DWSWL 743

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Sequence:

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029756 archaeoglob
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046547 pan troglod
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 ralstonia s
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 rattus norv
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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ACE RAT
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 Perfect score:
 Database :
```

Result No.

| 38.5         249         1 CYSH_SYNY3         P72794 Bynechocyst           38.6         249         1 STXA_HUMAN         060499 homo aspien           38.6         295         1 KPRS_METMA         Q9bux3 methanosarc           38.6         35.1         1 LEU3_SPIPL         Q00412 spirulina p           38.5         35.5         1 LEU3_SPIPL         Q00412 spirulina p           38.5         37.2         MTOX_SALTY         P58524 salmonella           38.5         37.2         MTOX_SALTY         P58525 salmonella           38.5         37.2         MTOX_SALTY         Q05361 streptomyce           38.5         38.0         1 SCHA_STRIAA         Q05361 streptomyce           38.5         38.6         1 BRB2_MOUSE         Q04536 salmonella           38.5         38.6         1 BRB2_MOUSE         Q054575 zea may9 (m | ALIGNMENTS | OCA STANDARD; PRT; 214 AA.        | P7125.5;<br>15-JUL-1998 (Rel. 36, Created)<br>28-FEB-2003 (Rel. 31, Last annotation update)<br>DNA repair protein radC homolog. | Andobacter capsulatus (Rhodopseudomonas capsulata).<br>Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;<br>Rhodobacteraceae; Rhodobacter.<br>NCBI_TaxID=1061; | [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=20118379; PubMed=10652786; MEDLINE=20118379; PubMed=10652786; MACHOCULAR analysis and identification of the radC gene from the "Mochercuphic bacterium Rhodobacter capsulatus B10."; Microbiol. Res. 154:233-239(1999)!- FUNCTION: INVOIVED IN DNA REPAIR (BY SIMILARITY)!- INDUCTION: Induced about five-fold after UV-irradiation. | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). | 4017; AAB18255.1; F_00018; -; 1. 6.0002; RadC. 04002; RadC, 1. PD007415; RadC; 1. 7 TIGR00608; radC; 1. PS01302; RADC; 1. 1r. 214 AA, 23792 MW; D008997B20C6743D CRC64; | n 100.0%; Score 26; DB 1; Length 214; Similarity 100.0%; Pred. No. 16; 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | LDASAL 6<br>       <br>  LDASAL 159 | PRT; 259 AA.                                          |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|-----------------------------------|---------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------|-------------------------------------|-------------------------------------------------------|
| 2334<br>2338<br>2338<br>2338<br>2338<br>2338<br>2338<br>2338                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |            | RESULT 1 RADC_RHOCA ID RADC_RHOCA | P72255;<br>15-JUL-1998<br>15-JUL-1998<br>28-FEB-2003<br>DNA repair p                                                            | Rhodobacter caps<br>Bacteria; Proteo<br>Rhodobacteraceae                                                                                                                     | [1] SEQUENCE STAIN=AT STAIN=AT STAIN=2 MEDLINE=2 "Molecula phototrop  Microbiol -!- FUNCT -!- INDUC                                                                                                                                                                                                                                                                                    | This SWIS. between the Europ use by modified entities or send a                                                                                                                                                                                                                                                                                                                                                                                                                        | EMBL; U74 HAMAP; MF INTERPRO; Pfam; PFO ProDom; P TIGRFAMS; PROSITE; DNA repai                                                                                          | Matc}<br>Local                                                                                                            | 1                                   | RESULT 2<br>ECX2 ARCFU<br>ID ECX2 ARCFU<br>AC 029756; |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |            | RESUL                             |                                                                                                                                 |                                                                                                                                                                              | 2 C C E E E E E C C C E                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 8.4.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.                                                                                                                                | Query<br>Best 1                                                                                                           | <i>8</i> %                          | RESULT<br>ECX2 A<br>ID E                              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |            |                                   |                                                                                                                                 |                                                                                                                                                                              |                                                                                                                                                                                                                                                                                                                                                                                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                                                                                                                         |                                                                                                                           |                                     |                                                       |

homo sapien pseudomonas mycobacteri

P58902 Q16619 Q9ev79

genome po genome po

dermatophag synechococc xanthomonas

P39674 P06113

saccharomyc chlamydia p

 $^{3}$ 

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Harris

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MEDLINE=98295987; PubMed=9634230;
MEDLINE=98295987; PubMed=9634230;
Gordon S.V., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Elglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamin N., Holroyd Hornsby T., Jagels K., Kroph A., McLean J., Moule S., Hamin N., Holroyd Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Sulston J.S., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
 NCBI_TaxID=1773;
 TIGR; MT1331;
 Bishai W.;
 SEQUENCE
 23
 Query Match
 Best Loca
Matches
 SCAD_HUMAN
 RESULT 4
 셤
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 ö
 Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey B.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G. (311 S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Sadow P.W., D'Andrea K.P., Bowman C., Faine B.P., Sykes S.M.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 -!- FUNCTION: Probably involved in the 3'->5' degradation of a variety
 (ArgRS).
 Gaps
 "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
 ö
 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Arginyl-ENNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase)
ARGS OR RV1292 OR MT1331 OR MTCX373.12.
 Tick; Arcara,
HAMAP; MF_00622; -; 1.
InterPro; IPR001247; 3 ExoRNase.
Pfam; PF01138; RNase_PH; 1.
Pfam; PF07725; RNase_PH C; 1.
ExoSome; Hydrolase; Nuclease; Exonuclease; Complete proteome.
eroHRNCR 259 AA; 28646 MW; E8289D46F9DDCCB3 CRC64;
 Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 100.0%; Score 26; DB 1; Length 259; 100.0%; Pred. No. 20;
 of RNA species (Potential).
-!- SUBUNIT: Component of the archaeal exosome multienzyme ribonuclease complex (Potential).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: BELONGS TO THE RNASE PH FAMILY.
 0; Indels
 Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Probable exosome complex exonuclease 2 (EC 3.1.13.-).
 550 AA.
 0; Mismatches
 or send an email to license@isb-sib.ch).
 / DSM 4304 / ATCC 49558;
 MEDLINE=98049343; PubMed=9389475;
 Archaeoglobaceae; Archaeoglobus
 EMBL; AE001070; AAB90743.1; -.
PIR; F69311; F69311.
 Local Similarity 100.
 STANDARD;
 Archaeoglobus fulgidus.
 149 LDASAL 154
 SEQUENCE FROM N.A.
 1 LDASAL 6
 Venter J.C.;
 SYR_MYCTU
010609:
 Query Match
 Best Loc
Matches
 RESULT 3
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 ö
 Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haff D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 PRINTS; PRO1038; TRNAŠYNTHARG.
TIGRARMS; TIGRO0465, args; L1.
PROSITE; PS00178; AA TRNA LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 Gaps
 diphosphate + L-arginyl-tRNA(Arg).
--- SUBUNIT: Monomer (By similarity).
--- SUBCELLULAR LOCATION: Cytoplasmic.
--- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
 "Whole genome comparison of Mycobacterium tuberculosis clinical and
 ö
 100.0%; Score 26; DB 1; Length 550; 100.0%; Pred. No. 45; 0; Indels tive 0; Mismatches 0; Indels
 laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP
 130 140 "HIGH" REGION.
550 AA; 59709 MW; 4F11239A6238124D CRC64;
 638 AA
 or send an email to license@isb-sib.ch).
 HAMAP; MF_00123; -; 1.
InterPro; IPR001278; Arg_tRNA-synt_lc.
InterPro; IPR005148; N.
InterPro; IPR001412; tRNA-synt_l.
Pfam; PF03485; N.Arg; 1.
Pfam; PF03750; tRNA-synt_ld; 1.
 100.0%; FAL.
 EMBL; AE007007; AAK45593.1; -. PIR; H70772; H70772.
 SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D
 EMBL; Z73419; CAA97757.1;
Nature 393:537-544 (1998).
 Local Similarity 100.
Les 6; Conservative
 STANDARD;
 Tuberculist; Rv1292; -.
 Complete proteome.
 1 LDASAL 6
 SCAD HUMAN
P51172;
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 15-5EP-2003 (Rel. 42, Created)
15-5EP-2003 (Rel. 42, Last sequence update)
15-5EP-2003 (Rel. 42, Last annotation update)
15-5EP-2003 (Rel. 42, Last annotation update)
5-methyltetrahydropteroyltrigluteamate--homocysteine methyltransferase
(EC 2.1.1.4) (Methionine synthase, vitamin-B12 independent isozyme)
 28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Amiloride-sensitive sodium channel delta-subunit (Epithelial Na+
channel delta subunit) (Delta ENAC) (Nonvoltage-gated sodium channel
scunID OR DNACH.
 SUBCELLULÂR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNEL
 Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
 100.0%; Score 26; DB 1; Length 638;
 InterPro; LEAL.
PERM; PF00858; ASC; 1.
PRINTS; PR01078; AMINACHANNEL.
TIGROMS; TIGRO0859; ENAC; 1.
PROSITE; PS01206; ASC; 1.
PROSITE; PS01206; ASC; 1.
CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
 321E9597D6A78D38 CRC64;
 745 AA
 Pred. No. 53;
0; Mismatches
 POTENTIAL.
 EMBL; AF038165; AAB92659.1; -.
InterPro; IPR004724; EnaC.
InterPro; IPR001873; Na+channel_ASC.
 70187 MW;
 100.08;
 6; Conservative
 STANDARD;
 530
551
 531
552
166
211
384
384
 551 LDASAL 556
 Best Local Similarity
 1 LDASAL 6
 NCBI_TaxID=9598;
 CORGL
 TRANSMEM
 CARBOHYD
 Query Match
 CARBOHYD
 SEQUENCE
 METE COR
QBNRE3;
 DOMAIN
 RESULT 6
METE_CORGL
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 2244488
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 ö
 Gaps
 01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Amiloride sensitive sodium channel delta-subunit (Epithelial Na+
channel delta subunit) (Delta ENSC) (Nonvoltage-gated sodium channel
1 delta subunit) (SCNED) (Delta NaCH).
 SEQUENCE FROM N.A.
MEDLINE=96070858; PubMed=7499195;
Waldmann R., Champigny G., Bassilana F., Voilley N., Lazdunski M.
"Molecular cloning and functional expression of a novel amiloride
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 POTENTIAL.
(YTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
 ö
 Score 26; DB 1; Length 638;
Pred. No. 53;
 Interpro; Leaves ASC; 1.
Pfam; PP00858; ASC; 1.
TIGREAMS; TICR00859; ENAC; 1.
PROSITE; PS01206; ASC; 1.
Ionic channel; Transmembrane; Ion transport; Glycoprotein.
 Indele
 EXTRACELLULAR (POTENTIAL).
 7CD5181F8497F5CF CRC64;
 ö
 638 AA.
 0; Mismatches
 PRT;
(Rel. 34, Created)
 70274 MW;
 100.08;
 EMBL; U38254; AAC50283.1; -.
 100.00
 PIR; 139196; 139196.
Genew; HGNC:10601; SCNNID.
 Conservative
 STANDARD;
 Homo sapiens (Human)
 166
211
384
638 AA;
 LDASAL 556
 Best Local Similarity
Matches 6; Conser
 1 LDASAL 6
 NCBI_TaxID=9606;
 SCAD PANTR
046547;
 FAMILY.
 DOMAIN
TRANSMEM
DOMAIN
 551
 FRANSMEM
 CARBOHYD
 SEQUENCE
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Gaps

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0; Indels

CARBOHYD

Query Match

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SCAD\_PANTR RESULT 5

us-09-643-260-3.rsp

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SEQUENCE
 Query Match
 Matches
 RESULT 8
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 ;
0
 "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBD databases.
-!- FUNCTION: Catalyzes the transfer of a methyl group from 5-
methyltetrahydrofolate to homo
 HAMAP; MF_0017; -; 1.
InterPro; IRR005629; Met syn Bl2ind.
InterPro; IPR006276; Met syn Bl2ind.
Pfam; PF01717; Methionine synt; 1.
Probom; PD046692; Methionine synt; 2.
TIGRPAMS; TIGR01371; met synt; 2.
TIGRPAMS; Methyltransferase; Methionine biosynthesis; Zinc; Repeat;
 formation (By similarity).
--- CATALYTIC ACTIVITY: 5-methyltetrahydropteroyltri-L-glutamate + L-monocygtefine = tetrahydropteroyltri-L-glutamate + L-methionine.
--- COFACTOR: Zinc; binds one ion per subunit (By similarity).
--- PATHWAY: Terminal step in the de novo biosynthesis of methionine.
--- SIMILARITY: Belongs to the vitamin-B12 independent methionine.
 Gaps
 MEDLINE=21848401; PubMed=11859360;
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 .
0
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 100.0%; Score 26; DB 1; Length 745; 100.0%; Pred. No. 62;
 Indels
 81312 MW; 856E05DE7398ED1F CRC64;
 0.00280; 094482; 0905K9; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 17-28-FEB-2003 (Rel. 41, Last annotati
 Corynebacterium glutamicum (Brevibacterium flavum).
 ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
 ;
 PRT; 855 AA.
(Cobalamin-independent methionine synthase)
 SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 0; Mismatches
 EMBL; AP005277; BAB98532.1; -.
 6; Conservative
 STANDARD;
 synthase family.
 140 LDASAL 145
 745 AA;
 Schizosaccharomyces
 Best Local Similarity
Matches 6; Conserv
 Complete proteome.
 SEQUENCE FROM N.A.
 1 LDASAL 6
 NCBI_TaxID=4896;
 NCBI_TaxID=1718;
 Nakagawa S.;
 SCHPO
 SEQUENCE
 Query Match
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SCHPO
 1D PAC DATE OF THE PACE OF THE
SO THE TENT AND DESCRIPTION OF
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RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornaby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
A James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Monory P., Moule S., Mungall K., Murphy L., Nibhett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Faylor K., Taylor R.G., Holzer R., Schaefer M., Mullbert H.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Mocstl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Mocstl D., Hilbert H.,
RA Gabel C., Fuchs W., Enger M., Schaefer M., Mullbert H.,
RA Gabel C., Fuchs W., Fritzc C., Holzer E., Mocstl D., Hilbert H.,
RA Goffeau A., Cadieu B., Dreano S., Caloux S., Lelaure V., Mottier S.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
A Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RT "The genome sequence of Schizosaccharomyces pombe.";
RT "The genome sequence of Schizosaccharomyces pombe.";
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 ö
 SEQUENCE OF 566-855 FROM N.A.
MEDLINE=98382525; PubMed=9714831;
Hoe K.-L., Won M.S., Chung K.-S., Park S.-K., Kim D.-U., Jang Y.-J.,
Yoo O.-J., Yoo H.-S.,
"Molecular cloning of gafl, a Schizosaccharomyces pombe GATA factor,
which can function as a transcriptional activator.";
Gene 215:319-328(1988).
 Gaps
 ;
0
 GRAKEL; SM00401; ZDF GATA; 1.

PROSITE; PS00344; GĀTA_ZN_FINGER_1; 1.

PROSITE; PS50114; GATA_ZN_FINGER_2; 1.

Transcription regulation; Activator; DNA-binding; Zinc-finger; ZN_FING
 100.0%; Score 26; DB 1; Length 855; 100.0%; Pred. No. 72;
 Indels
 855 AA; 91776 MW; 3D932F83D2DE6774 CRC64;
 -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: Contains 1 GATA-type zinc finger.
 Mismatches
 .
0
 EMBL; AL035076; CAA22647.1; -. EMBL; AL049521; CAB40003.1; -.
 GeneDB SPombe; SPCC1902.01; -.
InterPro; IPR000679; Znf_GATA.
Pfam; PF00120; GATA.1.
PRINTS; PR0019; GATAZNFINGER.
SWART; SM00401; ZnF_GATA; 1.
 EMBL; L31601; AAC35593.1; -. PIR; T41336. HSSP; P17429; 4GAT. TRANSFAC; T02831; -.
 6; Conservative
 211 LDASAL 216
 Local Similarity
 1 LDASAL 6
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FUNCTION: THIS ENZYME CATALYZES THE 6-ELECTRON REDUCTION OF SULFITE TO SULFIDE. THIS IS ONE OF SEVERAL ACTIVITIES REQUIRED FOR THE BIOSYNTHESIS OF L-CYSTEINE FROM SULFATE (BY SIMILARITY). CATALYTIC ACTIVITY: H(2)S + 3 NADP(+) + 3 H(2)O = sulfite + 3
 Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
 Schizosaccharomyces pombe (Fission yeast)
 6; Conservative
 699
 Cysteine biosynthesis.
NP_BIND 658 669
NP_BIND 788 798
 Schizosaccharomyces
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=4896
 NADPH.
 SEQUENCE
 Matches
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 ö
 SEQUENCE FROM N.A.
STRAIN=El Tor N16961 / Serotype Ol;
STRAIN=El Tor N16961 / Serotype Ol;
STRAIN=El Tor N16961 / Serotype Ol;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson M.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermoleava M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 HAMAP; ME 00049; -; 1.

INTERPOS; IRRO02302; LEG-TRNABYNTIA.
INTERPOS; IRRO01320; LEG-TRNABYNTIA.
INTERPOS; IRRO01412; LRNA-BYNTE_IA.
PRINTS; PRO00355; TRNA-SYNTE_I; 1.
PRINTS; PRO00355; TRNA-SYNTE_II.
TIGRFAMS; TIGRESS; TRNA-LIGASE_I; 1.
PROSITE; PS00178; AA TRNA-LIGASE_I; 1.
Aninoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 Gaps
 -1- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP + diphosphate + L-leucyl-tRNA(Leu).
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family
SYL_VIBCH STANDARD; PRT; 858 AA.
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last annotation update)
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeurS).
 "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 ;
 100.0%; Score 26; DB 1; Length 858; 100.0%; Pred. No. 73; 1. Indels tive 0; Mismatches 0; Indels
 Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales,
Vibrionaceae, Vibrio.
 01-FEB-1996 (Rel. 33, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
Probable sulfite reductase [NADPH] flavoprotein component (EC 1.8.1.2).
 "HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY).
A4D59A2E1C9F1292 CRC64;
 PRT; 1006 AA.
 EMBL; AE004177; AAF94118.1; ALT_INIT.
TIGR; VC0956; -
 96621 MW;
 Query Match
Beet Local Similarity lou.v.
Est Conservative
 Nature 406:477-483 (2000).
 STANDARD;
 621
 858 AA;
 688 LDASAL 693
 Complete proteome.
 1 LDASAL 6
 618
 Vibrio cholerae
 NCBI_TaxID=666;
 MT10 SCHPO
Q09878;
 cholerae.
 SEQUENCE
 BINDING
 MT10_SCHPO
 RESULT 9
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 8844488
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 ö
 Gaps
COFACTOR: THIS SUBUNIT IS A FLAVOPROTEIN THAT BINDS ONE FMN AND
 Pfam; PF00667; FAD binding 1; 1.
Pfam; PF00175; NAD binding 1; 1.
PRINTS; PR00371; PPNCR.
Oxidoreductase; Flavoprotein; NADP; FAD; FWN; Electron transport;
 ö
 788 798 FAD (FLAVIN PART) (BY SIMILARITY)
1006 AA; 111352 MW; 2EA2086D69561D33 CRC64;
 DB 1; Length 1006;
 (ADP PART) (BY SIMILARITY)
 0; Indels
 Score 26; DB
Pred. No. 86;
 0; Mismatches
 ONE FAD PER CHAIN (BY SIMILARITY).
 GeneDB_SPombe, SPCC584.01c; -.
InterPro, 18R003097; FAD_binding.
InterPro, 18R001709; FW Cyt_redctes.
InterPro, 18R001433; Oxred_FAD/NAD(P)
 FAD
 EMBL; AL032824; CAA21818.2; -. PIR; T41439; T41439.
HSSP; P00388; IAMO.
 100.0%;
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 01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Angiotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1)
(ACE) (Dipeptidyl carboxypeptidase I) (Kininase II).
 kattus norvegicus (kat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF THE TERMINAL HIS-LEU, THIS RESULTES IN AN INCREASE OF THE VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN.

-!- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide, oligopeptide |- Xaa-Xbb, when Xaa is not Pro, and Xbb is neither Asp nor Glu. Converts angiotensin I to angiotensin II.

-!- COPACTOR: Binds 2 zinc ions (By similarity).
-!- SUBCELLUAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
EVent-Alternative splicing; Named isoforms=2;
 SEQUENCE FROM N.A. STRAIN=Lewis/N; TISSUB=Lung; Jatarian-Tehrani M., Listwak S., Barrientos R.M., Michaud A., Jatwak S., Barrientos R.M., Michaud A., Corvol P., Sternberg E.M.; "Characterization of a missense mutation in the angiotensin I-converting enzyme cDNA in exudative inflammation resistant F344/N
 "Angiotensin converting enzyme and genetic hypertension: cloning of rat cDNAs and characterization of the enzyme."; Biochem. Biophys. Res. Commun. 198:380-386 (1994).
 ProDom; PD004184; Peptidase M2; 2.
PROSITE; PS00142; ZINC PROTEASE; 2.
Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;
 TISSUE=Lung;
MEDLINE=94121658; PubMed=8292044;
Koike G., Krieger J.E., Jacob H.J., Mukoyama M., Pratt R.E.,
 Name=Testis-specific;
IsoId=P47820-2; Sequence=Not described;
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
 PRT; 1313 AA.
 IsoId=P47820-1; Sequence=Displayed;
 InterPro, IPR001548; Peptidase M2.
InterPro; IPR006025; Zn MTpeptdse.
Pfam: PF01401; Peptidase M2; 2.
PRINTS; PR00791; PEPDIFTÄAEA.
 EMBL; AF201332; AAG35597.1; -.
 (Rel. 33, Created)
 EMBL; U03708; AAA82110.1; -.
EMBL; U03734; AAA82111.1; -.
 STANDARD;
 Rattus norvegicus (Rat)
 PIR; JC2038; JC2038.
MEROPS; M02.001; -.
 LDASAL 559
 SEQUENCE FROM N.A.
 NCBI_TaxID=10116;
 Name=Somatic
 01-FEB-1996
 ACE OR DCP1
 554
 RESULT 10
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 STRAIN=JAL-1 DSN 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Karlavage A.R., Budherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Stott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
 Gaps
 ANGIOTENSIN-CONVERTING ENZYME, SOMATIC
Repeat; Signal; Alternative splicing
 SIMILARITY)
SIMILARITY)
 (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 ;
0
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 Length 1313;
 0; Indels
 8CB5D0015F129591 CRC64;
 Methanococcus jannaschii.
Archaea; Buryarchaeota; Methanococci; Methanococales;
Methanocaldococcaceae; Methanocaldococcus.
NCBI_TaxID=2190;
 EXTRACELLULAR (POTENTIAL)
 CYTOPLASMIC (POTENTIAL)
 (BY
(BY
 (BY
 Score 26; DB 1; I
Pred. No. 1.1e+02;
 1 (BY SIMILARITY).
ZINC 1 (CATALYTIC)
ZINC 2 (CATALYTIC)
2 (BY SIMILARITY).
 jannaschii.";
Science 273:1058-1073(1996).
-i- SIMILARITY: BELONGS TO THE UPF0129 FAMILY.
 (GLCNAC
 (GLCNAC
 (GLCNAC.
 (GLCNAC
 (GLCNAC
 (GLCNAC
 (GLCNAC
 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
 (GLCNAC
 197 AA
 Mismatches
 SIMILARITY
 ZINC 2 (CA
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
N-LINKED
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N-LINKED
 N-LINKED
 N-LINKED
 ZINC 1
 ISOFORM
 150907 MW;
 ;
 100.0%;
 31ycoprotein; Transmembrane;
 Hypothetical protein MJ1474.
 6; Conservative
 STANDARD;
 1313 AA;
 600 LDASAL 605
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 1 LDASAL 6
 36
 28-FEB-2003
 YE74 METUA
 METAL
ACT_SITE
METAL
 METĀL
CARBOHYD
 CARBOHYD
CARBOHYD
CARBOHYD
 RANSMEM
 SITE
 CARBOHYD
 SEQUENCE
 CARBOHYD
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 CARBOHYD
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 CARBOHYD
 CARBOHYD
 CARBOHYD
 CARBOHYD
 VARIANT
 058869;
 SIGNAL
 DOMAIN
 DOMAIN
 REPEAT
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 MEDLINE=91330891; PubMed=1714386;
Elledge S.J., Spottswood M.R.;
"A new human p34 protein kinase, CDK2, identified by complementation
of a cdc28 mutation in Saccharomyces cerevisiae, is a homolog of
 Rieder M.J., Livingston R.J., Braun A.C., Montoya M.A., Chung M.-W., Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A., Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
 Α.
 MEDLINE=91367262; PubMed=1653904;
TBai L.-H., Harlow E., Meyerson M.;
Tsolation of the human cdk2 gene that encodes the cyclin A- and adenovirus E1A-associated p33 kinase.";
Nature 353:174-177(1991).
 01-MAR-1992 (Rel. 21, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Cell division protein kinase 2 (EC 2.7.1.-) (p33 protein kinase)
 .
 MEDLINE=92020980; PubMed=1717994;
Ninomiya-Teuji J., Nomoto S., Yasuda H., Reed S.I., Matsumoto Ninomiya-Teuji J., Nomoto S., Yasuda H., Reed S.I., Matsumoto I "Cloning of a human cDNA encoding a CDC2-related kinase by complementation of a budding yeast cdc28 mutation.";
Proc. Natl. Acad. Sci. U.S.A. 88:9006-9010(1991).
 Score 24, DB 1; Length 197;
Pred. No. 51;
1; Mismatches 0; Indels
 70075BB626934F58 CRC64;
 TIGR; MJ1474; -...
HAMAP; MF 00265; -; 1.
InterPro; IPR002651; DIF133.
InterPro; IPR002716; PIN.
InterPro; IPR006596; PIN.
Promo, PP0113236; PINC.
Promo, PP0113236; PINC.
Propon; PD013236; PINC; 1.
Propothetical protein; Complete proteome.
DOMAIN 181 197 LYSTRICH.
 298 AA.
 SEQUENCE 197 AA; 22781 MW;
 92.3%;
83.3%;
 EMBL; U67588; AAB99480.1; -.
 Xenopus Egl.";
EMBO J. 10:2653-2659(1991).
 Query Match
Best Local Similarity 83.3.
 STANDARD;
 PIR; A64484; A64484.
 sapiens (Human)
 |||||:
36 LDASAI 41
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 1 LDASAL 6
 SEQUENCE FROM N.A.
TISSUE=Placenta;
 NCBI_TaxID=9606;
 CDK2 HUMAN
 CDK2_HUMAN
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
Richards S.A., McEwan P.J., McKernan K.J., Lu X., Gibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Kachards J., Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Kzzywinski M.I., Skalska U., Smailus D.E.,
Rodriguez A.C., Grimwood J., Schmutz J., Myere R.M.,
Butterfield Y.S.N., Kzzywinski M.I., Skalska U., Smailus D.E.,
Mhan and mouse cDNA sequences."
 MEDLINE-97075215; PubMed=8917641; Schulze-Gahmen U., de Bondt H.L., Kim S.-H.; Schulze-Gahmen U., de Bondt H.L., Kim S.-H.; High-resolution crystal structures of human cyclin-dependent kinase 2 with and without ATP: bound waters and natural ligand as guides for inhibitor design."; J. hed. Chem. 39:4540-4546(1996).
 PHOSPHORYLATION SITES.
MEDLINE=33010995; PubMed=1396589;
Gu Y., Rosenblatt J., O'Morgan D.O.;
"Cell cycle regulation of CDK2 activity by phosphorylation of Thr160 and Tyr15.";
 X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF COMPLEX WITH CG2A AND KIP1. MEDLINE=96300318; PubMed=8684460; Russo A.A., Jeffrey P.D., Patten A.K., Massague J., Pavletich N.P.; "Crystal structure of the p27Kip1 cyclin-dependent-kinase inhibitor bound to the cyclin A-Cdk2 complex."; Mature 382:325-331(1996).
 X-RAY CRYSTALLOGRAPHY (2.33 ANGSTROMS) OF COMPLEX WITH L868276. WEDLINES=95181476; PubMed=6861010, de Azevedo WF. Jr., Muleer-Dieckann H.-J., Schulze-Gahmen U., Worland P.J., Sausville E., Kim S.-H.; potency of a flavonoid "Structural basis for specificity and potency of a flavonoid inhibitor of human CDE2, a cell cycle kinase."; Proc. Natl. Acad. Sci. U.S.A. 93:2735-2740(1996).
 Ä
 X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF COMPLEX WITH CYCLIN
 MEDLINE-95356811; Pubmed-7630397;
Jeffrey P.D., Russo A.A., Polyak K., Gibbs E., Hurwitz J.,
Massague J., Pavletich N.P.;
 K-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH CG2A
 MEDLINE=96313126; PubMed=8756328;
Russo A.A., Jeffrey P.D., Pavletich N.P.;
"Structural basis of cyclin-dependent kinase activation by
 "Mechanism of CDK activation revealed by the structure cyclinA-CDK2 complex.";
 MEDLINE=93288132; PubMed=8510751; de Bondt H.L., Jones H.D. de Bondt H.L., Rosenblatt J., Jancarik J., Jones H.D. Morgan D.O., Kim S.-H., "Crystal structure of cyclin-dependent kinase 2.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 Nat. Struct. Biol. 3:696-700(1996).
 EMBO J. 11:3995-4005 (1992).
 Nature 363:595-602(1993).
 Nature 376:313-320(1995).
 phosphorylation
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298 AA
 Pred. No. 80;
1; Mismatches
 IsoId=Q63699-1; Sequence=Displayed;
 92.3%;
83.3%;
 SIMILARITY).
ALTERNATIVE PRODUCTS:
 5; Conservative
 STANDARD;
 Rattus norvegicus (Rat).
 CDC2/CDKX SUBFAMILY.
PDB; 1H1S; 19-SEP-02.
PDB; 1H24; 01-FEB-03.
PDB; 1H25; 01-FEB-03.
PDB; 1H26; 01-FEB-03.
PDB; 1H26; 01-FEB-03.
PDB; 1H28; 01-FEB-01.
PDB; 1H29; 11-DEC-01.
PDB; 1KE5; 14-MAY-02.
PDB; 1KE7; 14-MAY-02.
PDB; 1KE9; 14-MAY-02.
PDB; 1KE9; 14-MAY-02.
PDB; 1KE9; 14-MAY-02.
 Name=CDK2-alpha;
 Name=CDK2-beta;
 Query Match
Best Local Similarity
Matches 5; Conserv
 91 MDASAL 96
 SEQUENCE FROM N.A.
 1 LDASAL 6
 NCBI_TaxID=10116;
 063699; 009136;
 CDK2 RAT
 RESULT 13
 -
 <u>-</u>;
 CDK2_RAT
 22222222222
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 -i - FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYCLE.
INTERACTS WITH CYCLINS A, D, OR E. ACTIVITY OF CDK2 IS MAXIMAL
DURING S PHASE AND G2.
-i - ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES
THE REXAME, WHILE PHOSPHORYLATION AT THR-160 ACTIVATES IT.
-i - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
-CDC2/CDKX SUBFAMILY.
 X-RAY CRYSTALLOCRAPHY (2.05 ANGSTROMS).
MEDLINE=99342369; PubMed=9677190;
Gray N.S., Wodicka L., Thunnissen A.-M.H., Norman T.C., Kwon S.,
Espinoza F.H., Morgan D.O., Barnes G., Leclerc S., Meijer L.,
Kim S.H., Lockhart D.J., Schultz P.G.;
"Exploiting chemical libraries, structure, and genomics in the search
for kinase inhibitors.";
Science 281:533-538(1998).
 MEDLINE=96182647; PubMed=8601310;
Bourne Y., Watson M.H., Hickey M.J., Holmes W., Rocque W., Reed S.I.,
Tainer J.A.;
 "Crystal structure and mutational analysis of the human CDK2 kinase complex with cell cycle-regulatory protein CksHs1."; Cell 84:863-874(1996).
 "Protein kinase inhibition by staurosporine revealed in details of
the molecular interaction with CDK2.";
Nat. Struct. Biol. 4:796-801(1997).
 Lawrie A.M., Noble M.E.M., Tunnah P., Brown N.R., Johnson L.N.,
 X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITG CKS1.
 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 MEDLINE=97475219; PubMed=9334743;
 AF512553; AAM34794.1; -. BC003065; AAH03065.1; -. A41227; A41227.
 EMBL; X61622; CAA43807.1; -.
EMBL; X62071; CAA43985.1; -.
EMBL; M68520; AAA35667.1; -.
 19-SEP-02.
19-SEP-02.
19-SEP-02.
 09-MAY-01
 14-NOV-01.
06-FEB-02.
 06-NOV-02.
06-FEB-02.
 07-DEC-96
 31-MAY-00
 27-JAN-97
 12-NOV-97
 29-JUL-97
 28-JAN-03
 10-MAY-01
 27-DEC-00
 17-JAN-01
 17-JAN-01
 11-JAN-97
 CKP;
 AQ1;
 DM2;
 E1X;
 FW;
 MBL;
 EMBL;
 PTR (2008) (2008
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 SEQUENCE OF 19-124 FROM N.A.

REDLINE=96113578; Pubmed=8673024;

REDLINE=96113578; Pubmed=8673024;

HOSGNAWA Y., Yang M., Kaneko S., Tanaka M., Nakashima K.;

HOSGNAWA Y., Yang M., Kaneko S., Tanasition in rat Nb2 pre-T during the prolactin-induced G1/S transition in rat Nb2 pre-T lymphoma cells.";

Biochem. Mol. Biol. Int. 37:393-399(1995).

-! FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYCLE.

INTERACTS WITH CYCLINS A, D, OR E. ACTIVITY OF CDK2 IS MAXIMAL DURING S PHASE AND G2.

-! ENZYME REGULATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES

-!- ENZYME, WHILE PHOSPHORYLATION AT THR-160 ACTIVATES IT (BY
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 TISSUB=Thyroid;
MEDLINE=95166553; PubMed=7862443;
Kotani S., Endo T., Kitagawa M., Higashi H., Onaya T.;
"A variant form of cyclin-dependent kinase 2 (Cdk2) in a malignantly transformed rat thyroid (FRTL-TC) cell line.";
Oncogene 10:663-669(1995)
 IsoId=Q63699-2; Sequence=Not described;
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 ;
0
Score 24; DB 1; Length 298;
Pred. No. 80;
 0; Indels
 Event=Alternative splicing; Named isoforms=2;
 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-BEB-2003 (Rel. 41, Last annotation update)
Cell division protein kinase 2 (EC 2.7.1.).
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Best Local Similarity 83.3
Matches 5, Conservative
 STANDARD;
 Shigella flexneri.
 91 MDASAL 96
 1 LDASAL 6
 ALF ECOLI
P11604;
 NP BIND
BINDING
ACT SITE
MOD RES
MOD RES
 MOD_RES
VARSPLIC
 SEQUENCE
 Query Match
 Matches
8
 名
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 STRAIN=CS7BL/6;
Jun D., Lee Y.H., Park H.K., Kim Y.H.;
"Exon-intron organization of the murine cyclin-dependent kinase-2 genes Cdk2-alpha and Cdk2-beta.";
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
 ;
0
 92.3%; Score 24; DB 1; Length 298; 83.3%; Pred. No. 80; ive 1; Mismatches 0; Indels
 V -> C (IN REF. 2).
L -> I (IN REF. 2).
L -> C (IN REF. 2).
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MEDLINE=21156231; Pubmed=11258796;
Hayashi T., Makino K., Ohnelbi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Ilda T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
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O157:H7 and genomic comparison with a laboratory strain K-12.";
 "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
 MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Xang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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 SPECIES=E.coli; STRAIN=KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
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Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.",

Nature 409:529-533(2001).
 Alefounder P.R., Baldwin S.A., Perham R.N., Short N.J.; "Cloning, sequence analysis and over-expression of the gene for the class II fructose 1,6-bisphosphate aldolase of Escherichia coli."; Biochem. J. 257:529-534 (1989)
 SPECIES=E.coli; STRAIN=K12 / W3110;
MEDLINE=98263247; PubMed=9600841;
Wilkins M.R., Gasteiger E., Tonella L., Ou K., Tyler M.,
Sanchez J.-C., Gooley A.A., Walsh B.J., Bairoch A., Appel R.D.,
Williams K.L., Hochstrasser D.F.;
"Protein identification with N and C-terminal sequence tags in
 "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
 SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
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Link A.J., Robison K., Church G.M.;
Comparing the predicted and observed prop
in the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313(1997).
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 MEDLINE=89193446; PubMed=2649077;
 J. Mol. Biol. 278:599-608(1998).
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[9]
ZINC-LIGANDS, AND MUTAGENESIS.

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 Hall D.R., Leonard G.A., Reed C.D., Watt C.I., Berry A., Hunter W.N.;
"The crystal structure of Escherichia coli class II fructose-1,
"Disphosphate aldolase in complex with phosphoglycolohydroxamate
reveals details of mechanism and specificity.";
J. Mol. Biol. 287:383-394(1999).
-!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
phosphate + D-glyceraldehyde 3-phosphate.
-!- CATALYTIC ACTIVITY: altoriance aldolase.
-!- Grammax Glycolysis; sixth step.
-!- SUBUNT: Homodimer.
-!- SUBUNT: Belongs to class II fructose-bisphosphate aldolase
 Berry A., Marshall K.E.;
"Identification of zinc-binding ligands in the class II fructose-1,6-
bisphosphate aldolase of Escherichia coli.";
 Cooper S.J., Leonard G.A., McSweeney S.M., Thompson A.W.,
Naismith J.H., Qamar S., Plater A., Berry A., Hunter W.N.;
"The crystal structure of a class II fructose-1,6-bisphosphate
aldolase shows a novel binuclear metal-binding active site embedded
in a familiar fold.";
 SPECIES=E.coli;
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 FEBS Lett. 318:11-16(1993).
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US-10-044-957-18

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US-10-10-170-1612

US-10-171-161A-187

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FRIOR FILING DATE: 2000-08-22
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Sequence 8434, Satoshi
APPLICANT: SHERA, HARNO
APPLICANT: HARNA, UNN
APPLICANT: HARNA, HROSHI
APPLICANT: SHERA, TAPAYOSHI
APPLICANT: SAKAKI, YOSHTVUKI
APPLICANT: HATTORI, MASAHIRA
TITLE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2001-05-30
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Publication No. US20030119018A1
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APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
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APPLICANT: SHIRAMA, HROSHI
APPLICANT: SHIBA, TADAYOSHI
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 20 LDASAL 25
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 US-10-156-761-13332
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 APPLICANT: Findeis, Mark A
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APPLICANT: Phillips, Kathryn
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APPLICANT: May, Michael J.
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APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
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ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
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SENOO, AKIHIRO
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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HINOSHI
APPLICANT: SHIBA, HADAYOSHI
APPLICANT: SHARA, HONSHI
APPLICANT: SHARA, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-26
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13333
LENGTH: 191
 APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPRENDENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PELLING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13332
LENGTH: 191
 Sequence 14915, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
 Sequence 13333, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
 ORGANISM: Streptomyces avermitilis US-10-156-761-13332
 , ORGANISM: Streptomyces avermitilis US-10-156-761-13333
SAKAKI, YOSHIYUKI
 6; Conservative
 41 LDASAL 46
 Query Match
Best Local Similarity
 41 LDASAL 46
 1 LDASAL 6
 1 LDASAL 6
 RESULT 8
US-10-156-761-14915
APPLICANT:
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Matches

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SEQ ID NO 18
LENGTH: 638
 US-10-133-157-8
 TYPE: PRT
 FEATURE:
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 Gaps
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 APPLICANT: Habernauer, Gregor
APPLICANT: Habernauer, Gregor
APPLICANT: Habernauer, Gregor
APPLICANT: Lee, Heung-Schick
APPLICANT: Lee, Heung-Schick
APPLICANT: Hwang, Byung-Joon
TITLE OF INVENTION: CRENBEACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-1212C2
CURRENT FILING DATE: 2000-12-22
PRIOR PLICATION NUMBER: US/605124
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR PLICATION NUMBER: 60/14031
PRIOR PLILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-02
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PRIOR FILING DATE: 2000-03-09
PRIOR FILING DATE: 2000-03-09
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 100.0%; Score 26; DB 11; Length 600; 100.0%; Pred. No. 5.3e+02;
 Indels
TITLE OF INVENTION: No. US20030236392Alel full length cDNA
 0; Mismatches
 FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE:
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3578
LENGTH: 374
 Sequence 106, Application US/09746660A Publication No. US20030049804A1 GENERAL INFORMATION:
 TYPE: PRT ORGANISM: Corynebacterium glutamicum
 Schroder, Hartwig
Zelder, Oskar
Haberhauer, Gregor
 APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
 Query Match
Best Local Similarity 100.
Matches 6; Conservative
 TYPE: PRT
CORGANISM: Homo sapiens
US-10-104-047-3578
 287 LDASAL 292
 1 LDASAL 6
 US-09-746-660A-106
 US-09-746-660A-106
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140 LDASAL 145

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RESULT 12

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 Sequence 8, Application US/10133157
Publication No. US20020184054A1
GENERAL INFORMATION:
APPLICANT: CALLAMARAS, NICHOLAS
APPLICANT: CHANG, HONG
TITLE OF INVENTION: HIGH THROUGHPUT CELL-BASED ASSAY FOR MONITORING SODIUM
TITLE OF INVENTION: CHANNEL ACTIVITY AND DISCOVERY OF SALIY TASTE
TITLE OF INVENTION: MOULLATING COMPOUNDS
FILE REFERENCE: 078003-0280790
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 100.0%; Score 26; DB 10; Length 638; 100.0%; Pred. No. 5.6e+02; tive 0; Mismatches 0; Indels
 Length 638;
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 100.0%; Score 26; DB 14; 100.0%; Pred. No. 5.6e+02;
Sequence 18, Application US/09983204
Patent No. US20020173000A1
GENERAL INFORMATION:
APPLICANT: RENARD, STEPHANE
APPLICANT: BESNARD, FRANCOIS
APPLICANT: BESNARD, FRANCOIS
APPLICANT: RENARM, DAVID
ITLE OF INVENTION: SODIUM CHANNEL RECEPTOR
FILE REPERENCE: 07586.0010
CURRENT FILING DATE: 2001-10-23
FRIOR APPLICATION NUMBER: 09/424,666
PRIOR PILING DATE: 2001-02-22
RIOR APPLICATION NUMBER: PCT/FP98/02884
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 97401196.7
PRIOR PILING DATE: 1997-05-30
NUMBER OF SEQ 1D NOS: 19
SOFTWARE PLANCE DATE: 1997-05-30
NUMBER OF SEQ 1D NOS: 2.0
 CURRENT APPLICATION NUMBER: US/10/133,157
CURRENT FILING DATE: 2002-04-26
PRIOR PILING DATE: 2002-05-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENT VET: 2.1
SEQ ID NO 8
LENGTH: 638
 US-09-738-626-6815
; Sequence 6815, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
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Best Local Similarity 10v.
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Best Local Similarity 100.
Matches 6; Conservative
 ; OTHER INFORMATION: HNACHD US-09-983-204-18
 TYPE: PRT
ORGANISM: Homo sapiens
 ; ORGANISM: Homo sapiens US-10-133-157-8
 551 LDASAL 556
 551 LDASAL 556
 1 LDASAL 6
 1 LDASAL 6
 RESULT 14
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 Query Match

100.0%; Score 26; DB 12; Length 704;

Best Local Similarity 100.0%; Pred. No. 6.2e+02;

Matches 6; Conservative 0; Mismatches 0; Indels (
 Sequence 3501, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1
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; TITLE OF INVENTION: No. US20030236392A1e1
; CURRENT APPLICATION NUMBER:
; CURRENT FILING DATE: 2002-03-25
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3501
 Query Match 100.0%; Score 26; DB 10; Length 659; Best Local Similarity 100.0%; Pred. No. 5.8e+02; Matches 6; Conservative 0; Mismatches 0; Indels
APPLICANT: NAKAGAWA, SATUSHI,
APPLICANT: MAZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, ARIO
APPLICANT: OZAKI, ARIO
APPLICANT: OYOUE POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-12-9
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PALGHIN VET: 3.0
LENGTH: 659
 ORGANISM: Corynebacterium glutamicum US-09-738-626-6815
 TYPE: PRT
GRGANISM: Homo sapiens
US-10-104-047-3501
 617 LDASAL 622
 132 LDASAL 137
 1 LDASAL 6
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us-09-643-260-3.rai

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ZIP: 02109-2170
COMPUTER READABLE FORM:
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 US-08-989-299-9
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and is derived by analysis of the total score distribution.
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 US-09-252-991A-17296
US-08-989-299-9
US-09-149-9
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US-09-480-991-18
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US-08-370-225-16
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US-09-417-197-115
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Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Issued_Patents_AA:*
 Minimum DB seq length: 0
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 US-09-643-260-3
26
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Match Length DB
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 Title:
Perfect score:
 Sequence:
 Searched:
 Database
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 Result
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APPLICATION TO RUBERIAL AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE DE TUNENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PAPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR APPLICATION NUMBER: US 60/094,190
FRIOR APPLICATION NUMBER: US 60/094,190
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17296
LENGTH: 293
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TYPE: PRT
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J. SEQUENCE OF SQUARE

J. PARPLICANT: ACTON, SUBBAL L.

APPLICANT: RObinson, Keith B.

JITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG

TITLE OF INVENTION: ANGIOTENSIN CONVERTION OF SQUARE

CORRESPONDENCE ADDRESS:

J. STATE: MA

COUNTRY: MA

COUNTRY: MA

COUNTRY: MA

COUNTRY: MA
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 100.0%; Score 26; DB 4; Length 293; 100.0%; Pred. No. 72;
 0; Indels
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US-08-227-36-6
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US-08-98-911-8
US-08-98-911-8
US-09-016-534-11
 US-09-648-183-3
PCT-US95-04467-8
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Best Local Similarity 100.
Matches 6; Conservative
 91 LDASAL 96
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11 MDASAL 16
 33 MDASAL 38
 1 LDASAL 6
 US-09-480-993-18
 US-09-615-917-9
 Query Match
 TYPE: PRT
 FEATURE:
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 0; Gaps
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 OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: peptide
 100.0%; Score 26; DB 3; Length 1313; 100.0%; Pred. No. 4e+02;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,299
FILING DATE: 11-DEC-1997
 0; Mismatches
 FILING DATE: 11-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: ATNOID E., Beth
REGISTRATION NUMBER: 35,430
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-1000
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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US-08-989-299-9
 600 LDASAL 605
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11 MDASAL 16
 1 LDASAL 6
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 JS-09-140-149-9
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Sequence 9, Application US/09615917

Patent No. 6479653

GENERAL INFORMATION:

APPLICANT: Gilman, Michael Z

TITLE OF INVENTION: No. 6479653el Compositions and Methods for Regulation of

TITLE OF INVENTION: Transcription

FILE REFERENCE: 363C continuation

CURRENT APPLICATION NUMBER: US/09/615,917

CURRENT APPLICATION NUMBER: 08/918,401

PRIOR PLING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 08/920,610

PRIOR APPLICATION NUMBER: 08/920,610

PRIOR APPLICATION NUMBER: 09/126,009

PRIOR PRILING DATE: 1998-08-26

PRIOR PRILING DATE: 1998-08-26

PRIOR PRILING DATE: 1998-08-26

PRIOR PRILING DATE: 1998-08-26

PRIOR PRILING DATE: 1998-08-26

PRIOR PRILING DATE: 1998-08-26

PRIOR PRILING DATE: 1998-08-26
 sequence 18, Application US/09480993

Sequence 18, Application US/09480993

Patent No. 6383790

GENERAL INFORMATION:

APPLICANT: Shokat, Kevan M.

TITLE OF INVENTION: And Uses Thereof

TITLE OF INVENTION: and Uses Thereof

TITLE OF INVENTION: And Uses Thereof

CURRENT APPLICATION NUMBER: US/09/480,993

CURRENT APPLICATION NUMBER: US 60/115,340

EARLIER PILING DATE: 1999-01-11

NUMBER OF SEQ ID NOS: 20

SEQ ID NO 18

LENGTH: 40
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 0; Indels
 ; OTHER INFORMATION: Cdk2, cyclin-dependent kinase US-09-480-993-18
 1; Mismatches
 TYPE: PRT
ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 83,33,
 PatentIn Ver. 2.0
 Best Local Similarity 83.3
Matches 5; Conservative
 ORGANISM: Homo sapiens
 NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve
SEQ ID NO 9
LENGTH: 20
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RESULT 6 US-08-370-225-16

RESULT 4

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Sequence 16, Application PC/TUS9310069
GENERAL INFORMATION:
APPLICANT: Brent, Roger
APPLICANT: Gyuls, Jeno
APPLICANT: Gylemis, Line
TITLE OF INVENTION: Interaction Trap System for Isolating
TITLE OF INVENTION: Interaction Trap System for Isolating
TITLE OF INVENTION: Novel Proteins
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
 Score 24; DB 1; Length 83;
Pred. No. 54;
 0; Indels
 OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,859
FILING DATE: June 5, 1995
CLASSIFICTATION: 330
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/370,225
FILING DATE: January 9, 1995
FILING DATE: January 9, 1995
FILING DATE: OCCOBER 30, 1995
FILING DATE: OCCOBER 30, 1995
FILING DATE: OCCOBER 30, 1992
ATTORNEY/AGENT INFORMATION:
NAME: LECH, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/143002
TELECOMMUNICATION NUMBER: 00786/143002
TELECOMMUNICATION NUMBER: 00786/143002
TELECOMMUNICATION NUMBER: 00786/143002
TELECOMMUNICATION NUMBER: 00786/143002
 COUNTY: U.S.A.

ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordbefrect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10069
FILING DATE: 20-OCT-1993
 1; Mismatches
 NAME: Clark, Paul T.
REGIGSTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/143001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/969,038
FILING DATE: 10/30/92
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
 (617) 542-8906
 TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 Best Local Similarity 83. Matches 5; Conservative
 CITY: Boston
STATE: Massachusetts
 TYPE: amino acid STRANDEDNESS:
 ; TOPOLOGY: linear
US-08-461-859-16
 :|||||
18 MDASAL 23
 1 LDASAL 6
 Boston
 PCT-US93-10069-16
 Query Match
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 NS-08-461-859-16

Sequence 16, Application US/08461859
Facent No. 57661639
GENERAL INFORMATION:
APPLICANT: Gyuris, Jeno
APPLICANT: Gyuris, Jeno
TITLE OF INVENTION: Interaction Trap System for Isolating
TITLE OF INVENTION: No. 578616991 Proteins
VUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
COUNTRY: Moston
STATE: Massachusetts
COMPUTRY: US.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
Sequence 16, Application US/08370225
Patent No. 5580736
GENERAL INFORMATION:
APPLICANT: Brent, Roger
APPLICANT: Gyuris, Jeno
APPLICANT: Golemis, Erica
TITLE OF INVENTION: Interaction Trap System for Isolating
TITLE OF INVENTION: No. 5580736el Proteins
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
 92.3%; Score 24; DB 1; Length 83; 83.3%; Pred. No. 54;
 COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 553X

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: Wordberfect (Version 5.1)

CURRENT APPLICATION DATA: US/08/370,225

FILING DATE:
 1; Mismatches
 CLASSIFICATION: 435
CCLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/969,038
FILING DATE: 10/30/92
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00/186/1.
TELECOMUNICATION INFORMATION:
TELEPAN: (617) 542-8906
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 16:
 E: Fish & Richardson 225 Franklin Street
 Query Match
Best Local Similarity 83.3.
 CITY: Boston
STATE: Massachusetts
 TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-370-225-16
 18 MDASAL 23
 1 LDASAL 6
 STREET: 225 F
CITY: Boston
 ADDRESSEE:
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 RESULT 11
US-08-31B-947A-20
i Sequence 20, Application US/08318947A
i Sequence 20, Application US/08318947A
i Sequence 20, Application US/08318947A
i SPECT INFORMATION:
i APPLICANT: Anderson, Paul J.
i APPLICANT: Tian, Qingsheng
i TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED
i TITLE OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME
i NUMBER OF SEQUENCES: 21
i CORRESPONDENCE ADDRESS:
i ADDRESSEE: Sughtne, Mion, Zinn, Macpeak & Seas
i STREET: 2100 Pennsylvania Avenue, NW Suite 800
i STATE: DRAWENCE ADDRESS:
i STATE: DRAWENCE ADDRESS:
i STREET: AMBADIAGEN
 Score 24; DB 1; Length 274;
Pred. No. 2.1e+02;
1; Mismatches 0; Indels
 Sequence 20, Application US/08795303
Patent No. 5948656
GENERAL INFORMATION:
APPLICANT: Anderson, Paul J.
APPLICANT: Tian, Qingsheng
TITLE OF INVENTION: TIA.1 BINDING PROTEINS AND ISOLATED
TITLE OF INVENTION: TOALLEMENTARY DNA ENCODING THE SAME
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGBLUE, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, NW Suite 800
 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPATION

COMPUTER: IBM PC COMPATION

COMPUTER: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/318,947A

FILING DATE: 06-OCT-1994

CLASSIFICATION: 435
 1; Mismatches
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/133,530
FILING DATE: 07-0CT-1993
ATTORNEY AGENT INFORMATION:
NAME: MACK, SUSAN J.
REGISTRATION NUMBER: 30,951
 REFERENCE/DOCKET NUMBER: A6
TELECOMMUNICATION INFORMATION:
 TELEX: 6491103
INFORMATION FOR SEQ ID NO: 20:
 92.3%;
 : 274 amino acids
amino acid
 (202) 293-2920
 SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acic
 Query Match
Best Local Similarity 83.3
Matches 5, Conservative
 , MOLECULE TYPE: protein US-08-318-947A-20
 Washington
 linear
 :|||||
5 IDASAL 10
 91 MDASAL 96
 1 LDASAL 6
 TELEPHONE:
 TOPOLOGY:
 RESULT 12
US-08-795-303-20
 TELEFAX:
 COUNTRY:
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 Sequence 4324, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
BELON BELON BELON Et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4324
LENGTH: 257
 Sequence Seq
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 Gaps
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 92.3%; Score 24; DB 4; Length 165; 83.3%; Pred. No. 1.2e+02; tive 1; Mismatches 0; Indels
 Score 24; DB 4; Length 257; Pred. No. 2e+02;
 Score 24; DB 5; Length 83;
Pred. No. 54;
 0; Indels
 1; Mismatches
 Mismatches
 TYPE: PRT GRGANISM: Acinetobacter baumannii US-09-328-352-4324
 ORGANISM: Pseudomonas aeruginosa
 92.3%;
 Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
 (617) 542-8906
 Query Match
Best Local Similarity 83...
Si Conservative
TELEFAX: (617) 542-890.
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 Query Match
Best Local Similarity 83.5.
 TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-10069-16
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150 IDASAL 155
 18 MDASAL 23
 1 LDASAL 6
 1 LDASAL 6
 US-09-252-991A-23877
 US-09-252-991A-23877
 US-09-328-352-4324
 TYPE: PRT
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1 LDASAL 6

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ö
 Sequence 25, Application US/08874347

Patent No. 5863741

GENERAL INFORMATION:
APPLICANT: Lief, Edward B.
APPLICANT: Thomas, Charles F.
APPLICANT: Guetafson, Michael P.
TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
TITLE OF INVENTION: CARINII
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C., P.A.
STREET: 60 South Sixth Street, Suite 3300
CITY: Minneapolis
 Score 24; DB 4; Length 289; Pred. No. 2.2e+02; 1; Mismatches 0; Indels
 OPERATING SYSTEM: DOS
SOFTWARE: FASLERQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,347
FILING DATE: 13-JUN-1997
CLASSIFICATION: 435
ATTORNAY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
) NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...289
; SEQUENCE DESCRIPTION: SEQ ID NO: 4402:
US-09-107-532A-4402
 07039/055001
 ORIGINAL SOURCE: ORIGINAL SOURCE:
 INFORMATION FOR SEQ ID NO: 4402:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: protein
HYPOTHETICAL: YES
 TELECOMMUNICATION INFORMATION
 TELEFAX: (781)893-8277
 REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-335-5070
 92.3%;
 ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
 298 amino acids
 Query Match
Best Local Similarity 83.3
Matches 5; Conservative
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 TELEFAX: 612-288-9696
 MOLECULE TYPE: protein
 TELEPHONE:
 amino acid
 linear
 96 IDASAL 101
 1 LDASAL 6
 TYPE: amino a STRANDEDNESS:
 Ž
 FEATURE:
 US-08-874-347-25
 US-08-874-347-25
 COUNTRY:
 LENGIH:
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 g
 Sequence 4402, Application US/09107532A
Patent No. 6583275
GENERAL INPORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
 ö
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 Length 274;
 0; Indels
COMPUTER REABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,303
FILING DATE: 04-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/318,947
FILING DATE: 06-OCT-1994
APPLICATION NUMBER: 08/318,530
FILING DATE: 07-OCT-1994
APPLICATION NUMBER: 08/133,530
FILING DATE: 07-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
REFERENCE/DOCKET NUMBER: 30,951
TELECOMMUNICATION NUMBER: A6462
 CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
CRNOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STREET: Massachusetts
COUNTR: USA
ZIP: 02354
 Score 24; DB 2; I Pred. No. 2.1e+02;
 COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <UNKNOWN>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107, S32A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAMME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
 1; Mismatches
 TELEX: 6491103
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
 NUMBER OF SEQUENCES: 7310
 92.3%;
 (202) 293-7060
 (202) 293-2920
 Query Match
Best Local Similarity 83.3
Matches 5; Conservative
 MOLECULE TYPE: protein
 91 MDASAL 96
 1 LDASAL 6
 US-09-107-532A-4402
 TELEPHONE:
 TOPOLOGY:
 US-08-795-303-20
 TELEFAX:
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Score 24; DB 2; Length 298; Pred. No. 2.3e+02; 1; Mismatches 0; Indels
 92.3%;
Query Match 92.3
Best Local Similarity 83.3
Matches 5; Conservative
 TOPOLOGY: unknown; MOLECULE TYPE: protein US-08-969-106-2
 . :|||||
91 MDASAL 96
 1 LDASAL 6
 1 LDASAL 6
 US-08-969-106-2
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Search completed: February 18, 2004, 14:41:45
Job time : 7.06579 secs

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Sequence 131, App Sequence 135, App Sequence 133, App Sequence 134, App Sequence 137, App Sequence 139, App Sequence 139, App Sequence 18, App Sequence 18, App Sequence 10, App Sequence 2, Appli Sequence 10, Appl Sequence 10, Appl Sequence 32, Appli Sequence 32, Appli Sequence 34, Appli Sequence 16, Appli Sequence 16, Appli Sequence 17, Appli Sequence 18, Appli Sequence 18, Appli Sequence 11, Appli Sequence 11, Appli Sequence 12, Appli Sequence 11, Appli Sequence 12, Appli Sequence 15, Appli Sequence 15, Appli

Scoring table:

Searched:

Minimum DB e Maximum DB e

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Database

Title: Perfect score:

Sequence:

OM protein

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Sequence 2, Application US/09847940B
; Sequence 2, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: MAY, Michael J.
; APPLICANT: Ghosh, SANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; TITLE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILIATION NUMBER: US/09/847,940B
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR PILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO :
 OTHER INFORMATION: Description of Artificial Sequence: NBD mutants
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 100.0%; Score 40; DB 10; Length 100.0%; Pred. No. 7e+05; ive 0; Mismatches 0; Indels
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US-09-771-161A-232
 US-09-844-908-9
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 ; Sequence 2, Application US/09847946A; Publication No. US20030054999A1; EDEREAL INFORMATION; APPLICANT: May, Michael J
 TYPE: PRT
ORGANISM: Artificial Sequence
 Similarity 100.
 1 LDWSWL 6
 LDWSWL
 RESULT 2
US-09-847-946A-2
 US-09-847-940B-2
 US-09-847-940B-2
 Query Match
Best Local S:
Matches 6,
 FEATURE:
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 셤
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 February 18, 2004, 14:36:10; Search time 16.6974 Seconds (without alignments) 75.239 Million cell updates/sec
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 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 US-09-847-940B-2
US-09-847-946A-33
US-09-847-946A-33
US-09-847-946A-30
US-09-847-946A-30
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US-09-847-946A-35
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US-09-847-946A-13
US-09-847-946A-13
US-09-847-946A-13
 Total number of hits satisfying chosen parameters:
 801455 seqs, 209382283 residues
 SUMMARIES
 Published Applications AA:*
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 seq length: 0
seq length: 200000000
 US-09-643-260-2
40
 Query
Match Length
 1 LDWSWL 6
 000000
 000
 100.
111.
112.
114.
115.
116.
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 100.
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Score

Result

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Sequence 30, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION: APPLICANT: May, Michael J APPLICANT: Ghosh, Sankar APPLICANT: Findeis, Mark A
 TYPE: PRT
ORGANISM: Artificial Sequence
 TYPE: PRT
ORGANISM: Artificial Sequence
 Findeis, Mark A
 Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
 1 LDWSWL 6
 US-09-847-946A-30
 FEATURE:
 RESULT 6
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 Gaps
 Gaps
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Phillips, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 160
SOUTHWARE: PATENTIN VET: 2.0
SEQ ID NO S: 160
SEQ ID NO S: 160
SEQ ID NO S: 160
 APPLICANT: May, Michael J
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar .
APPLICANT: Ghosh, Sankar .
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Pinleis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMFOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR PRILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PALENTIN VEY: 2.0
SEQ ID NO 33
LENOTH: 6
) OTHER INFORMATION: Description of Artificial Sequence:NEMO binding ; OTHER INFORMATION: sequence US-09-847-946A-33
 FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-2
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 100.0%; Score 40; DB 11; Length 6; 100.0%; Pred. No. 7e+05;
 100.0%; Score 40; DB 11; Length 6; 100.0%; Pred. No. 7e+05; tive 0; Mismatches 0; Indels
 0; Indels
 0; Mismatches
 Sequence 33, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION:
 ; Sequence 37, Application US/09847946A ; Publication No. US20030054999A1
 TYPE: PRT ORGANISM: Artificial Sequence
 TYPE: PRT
ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 100.(
Matches 6, Conservative
 Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
 1 LDWSWL 6
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1 LDWSWL 6
 1 LDWSWL 6
 -09-847-946A-33
 US-09-847-946A-37
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Gaps
 Gaps
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REPERENCE: PPP-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/641,261
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PATCHLIN VEY: 2.0
 ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding ; OTHER INFORMATION: sequence US-09-847-946A-37
 OTHER INFORMATION: Description of Artificial Sequence:NEMO binding COTHER INFORMATION: sequence US-09-847-946A-30
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 APPLICANT: Phillips, Kathryn
PapLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE: REFERENCE: PPI-118
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 Query Match 100.0%; Score 40; DB 11; Length 8; Best Local Similarity 100.0%; Pred. No. 7e+05; Matches 6; Conservative 0; Mismatches 0; Indels
 CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
FRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
FRIOR APPLICATION NUMBER: 09/643,260
FRIOR APPLICATION NUMBER: 09/643,260
FRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
LENGTH: 8
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; Sequence 32, Application US/09847946A; Publication No. US20030054999A1; GENERAL INFORMATION:
 US-09-847-946A-35; Sequence 35, Application US/09847946A; Publication No. US20030054999A1; GENERAL INFORMATION:
 ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 35
LENGTH: 9
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 SEQ ID NO 32
 d
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 ö
 Sequence 29, Application US/09847946A
| Publication No. US2003005499A1
| GENERAL INFORMATION:
| APPLICANT: May, Michael J
| APPLICANT: Pindeis, Mark A
| APPLICANT: Pindeis, Mark A
| APPLICANT: Pillips, Kathryn
| TITLE OF INVENTION:
| TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
| FILE REFERENCE: POPI-119
| CURRENT APPLICATION NUMBER: US/09/847,946A
| PRIOR PLIING DATE: 2000-05-02
| PRIOR APPLICATION NUMBER: 60/201,261
| PRIOR PILING DATE: 2000-06-02
| PRIOR FILING DATE: 2000-08-22
| NUMBER OF SEQ ID NOS: 100
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| CONTINUED OF SECTION NOS: 100
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| CONTINUED OF SECTION NOS: 100
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 OTHER INFORMATION: Description of Artificial Sequence:NEMO binding OTHER INFORMATION: sequence US-09-847-946A-38
 OTHER INFORMATION: Description of Artificial Sequence:NEMO binding COTHER INFORMATION: sequence US-09-847-946A-29
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 APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Pinlips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
 Query Match

100.0%; Score 40; DB 11; Length 9;

Best Local Similarity 100.0%; Pred. No. 7e+05;

Matches 6; Conservative 0; Mismatches 0; Indels
 100.0%; Score 40; DB 11; Length 8; 100.0%; Pred. No. 7e+05; Live 0; Mismatches 0; Indels
 FILE REFERENCE: PPT-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR PILING DATE: 2000-08-22
PRIOR SEQ ID NOS: 160
NUMBER OF SEQ ID NOS: 160
Sequence 38, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION:
 ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
 1 LDWSWL 6
 LDWSWL 6
 LDWSWL 6
 SEQ ID NO 29
LENGTH: 9
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GENERAL INFORMATION

JAPPLICANT: May, Michael J

APPLICANT: Ghosh, Sankar

APPLICANT: Findels, Mark A

APPLICANT: Findels, Mark A

APPLICANT: Phillibs, Kathryn

APPLICANT: Phillips, Kathryn

APPLICANT: Hamig, Gerhard

TILE OF INVENTION ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REFERENCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2000-05-02

PRIOR PILING DATE: 2000-05-02

PRIOR PLILNG DATE: 2000-08-02

PRIOR PLILNG DATE: 2000-08-12

PRIOR PLILNG DATE: 2000-08-12

NUMBER OF SEQ ID NOS: 160

SOFTWARE: PatentIn Ver. 2.0
 APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Pindels, Mark A
APPLICANT: Pindels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR PILING DATE: 2000-06-03
PRIOR PLING DATE: 2000-06-03
PRIOR PILING DATE: 2000-06-03
 CTHER INFORMATION: Description of Artificial Sequence: NEMO binding CTHER INFORMATION: sequence US-09-847-946A-32
 ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding; OTHER INFORMATION: sequence
US-09-847-946A-35
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 Query Match 100.0%; Score 40; DB 11; Length 9; Best Local Similarity 100.0%; Pred. No. 7e+05; Matches 6; Conservative 0; Mismatches 0; Indels
 Query Match 100.0%; Score 40; DB 11; Length 9; Best Local Similarity 100.0%; Pred. No. 7e+05; Matches 6; Conservative 0; Mismatches 0; Indels
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APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Pindeis, Mark A
APPLICANT: Pindeis, Mark A
TITLE CF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/021,261
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR PILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PATENTIN VET. 2.0
 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Begringtion of Artificial Sequence: NEMO binding
OTHER INFORMATION: sequence
 OTHER INFORMATION: Description of Artificial Sequence:NEMO binding OTHER INFORMATION: sequence
 APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
 100.0%; Score 40; DB 11; Length 10; 100.0%; Pred. No. 19;
 Pred. No. 19;
Mismatches
 CURRENT APPLICATION NUMBER: US/09/847,946A;
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SEQ ID NO 28
 Mismatches
 Sequence 34, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION:
 Sequence 28, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION:
APPLICANT: May, Michael J
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Best Local Similarity 100.0%; P. Matches 6; Conservative 0;
 TYPE: PRT ORGANISM: Artificial Sequence
 6; Conservative
 Query Match
Best Local Similarity
Matches 6; Conserv
 1 LDWSWL 6
 LDWSWL 8
 2 LDWSWL 7
 1 LDWSWL 6
 RESULT 13
US-09-847-946A-28
 US-09-847-946A-34
 US-09-847-946A-34
 SEQ ID NO 34
LENGTH: 10
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 Gaps
 APPLICANT MAY, Michael J
APPLICANT: May, Michael J
APPLICANT: Glosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Findels, Mark A
APPLICANT: Pindlips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTIINFLAMMATORY COMPOUNDS AND USES THEREOF
TITLE PREPRENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 2000-08-02
NUMBER OF SEQ ID NOS: 160
SOFFWARE: PALENT OF 10 NOS: 160
SOFFWARE: PALENT OF 10 NOS: 160
 Sequence 31. Application US/09847946A
| Sequence 31. Application US/09847946A
| Publication No. US20030054999A1
| GENERAL INFORMATION:
| APPLICANT: May, Michael J
| APPLICANT: Findeis, Mark A
| APPLICANT: Findeis, Mark A
| APPLICANT: Phillips, Kark A
| APPLICANT: Phillips, Kark A
| APPLICANT: Phillips, Gerhard
| TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
| TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
| FILE REFERENCE: PPI-119
| CURRENT APPLICATION NUMBER: US/09/847,946A
| PRIOR APPLICATION NUMBER: 60/201,261
| PRIOR APPLICATION NUMBER: 09/643,260
| PRIOR PLING DATE: 2000-08-22
| PRIOR FILING DATE: 2000-08-22
| NUMBER OF SEQ ID NOS: 160
| SOFTWARE: PATENTIN NOS: 160
| CONTINUED ON TO NOS: 160
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| CONTINUED ON TO NOS: 160
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 ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding; OTHER INFORMATION: sequence
US-09-847-946A-36
 OTHER INFORMATION: Description of Artificial Sequence:NEMO binding OTHER INFORMATION: sequence
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 100.0%; Score 40; DB 11; Length 9; 100.0%; Pred. No. 7e+05; Live 0; Mismatches 0; Indels
 100.0%; Score 40; DB 11; Length 10
 Sequence 36, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION:
 ORGANISM: Artificial Sequence
 TYPE: PRT ORGANISM: Artificial Sequence
 Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
 ||||||
LDWSWL 8
 1 LDWSWL 6
 2 LDWSWL 7
 US-09-847-946A-36
 US-09-847-946A-31
 US-09-847-946A-31
 SEQ ID NO 36
LENGTH: 9
 SEQ ID NO 31
LENGTH: 10
 Query Match
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 Sequence 132, Application US/09847946A

Sequence 132, Application US/09847946A

Publication No. US2030054999A1

GENERAL INFORMATION:

APPLICANT: Handel J

APPLICANT: Findels, Mark A

APPLICANT: Findels, Mark A

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REPERENCE: PPL119

CURRENT FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 60/201,261

PRIOR APPLICATION NUMBER: 60/201,261

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR PILING DATE: 2000-08-22

NUMBER: PREDICATION NUMBER: 09/641,260

SOFTWARE: PatentIN Ver. 2.0

SEQ 1D NO 132

LENGTH: 11

TUTLE OF INVENTION NUMBER: 09/641,260

SEQ 1D NO 132
 Sequence 100 Application US/09847946A

Figure 100 Application US/09847946A

Fortication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: Ghosh, Sankar

APPLICANT: Pindeis, Mark A

APPLICANT: Phillips, Kathryn

APPLICANT: Phillips, Kathryn

APPLICANT: Phillips, Kathryn

APPLICANT: Phillips, Kathryn

APPLICANT: Phillips, Wark A

APPLICANT: Phillips, Wark A

APPLICANT: Phillips, Wathryn

APPLICANT: Phillips, Wathryn

APPLICANT: Phillips, Wathryn

APPLICANT: Phillips, Wathryn

FILE REFERENCE: PPI-119

CURRENT FILING DATE: 2000-05-02

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR PELING DATE: 2000-05-22

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SEQ ID NO 140

LENGTH: 11
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 100.0%; Score 40; DB 11; Length 11; 100.0%; Pred. No. 20; ive 0; Mismatches 0; Indels
 Query Match 100.0%; Score 40; DB 11; Length 11; Best Local Similarity 100.0%; Pred. No. 20; Matches 6; Conservative 0; Mismatches 0; Indels
) OTHER INFORMATION: Description of Artificial ; OTHER INFORMATION: Sequence:anti-inflammatory compound US-09-847-946A-132
 TYPE: PRT ORGANISM: Artificial Sequence
 TYPE: PRT ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 100.
Matches 6; Conservative
 LDWSWL 8
 1 LDWSWL 6
 US-09-847-946A-140
 US-09-847-946A-132
US-09-847-946A-28
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; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:anti-inflammatory compound
US-09-847-946A-140

Query Match

Query Match

Best Local Similarity 100.0%; Score 40; DB 11; Length 11;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6

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Db 3 LDWSWL 8

Search completed: February 18, 2004, 15:41:54
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Sequence 2 Sequence 2 Sequence 4 Sequence 4 Sequence 1

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Result

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Sequence 3, Application US/08887518
Patent No. 5843721
GENERAL INFORMATION:
APPLICANT: Wothe, Mike
APPLICANT: Wothe, Mike
APPLICANT: Wother With Application of INVENTION: NIK Proteins, Nucleic Acids and Methods NUMBER OF SEQUENCES: 4
CORRESPONDENCES: ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
 Query Match 100.0%; Score 40; DB 2; Length 745; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 6; Conservative 0; Mismatches 0; Indels
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COMPUTRY: USA
ZIP: 94104
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTRI: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
CURRENT APPLICATION DATA:
RELICATION NUMBER: US/08/887,518
FILING DATE:
CLASSIFICATION: A435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 36,627
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TYPE: amino acid
STRANDEDNESS: single
 TOPOLOGY: linear
MOLECULE TYPE: peptide
CITY: SAN FRANCISCO
STATE: CALIFORNIA
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US-09-109-986-2
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Maximum Match 100%
Listing first 45 summaries
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 Issued Patents AA:*
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(415) 343-4341
 SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
 TELEFAX: (415) 343-4342 INFORMATION FOR SEQ ID NO:
 : 745 amino acids
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 Best Local Similarity 100.
Matches 6; Conservative
 SEQUENCE CHARACTERISTICS
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 ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-890-853-4
 ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-032-475-3
 TYPE: amino acid
STRANDEDNESS: si
 738 LDWSWL 743
 1 LDWSWL 6
 STRANDEDNESS:
 FILING DATE:
 ZIP: 94104
 TELEPHONE:
 COUNTRY:
 US-09-032-475-3
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 Sequence 4, Application US/08890853
Patent No. 5851812
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALLFORNIA
COUNTRY: USA
 Sequence 3. Application US/09023321

Patent No. 5844073

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCES: ADDRESSEE: ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
 0; Mismatches
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
 FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFRENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 TELEFAR. (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
 TELEPHONE: (415) 343-4341
 745 amino acids
 6; Conservative
 single
 ZIP: 94104
COMPUTER READABLE FORM:
 MOLECULE TYPE: peptide
 TYPE: amino acid
STRANDEDNESS: si
 linear
 Query Match
Best Local Similarity
Matches 6; Conserv
 738 LDWSWL 743
 1 LDWSWL 6
 FILING DATE:
 COUNTRY: U
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 US-09-023-321-3
 US-08-890-853-4
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Gaps
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 GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INFORMATION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: SCIENCE & TECHNOLOGY LAW GROUP
CITY: SAN FRANCISCO
STATE: CALIFORNIA
 Length 745;
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRATI APPLICATION DATA:
APPLICATION NUMBER: US/09/032,475
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ches 0;
 100.0%; Score 40; DB 2;
100.0%; Pred. No. 1.4e+02
Live 0; Mismatches 0
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEPHONE: (415) 343-4341
INFORMATION FOR SEQ ID NO: 4:
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,518
 Sequence 3, Application US/09032475 Patent No. 5854003
 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 797-,TELECOMMUNICATION:
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ADDRESSEE:
 US-09-099-124A-4
 COUNTRY:
 RESULT 7
US-09-032-476-4
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 Gaps
 ; Sequence 4, Application US/09099125A; Patent No. 5916760; GENERAL INFORMATION: APPLICANT: Geodel, David V. APPLICANT: Geodel, David V. TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods ITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods NUMBER OF SEQUENCES: ADDRESSE: ADDRESS
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 Sequence 4, Application US/09099124A

Patent No. 5939302

GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
APPLICANT: Woronicz, John
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
 100.0%; Score 40; DB 2; Length 745; 100.0%; Pred. No. 1.4e+02;
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 ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,125A
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100.0%; Score 40; DB 2; L
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0;
 0; Mismatches
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
APTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERRNCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
 Best Local Similarity 100.
Matches 6; Conservative
 TYPE: amino acid
STRANDEDNESS: single
 MOLECULE TYPE: peptide
 TOPOLOGY: linear
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 Sequence 4, Application US/09032476

Sequence 4, Application US/09032476

Patent No. 6235492

GENERAL INFORMATION:

APPLICANT: Cather, Mike

APPLICANT: R gnier, Catherine

TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA
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MEDIUM TYPE: Floppy disk
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 ZIP: 94104

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SOFTWARE: PatentIn Release #1.0, Version #1.30
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SSEE: SCIENCE & TECHNOLOGY LAW GROUP
S: 268 BUSH STREET, SUITE 3200
SAN FRANCISCO
CALIFORNIA
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 FILING DATE:
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFENCE/DOCKET NUMBER: 197-006-1
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION (415) 343-4341
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
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 TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
 Query Match
Best Local Similarity 100...
Si Conservative
 STRANDEDNESS: single
TOPOLOGY: linear
 MOLECULE TYPE: peptide
 738 LDWSWL 743
 1 LDWSWL 6
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amino acid
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 1 LDWSWL 6
 US-09-023-324-4
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 Gaps
 GENERAL INFORMATION:

APPLICANT: Rothe, Mike

APPLICANT: Rothe, Mike

APPLICANT: Cac, Zhaodan

APPLICANT: R gnier, Catherine

TITLE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA
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TELEFHONE: (415) 343-4342
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SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
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 GENERAL INFORMATION:
APPLICANT: No. 16721233
APPLICANT: Bibonato, Joseph A.
APPLICANT: Bibonato, Joseph A.
APPLICANT: Bibonato, Joseph A.
APPLICANT: Hayakawa, Makio
APPLICANT: Hayakawa, Makio
APPLICANT: Barakim
TITLE OF INVENTION: IkB Kinase, Subunits Thereof, and Methods of Using Same
FILE REPERSNOE: P-UD 3295
CURRENT APPLICATION NUMBER: US/09/168,629
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 60/061,470
BARLIER PILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 20
 Gaps
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 Query Match 100.0%; Score 40; DB 3; Length 745; Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 0; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/023,324 FILING DATE:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: USA
 0; Mismatches
 T97-006-1
 CLASSIFCATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A:
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 797-006
TELEPHONE: (415) 343-4341
TELEPHONE: (415) 343-4341
INFORMATION FOR SEQ ID NO: 4:
 ZIP: 94104
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 US-09-168-629-2; Sequence 2, Application US/09168629; Patent No. 6242253
 745 amino acids
 SEQUENCE CHARACTERISTICS:
 6; Conservative
 STRANDEDNESS: single
 MOLECULE TYPE: peptide
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; Sequence 4, Application US/09109986
; Patent No. 6479266
 : 745 amino acids
amino acid
 Query Match
Best Local Similarity 100.
 TOPOLOGY: linear
MOLECULE TYPE: protein
 738 LDWSWL 743
 1 LDWSWL 6
 US-08-810-131A-2
 RESULT 13
US-09-109-986-4
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 US-08-910-820-10

Sequence 10, Application US/08910820

Sequence 10, Application US/08910820

Sequence 10, Application US/08910820

Sequence 10, Application

APPLICANT: Zhu, Hengyl

APPLICANT: Li, Gian

APPLICANT: Li, Gian

APPLICANT: Li, Gian

TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR

NUMBER OF SEQUENCE: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: ADDRESSEE: SEED and BERRY LLP

STREET: ADDRESSEE: SEED and BERRY LLP

STREET: ADDRESSEE: SEED and BERRY LLP

STREET: ADDRESSEE: SEED and BERRY LLP

STREET: ADDRESSEE: SEED and BERRY LLP

STREET: ADDRESSEE: SEED and BERRY LLP
 100.0%; Score 40; DB 3; Length 745; 100.0%; Pred. No. 1.4e+02; Live 0; Mismatches 0; Indels
 100.0%; Score 40; DB 3; Length 745; 100.0%; Pred. No. 1.4e+02; Live 0; Mismatches 0; Indels
 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,820
FLING DATE: 12-AUG-1997
CLASSIFICATION: 435
ATTONREY/AGENT INPORMATION:
NAME: MAKA, DAVIG J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 360098.413C1
TELECOMMULCATION INFORMATION:
TELECOMMULCATION:
(206) 622-4900
 ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 ; Sequence 2, Application US/08810131A ; Patent No. 6268194
 TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
 SOFTWARE: Patentin Ver. 2.0
 Conservative
 ; ORGANISM: Homo sapiens
US-09-168-629-2
 CITY: Seattle
STATE: Washington
COUNTRY: USA
 738 LDWSWL 743
 amino acid
 ropology: linear
 738 LDWSWL 743
 Query Match
Best Local Similarity
Matches 6; Conserv
 1 LDWSWL 6
 1 LDWSWL 6
 STRANDEDNESS
 SEQ ID NO 2
LENGTH: 745
TYPE: PRT
 RESULT 12
US-08-810-131A-2
 US-08-910-820-10
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 GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaodan
APPLICANT: Catherine
TITLE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
 100.0%; Score 40; DB 3; Length 745; 100.0%; Pred. No. 1.4e+02;
APPLICANT: Dibonato, Joseph A.
APPLICANT: Rothwar, Makio
APPLICANT: Raykawa, Makio
APPLICANT: Zandi, Ebrahim
TITLE OF INVENTION: I-kappa-B Kinase and Methods of Using
TITLE OF INVENTION: Same
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
 0; Indels
 SIREET: 4370 La JOLIA VILIAGE DITVE, SUITE 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,131A
FILING DATE: 25-FEB-1997
CLASSIFICATION NUMBER: 31,815
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 31,815
REGISTRATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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LEMETHE FOR SEQ ID NO: 3:
LEMETHE FOR SEQ ID NO: 3:
LEMETHE FOR SEQ ID NO: 3:
LEMETHE FOR SEQ ID NO: 3:
LEMETH
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,986
 ADDRESS:
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
 0; Mismatches
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STRANDEDNESS: <Unknown>
 US-09-844-908-10
 RESULT 15
US-09-868-758-3
 US-09-868-758-3
 TYPE: PRT
 Query Match
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 Gaps
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0
 APPLICANT: Mercurio, Frank
Zhu, Hengyi
Barboea, Miguel
Li, Gian
Murray, Brion W.
TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
 Length 745;
 Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
 ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/844,908
FILING DATE: 27-Apr-2001
CILING DATE: 27-Apr-2001
FILING DATE: 12-AUC-1997
ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.413C1
TELECOMMUNICATION INFORMATION:
 100.0%; Score 40; DB 4;
100.0%; Pred. No. 1.4e+02;
 0; Mismatches
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECPHONE: (415) 343-4341
TELEPHONE: (415) 343-4341
INFORMATION FOR SEQ ID NO: 4:
 Sequence 10, Application US/09844908
Patent No. 6576437
GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
 TELEFAX: (206) 682-6031
 SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
STRANDEDNESS: single
 NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
 STATE: Washington
 (206)
 Query Match
Best Local Similarity 100.
Matches 6; Conservative
 TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-109-986-4
 CITY: Seattle
 COUNTRY: USA
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|38 LDWSWL 743
 1 LDWSWL 6
 US-09-844-908-10
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Gaps
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 100.0%; Score 40; DB 4; Length 745; 100.0%; Pred. No. 1.4e+02; ive 0; Mismatches 0; Indels
 100.0%; Score 40; DB 4; Length 745; 100.0%; Pred. No. 1.4e+02; ive 0; Mismatches 0; Indels
 Sequence 3, Application US/09868758; Sequence 3, Application US/09868758; Patent No. 6576439; GENERAL INPORMATION:
APPLICANT: Takemoto, Yoshihiro; APPLICANT: Sakai, Yutaka
TITLE OF INVENTION: IKK3
FILE REPERBNCE: 9950986P; CURRENT ALPLICATION NUMBER: US/09/868,758; CURRENT FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 45; SEQ ID NO 3
LENGTH: 745
 Search completed: February 18, 2004, 14:41:45
Job time : 8.06579 secs
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 Query Match
Best Local Similarity 100.
Matches 6; Conservative
 Best Local Similarity 100.
Matches 6; Conservative
 ORGANISM: Homo sapiens
 738 LDWSWL 743
 738 LDWSWL 743
 1 LDWSWL 6
 1 LDWSWL 6
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

; Search time 6.5921 Seconds (without alignments) 87.531 Million cell updates/sec February 18, 2004, 14:12:09 Run on:

US-09-643-260-2 Title: Perfect score:

40 1 LDWSWL 6 Seguence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

**Database** :

PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|               |       | 4              |      |    |          |                    |
|---------------|-------|----------------|------|----|----------|--------------------|
| Result<br>No. | Score | Query<br>Match | gth  | DB |          | Descripti          |
| 1             | 40    | 100.0          | 745  | -  | 149101   | conserved helix-lo |
| 7             | 38    | 95.0           | 1139 | ~  | AI0379   | probable potassium |
| m             | 37    | 92.5           | 322  | ~  | AI3395   | NADH2 dehydrogenas |
| ℴ             | 36    |                | 122  | 7  | 869909   | Ig V-D-J region (M |
| ហ             | 36    | 90.0           | 132  | ~  | S65785   | mel-13a protein -  |
| ø             | 36    | 90.0           | 277  | -  | JC5900   | bo-type ubiquinol  |
| 7             | 36    | 90.0           | 296  | N  | A84985   | cytochrome o ubiqu |
| 89            | 36    | 90.0           | 307  | н  | A36885 . | bo-type ubiquinol  |
| 6             | 36    | 90.0           | 318  | N  | AD0384   | cytochrome O ubiqu |
| 10            | 36    | 90.0           | 331  | ~  | D83480   | cytochrome o ubiqu |
| 11            | 36    | 90.0           | 344  | ~  | AG3489   | 0                  |
| 12            | 36    | 90.0           | 353  | 7  | A87469   | ubiquinol oxidase  |
| 13            | 36    | 90.0           | 362  | 7  | S23471   | uroporphyrinogen d |
| 14            | 36    | 90.0           | 386  | ~  | 200963   | probable cytochrom |
| 15            | 36    | 0.06           | 409  | 7  | T47298   | probable replicati |
| 16            | 36    | 90.0           | 747  | ~  | D70802   | hypothetical prote |
| 17            | 36    | 90.0           | 803  | ~  | F90485   |                    |
| 18            | 36    | 90.0           | 915  | N  | A43802   | ដ                  |
| 19            | 36    | 90.0           | 983  | ~  | B45583   | receptor tyrosine  |
| 20            | 36    | 90.0           | 983  | N  | A38224   | protein-tyrosine k |
| 21            | 36    |                | 983  | ~  | A45583   | receptor tyrosine  |
| 22            | 36    | 90.0           | 1039 | ~  | 802711   | cellulase (EC 3.2. |
| 23            | 36    |                | 1329 | ~  | D87226   | conserved hypothet |
| 24            | 35    |                | 162  | ~  | C70829   | hypothetical prote |
| 25            | 35    |                | 348  | N  | AE2733   | NADH ubiquinone ox |
| 26            | 35    | 87.5           | 348  | ~  | G97514   | NADH dehydrogenase |
| 27            | 35    |                | 443  | ~  | AE0309   | probable sugar tra |
| 28            | 34    | 85.0           | 82   | ~  | $\sim$   | hypothetical prote |
| 53            | 34    | 85.0           | 116  | N  | T03472   | conserved hypothet |

| prote              | denin             | ine D            | ine D            | denin              | prote              | ubidu              | (3)              | prote              | ylpol             | prote        | prote              | (3) c            | an 1,           | rogen              | (060          |
|--------------------|-------------------|------------------|------------------|--------------------|--------------------|--------------------|------------------|--------------------|-------------------|--------------|--------------------|------------------|-----------------|--------------------|---------------|
| hypothetical prote | DNA-3-methyladeni | 3-methyl-adenine | 3-methyl-adenine | DNA-3-methyladenin | hypothetical prote | cytochrome o ubiqu | cytochrome ba(3) | hypothetical prote | tetrahydrofolylpo | hypothetical | hypothetical prote | cytochrome ba(3) | probable glucan | formate dehydroger | cbbBc protein |
| G83692             | DGECMA            | E90988           | G85833           | AI0770             | B83243             | AH2593             | B97376           | C85064             | E84949            | B82408       | D85064             | A54759           | S45914          | AD3144             | H98143        |
| 0                  | -                 | ~                | N                | ~                  | N                  | ~                  | N                | ~                  | 7                 | 7            | ~                  | ~                | ~               | ~                  | ~             |
| 214                | 282               | 282              | 282              | 289                | 299                | 332                | 377              | 394                | 411               | 414          | 418                | 420              | 501             | 764                | 764           |
|                    |                   | _                | 0                | 0                  | 0                  | 0                  | 0                | 0                  | 0                 | 0            | 0                  | 0                | 0               | 0                  | 0.            |
| 85.0               | 85.0              | 85.              | 85.              | 85.                | 85.                | 85.                | 85.              | 85.                | 85.               | 85.          | 85.                | 85.              | 85.             | 85                 | 85            |
| 34 85.0            | 34 85.0           |                  |                  |                    |                    |                    |                  |                    |                   | 34 85.       |                    |                  |                 |                    |               |

## ALIGNMENTS

| RESULT 1                                                |            |   |
|---------------------------------------------------------|------------|---|
| I49101                                                  |            |   |
| conserved helix-loop-helix ubiquitous kinase (EC 2.7.1) | (EC 2.7.1) | E |
| C; Species: Mus musculus (house mouse)                  |            |   |

C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999
C;Accession: 149101
R;Mock, B.A.; Connelly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.
Genomics 27, 348-351, 1995
A;Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome A;Reference number: 149101
A;Reference number: 149101
A;Accession: 149101
A;Accession: 149101
A;Accession: 149101
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-745 <RES
A;Cross=references: EMBL:U12473; NID:g1079492; PIDN:AAC52589:1; PID:g1079493
C;Genetics:
A;Gene: CHUK

C;Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homol. C;Keywords: ATP; phosphotransferase F;13-283/Domain: protein kinase homology <KIN>

Gaps ö Query Match 100.0%; Score 40; DB 1; Length 745; Best Local Similarity 100.0%; Pred. No. 53; Matches 6; Conservative 0; Mismatches 0; Indels

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738 LDWSWL 743 1 LDWSWL 6 셤 ઠે

RESULT 2

probable potassium efflux system YPO3129 [imported] - Yersinia pestis (strain CO92)

C.Species: Yersinia pestis
C.Species: Yersinia pestis
C.Species: Yersinia pestis
C.Species: Yersinia pestis
C.Saccession: A10379
C.Saccession: A10379
C.Saccession: A10379
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C.Sacc

A; Cross-references: GB: ALS90842; PIDN: CAC92364.1; PID:g15981067; GSPDB: GN00175 C; Genetics:

Score 38; DB 2; Length 1139; Pred. No. 1.7e+02; 95.0%; 83.3%; Query Match Best Local Similarity us-09-643-260-2.rpr

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C;Genetics:
A;Gene: cyoA; BU472
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; respiratory chain
R;Tetsu, O.; Kanno, R.; Isono, K.; Taniguchi, M.; Kanno, M.
Biochim. Biophys. Acta 1305, 109-112, 1996
A;Title: Cloning and characterization of two transcripts generated from the mel-13 gene A;Reference number: 865785; MUID:96180310; PMID:8597592
 C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain C; Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; rest
 C;Accession: JC5900
R;Surpin, M.A.; Luebben, M.; Maier, R.J.
Gene 183, 201-206, 1996
A;Title: The Bradyrhizobium japonicum coxWXYZ gene cluster encodes a bb3-type ubiquinol
A;Reference number: JC5900; MUID:97149299; PMID:8996107
A;Accession: JC5900
 A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A;Reference number: A84930; MUID:20445173; PMID:10993077
 (strain APS)
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 Bradyrhizobium japonicum

 C;Species: Bradyrhizobium japonicum
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 Gaps
 Gaps
 C,Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-A;
C;Accession: A8498;
K;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
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 Length 296;
 Length 132;
 Length 277;
 1; Indels
 0; Indels
 cytochrome o ubiquinol oxidase subunit II [imported]
 90.0%; Score 36; DB 2;
 90.0%; Score 36; DB 2;
100.0%; Pred. No. 39;
iive 0; Mismatches
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 bo-type ubiquinol oxidase (EC 1.10.3.-) chain II
 Score 36; DB 1
Pred. No. 83;
0; Mismatches
 A;Residues: 1-296 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
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 C;Superfamily: mouse mel-13a protein C;Keywords: alternative splicing
 A; Accession: S65785
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-132 <TET>
A; Cross-references: EMBL: U35309
C; Genetics:
 Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
 Query Match 90.0
Best Local Similarity 100.
Matches 5; Conservative
 108 LDWKWL 113
 1 LDWSWL 6
 58 DWSWL 62
 9
 A;Status: preliminary
 A, Molecule type: DNA
 2 DWSWL
 A; Accession: A84985
 A;Gene: mel-13
 Query Match
 A; Gene: coxW
 C,Genetics:
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 Ig V-D-J region (MS) - human
C;Species: Homo sapiens (man)
C;Date: 1-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: 569909
R;Sahota, S; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.
Leukemia 8, 1285-1289, 1994
A;Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multi
A;Reference number: 569909; MUID:94335315; PMID:8057663
 Ribelvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. US.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
 A;Cross-references: EMBL:233399; NID:g871348; PIDN:CAA83850.1; PID:g871349
A;Note: the sequence of residues 112-122 and the corresponding nucleic acid sequence are C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-97/Domain: immunoglobulin homology <IMM>
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) [imported] - Brucella melitensis (strain
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 A;Cross-references: GB:AE008917; PIDN:AAL52332.1; PID:g17983126; GSPDB:GN00190 A;Experimental source: strain 16M C;Genetics: A;Genetics: A
 C,Species: Brucella melitensis
C,Date: 01-Peb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
C,Accession: A13395
 mel-13a protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
C;Accession: S65785
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 Length 122;
 Length 322
 Indels
 Indels
 Indels
 A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA
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0
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C;Superfamily: NADH dehydrogenase (ubiquinone) chain
C;Keywords: oxidoreductase
 Query Match 90.0%; Score 36; DB 2; Best Local Similarity 100.0%; Pred. No. 36; Matches 5; Conservative 0; Mismatches (
 2;
 DB '
 Score 37; DB 2
Pred. No. 67;
1; Mismatches
 Mismatches
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 92.5%;
 Best_Local Similarity 83.3
Matches 5; Conservative
 Conservative
 480 MDWSWL 485
 LDWNWL 179
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A;Molecule type: DNA
A;Residues: 1-322 <KUR>
 A; Residues: 1-122 <SAH>
 9
 1 LDWSWL 6
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DWSWL 37
 2 DWSWL 6
 1 LDWSWL
 A, Accession: A13395
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 Query Match
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Cytochrome o ubiquinol oxidase subunit II PA1317 [imported] - Pseudomonas aeruginosa (s. C;Species: Pseudomonas aeruginosa (s. C;Species: Pseudomonas aeruginosa (c. Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 [S. C;Accession: D83480] R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B: adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim J. Lory, S.; Olson, M.V. N. L. Coulter, S.N.; Folger, R.R.; Kas, A.; Larbig, K.; Lim Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathra. A;Reference number: A82950; MUID: 20437337; PMID: 10984043
 A Status: preliminary
A Molecule type: DNA
A; Residues: 1-31 <570>
A; Cross-references: GB:AE004561; GB:AE004091; NID:g9947253; PIDN:AAG04706.1; GSPDB:GN00
A; Experimental source: strain PAO1
 A;Gene: cyoA; PA1317
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; respiratory chain
 cytochrome o ubiquinol oxidase chain II (EC 1.10.3.-) [imported] - Brucella melitensis C;Species: Brucella melitensis C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 22-Mar-2002 C;Accession: AG3489 B;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002 A;Atitle: The genome sequence of the facultative intracellular pathogen Brucella meliten A;Accession: AG3489
 A;Map position: I
C;Superfamily: bo-rype ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; res
 A;Cross-references: GB:AE008917; PIDN:AAL53082.1; PID:g17983945; GSPDB:GN00190
A;Experimental source: strain 16M
 A87469
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C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 24-May-2001
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 Score 36; DB 2; Length 331;
Pred. No. 99;
0; Mismatches 1; Indels
 90.0%; Score 36; DB 2; Length 344; 83.3%; Pred. No. 1e+02; ive 0; Mismatches 1; Indels
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 135 LDWKWL 140
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A;Residues: 1-344 <KUR>
 1 LDWSWL 6
 1 LDWSWL 6
 A; Accession: D83480
 A; Gene: BMEI1901
 Query Match
 C, Genetica:
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 A; Description: terminal oxidase for ethanol oxidation
C; Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C; Keywords: copper; electron transfer; heterotecramer; membrane-associated complex; oxid
F; 1-23/Domain: signal sequence #status predicted <SIG>
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F; 89-105/Domain: transmembrane #status predicted <TM2>
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R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
G;Accession: AD0384
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.W.; Chillingworth, T.; Cronin, A.; Davies, R.W.; Davies, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AD0384
A;Status: preliminary
A;Molecule type: DNA
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
 T.; Ebisuya, H.; Okumura, H.; Kawamura, Y.; Horinouchi
 A;Gene: cyoA
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; resp
 NiAlternate names: Cytochrome al chain II precursor. Acetobacter acet. (Species: Acetobacter acet. (Species: Acetobacter acet.) Cispecies: Acetobacter acet. (Cispecies: Acetobacter acet.) Cyate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000 CyAccession: A36885 R:Fukaya, M.; Tayama, K.; Tamaki, T.; Ebisuya, H.; Okumura, H.; Kawamura, Y.; Horinouch A; Hattle: Characterial: 175, 4307-4314, 1993 A; Title: Characteriation of a cytochrome a-1 that functions as a ubiquinol oxidase in A; Reference number: A36885; MUID:93322308; PMID:8392509
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 bo-type ubiquinol oxidase (EC 1.10.3.-) chain II precursor - Acetobacter aceti
 A; Cross-references: GB: AL590842; PIDN: CAC92399.1; PID: 915981102; GSPDB: GN00175
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A;Cross-references: GB:D13185; NID:g409064; PIDN:BAA02480.1; PID:g433186
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 90.0%; Score 36; DB 1; Length 307; 83.3%; Pred. No. 92; ive 0; Mismatches 1; Indels
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 Indels
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tive 0; Mismatches
 Mismatches
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 83.3%;
 Query Match
Best Local Similarity 83.33
Matches 5; Conservative
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 A, Accession: A36885
A, Status: preliminary
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 Gene: cyaB
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C;Accession: C96006
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: C96006
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A;Molecule type: DNA
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A;Cross-references: GB:AL591985; PIDN:CAC49715.1; PID:g15141202; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
B;Galibert, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
Cscience 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Contents: annotation
 Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain Keywords: copper; electron transfer; membrane-associated complex; oxidoreductase; resp
 D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
 probable cytochrome o ubiquinol oxidase chain II protein (EC 1.10.3.-) [imported] C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 N.Alternate names: protein T14K23.110
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47298
R;Nyakatura, G:; Fartmann, B:; Dauner, D:; Sterr, W:; Holland, R:; Weichselg
 A;Map position: 3
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A;Note: T14K23.110
 Score 36; DB 2; Length 386;
Pred. No. 1.2e+02;
 cultivar Columbia; BAC clone T14K23
 Mayer, K.F.X. submitted to the Protein Sequence Database, April 2000
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100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0;
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 h 90.0%;
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A;Accession: T47298
 141 LDWKWL 146
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 1 LDWSWL 6
 190 LDWSW 194
 A; Experimental source:
 A; Gene: cyoA; SMb21487
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 A;Status: preliminary
 A; Molecule type: DNA
 plasmid
 Matches
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C;Accession: A87469

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, Y. T.; DeBoy, N.T.; DeBoy, N.T.; DeBoy, N.T.; DeBoy, N.T.; DeBoy, N.T.; Podson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon H. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

Rroc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Reference number: A87249; MUD:21173698; PMID:11259647

A;Accession: A87469

A;Accession: A87469

A;Accession: A87469

A;Accession: A87469

A;Cross-references: GB:AE005673; NID:g13423199; PIDN:AAK23749.1; GSPDB:GN00148
 uroporphyrinogen decarboxylase (EC 4.1.1.37) - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein YD9609.03; protein YD8047w
C;Species: Saccharomyces cerevisiae
C;Decies: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 22-Jun-1999
C;Accession: $23471; $33965; $54033; $20190; $27348; $31312
R;Garey, J.R.; Labbe-Bois, R.; Chelstowska, A.; Rytka, J.; Harrison, L.; Kushner, J.; Labe-Bois, Bur. J. Blochem. 205, 1011-1016, 1992
A;Title: Uroporphyrinogen decarboxylase in Saccharomyces cerevisiae. HEM12 gene sequence A;Reference number: $233471; MUID:92249304; PMID:1576986
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 Cross-references: EMBL:Z49209; NID:g798897; PIDN:CAA89078.1; PID:g798900; MIPS:YDR047w
 chain
 C;Genetics:
A;Gene: CC1773
C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chai
C;Superfamily: bo-type ubiquinol oxidase chain IC precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; respiratory chain
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 A, Molecule type: DNA
A, Residues: 1.362 < GAR>
A, Cross-treferences: EMBL:X63721; NID:g3766; PIDN:CAA45253.1; PID:g3767
R, Diflumeri, C.; Larocque, R.; Keng, T.
Yeast 9, 613-623, 1993
A, Fille: Molecular analysis of HEM6 (HEM12) in Saccharomyces cerevisiae, the gene 1
A, Reference number: S33965; MUID:93348774; PMID:8346678
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 A;Map position: 4R
C;Superfamily: uroporphyrinogen decarboxylase
C;Keywords: carbon-carbon lyase; carboxy-lyase; porphyrin biosynthesis
 A; Cross-references: EMBL: Z19089; NID: g4775; PIDN: CAA79514.1; PID: g4776
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 90.0%; Score 36; DB 2; Length 362; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
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 Gene: HEM12; HEM6; POP3
Cross-references: MIPS:YDR047w; SGD:S0002454
 R;Hunt, S.; Bowman, S.; Harris, D.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54031
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 Query Match 90.0
Best Local Similarity 100.
Matches 5; Conservative
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A, Molecule type: DNA
A, Residues: 1-362 <HUN>
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A; Residues: 1-362 <DIF>
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 LDWSW 283
 1 LDWSW 5
 A;Accession: S23471
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 Description
 P36590
P23135
P75227
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
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 SUMMARIES
 IKKA MOUSE
IKKA HUMAN
IKKB HUMAN
IKKB BAT
CYOA BUCAI
CYOA BUCAI
CYOA BEEN
CYOA BUCAI
CHARA
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Maximum Match 100%
Listing first 45 summaries
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 IKKA HUMAN
 BLOSUM62
Gapop 10.0 , Gapext 0.5
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1 LDWSWL 6
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 February 18,
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Perfect score:
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 Score
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 Result
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InterPro; IPR001299; Prot kinase.

R InterPro; IPR001299; Sert kinase.

R InterPro; IPR001299; Sert kinase.

R InterPro; IPR001299; Sert kinase.

R InterPro; IPR001299; Tyr pkinase.

R PR001099; PR001099; TYRKINASE.

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 -!- SUBUNIT: Preferentially found as a heterodiner with IKK-beta but also as an homodimer. Directly interacts with IKK-GAMMA/NEMO. Heterodiners form the active complex. The tripartite complex can also bind to MAP3K14/NIK, MEKK1, IKAP and IKB-alpha-P65-P50 complex. A weak interaction with TRAF2 cannot be excluded. Part of a complex. Composed of NCOA2, NCOA3, IKKB, IKBKG and CREBBP.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: Widely expressed.
-!- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by MEKK1, and dephosphorylated by PP2A. Autophosphorylated.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 Nemoto S., Dibonato J.A., Lin A.; "Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase kinase kinase kinase (1 and WF-kappaB-inducing kinase."; Mol. Cell. Biol. 18:7336-7343(1998).
 SUBJUIT OF A COMPLEX CONTAINING CREBBP; NCOA2; NCOA3; IKKB AND IKBKG. MEDLINE=21968797; PubMed=11971985; MCDLINE=21968797; PubMed=11971985; Ncoag J., Xu J., Tsai S.Y., Tsai M.J., O'Malley B.W.; Tsai M.J., O'Malley B.W.; Regulation of SRC-3 (PCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator activity by I kappa B kinase."; Mol. Cell. Biol. 22:3549-3561(2002).

-!-FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates
 AND SER-180.
MEDLINE=98188283; PubMed=9520446;
Ling L., Cao Z., Goeddel D.V.;
"NP-kappaB-inducing Kinase activates IKK-alpha by phosphorylation of
 MEDLINE=99212141; PubMed=10195894;
Delhase M., Hayakawa M., Chen Y., Karin M.;
"Positive and negative regulation of IkappaB kinase activity through
 ENZYME REGULATION: Activated when phosphorylated and inactivated
 PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179
 "NF-kappaB activation by tumour necrosis factor requires the Akt serine-threonine kinase."; Nature 401:82-85(1999).
 PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
MEDLINE=99413720; PubMed=10485710;
Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M.,
 Jobin C., Sartor R.B.;
"The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";
Am. J. Physiol. 278:C451-C462(2000).
 Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998)
 Cell. Mol. Biol. Res. 41:537-549(1995)
 IKKbeta subunit phosphorylation.";
Science 284:309-313(1999)
 MEDLINE=20178139; PubMed=10712233;
 IKK PHOSPHORYLATION.
MEDLINE=99038238; PubMed=9819420;
 when dephosphorylated
 IKKA-IKKB BINDING.
 NCOA3
 REVIEW
```

S-A: LOSS OF PHOSPHORYLATION AND OF ACTIVITY.
S-AE: FULL ACTIVATION.
S-A: NO CHANGE IN PHOSPHORYLATION.
S-A: NO CHANGE IN PHOSPHORYLATION.
E -> G (IN REF. 2).
L -> R (IN REF. 5).

CONFLICT CONFLICT

MUTAGEN MUTAGEN

LOSS OF AUTOPHOSPHORYLATION. LOSS OF PHOSPHORYLATION AND OF

ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (BY PKB/AKT1).
PHOSPHORYLATION (BY MAP3K14).
T->A: LOSS OF PHOSPHORYLATION AND DECREASE OF KINASE ACTIVITY.
K->A: LOSS OF KINASE ACTIVITY.
K->A: LOSS OF KINASE ACTIVITY.

LEUCINE-ZIPPER (POTENTIAL)
NEMO-BINDING.

PROTEIN KINASE.

ATP (BY SIMILARITY). ATP (BY SIMILARITY).

302 476 743 29 144 176 23

23 176 23

MUTAGEN MUTAGEN MUTAGEN MUTAGEN MUTAGEN

44 44 176

455 738 21 44 144

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 TKKA_MOUSE STANDARD; PRT; 745 AA.

Q60680, Q902X3;

16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last amnoration update)
15-SEP-2003 (Rel. 42, Last amnoration update)
15-SEP-2003 (Rel. 42, Last amnoration update)
16-Kappa-B kinase alpha) (IkBKA) (IKK-alpha) (IKK-A) (IkappaB kinase)
(I-kappa-B kinase alpha) (IkRX) (Conserved helix-loop-helix ubiquitous (Kinase) (Wuclear factor NFkappaB inhibitor kinase alpha) (NFKBIKA).

CHUK OR IKKA.
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 ;
 100.0%; Score 40; DB 1; Length 745; 100.0%; Pred. No. 32;
 0; Indels
 TS -> AY (IN REF. 5).
P -> A (IN REF. 3 AND 5).
 7A90B59BC98A56C2 CRC64;
 TS -> DL (IN REF.
 0; Mismatches
 84653 MW;
 6; Conservative
176
179
180
180
543
684
684
 Mus musculus (Mouse).
 LDWSWL 743
 745 AA;
 Local Similarity
 1 LDWSWL 6
 NCBI_TaxID=10090;
 CONFLICT
CONFLICT
SEQUENCE
 738
 Query Match
 IKKA MOUSE
 Matches
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TO STRAIN-CSTBL/63; TISSUB-COLON; A WARDINE-2108560; PubMed=11217851;

RAWAN J., Shinagawa A., Shibata K., Yonohino M., Itoh M., Ishii Y., Arawawa T., Shibata M., Kohosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R., Ashiburner M., Batalov S., Casavant T., Ashiburner M., Batalov S., Casavant T., Araburner M., Batalov S., Casavant T., Araburner M., Batalov S., Casavant T., Araburner M., Batalov S., Casavant T., Arabi P., Lowis S., Mateuo Y., Nikaido I., Fosole G., Quackenbush J., Arabi P., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Carninci M., Batashio T., Asha M., Bult C., Fletcher C., Fujita M., Gariboldi M., Bara J., Boffelli D., Hofmann M., Hume D.A., Kaniya M., Lee N.H., Lownsein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Loon P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Saco K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Marabizaki Y.;

Mayashizaki Y., Marthi M., Hasegawa Y., Kawaji H., Kohtsuki S., Maring M., Marting
 MEDLINE-99038238; PubMed-9819420;
Nemoto S., Dibonato J.A., Lin A.;
"Coordinate regulation of IkappaB kinases by mitogen-activated protein
kinase kinase kinase 1 and MF-kappaB-inducing kinase.";
Mol. Cell. Biol. 18:7336-7343(1998).
 Mock B.A., Connelly M.A., McBride O.W., Kozak C.A., Marcu K.B.; "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome 10 and mouse chromosome 19."; Genomics 27:348-351(1995).
 Connelly M.A., Marcu K.B.; "Chur, and leucine zipper "CHUK, a new member of the helix-loop-helix and leucine zipper families of interacting proteins, contains a serine-threonine kinase
 MEDLINE=20198447; PubMed=10733566; McKenzie F.R., Connelly M.A., Balzarano D., Mueller J.R., Geleziunas R., Marcu K.B.; "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking leucine zipper and helix-loop-helix domains reveal that IKKalpha and IKKbeta have different activation requirements."; Mol. Cell. Biol. 20:2635-2649(2000).
 Delhase M., Hayakawa M., Chen Y., Karin M.;
"Positive and negative regulation of IkappaB kinase activity through
IKKbeta subunit phosphorylation.";
Science 284:309-313(1999)
 PHOSPHORYLATION BY MAP3K14/NIK.
MEDLINE-98188238; Pubmed-9520401;
Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 "Differential regulation of IkappaB kinase alpha and beta by two upbrream kinases. NF-kappaB-inducing kinase and mitogen-activated procein kinase/ERK kinase kinase-1.";
Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 Cell. Mol. Biol. Res. 41:537-549(1996).
 MEDLINE-99212141; PubMed-10195894;
 MEDLINE=9604444; PubMed=7558004;
 MEDLINE=96258427; PubMed=8777433;
[1]
SEQUENCE FROM N.A. (ISOFORM 1).
 SEQUENCE FROM N.A. (ISOFORM 1).
 SEQUENCE FROM N.A. (ISOFORM 3).
 Nature 409:685-690(2001).
 ALTERNATIVE SPLICING
 PHOSPHORYLATION
 catalytic domain."
 KKA-IKKB BINDING.
 STRAIN-BALB/C;
 Okumura K.;
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 when dephosphorylated.
SUBUNIT: Preferentially found as a heterodimer with IKK-beta but also as an homodimer. Directly interacts with IKK-gamma/NEMO.
Heterodimers form the active complex. The tripartite complex can also bind to MAPSKIA, IKK, IKAP and IKB-alpha-P65-P50 complex. A weak interaction with TRAP2 cannot be excluded. Part of a complex composed of NCOA2, NCOA3, IKKB, IKBKG and CREBBP (By
 Name=2; Synonyms=Delta LH;
Isold=60680-2; Sequence=VSP_004866, VSP_004867;
Name=3; Synonyms=Delta H;
Isold=606680-3; Sequence=VSP_004868, VSP_004869;
Isold=606080-3; Sequence=VSP_004868, VSP_004869;
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 PIR; 149101; 149101.

**RISP; 063450; 1A06.

**RISP; 063450; 1A06.

**RICEPTO; IPR002290; Ser_Ehr_pkinase.

**InterPro; IPR002290; Ser_Ehr_pkinase.

**InterPro; IPR001245; Tyr_pkinase.

**InterPro; IPR001245; Tyr_pkinase.

**PEGM; PR00109; PRVEKINASE.

**PROSITE; PS00100; PROTEIN KINASE ATP; 1.

**PROSITE; PS001109; PROTEIN KINASE EX; 1.

**PROSITE; PS001109; PROTEIN KINASE EX; 1.

**PROSITE; PS001109; PROTEIN KINASE DOM; 1.

**PROSITE; PS50011; PROTEIN KINASE DOM; 1.

**PROSITE; PS50011; PROTEIN KINASE DOM; 1.

**PROSITE; PS50011; PROTEIN KINASE DOM; 1.

**PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 NEWO-BINDING.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (BY PKB/AKT1)
(BY SIMILARITY).
PHOSPHORYLATION (BY MAP3K14)
(BY SIMILARITY).
 Phosphorylation; Alternative splicing.

DOMAIN
15 300 PROTEIN KINASE.

DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL)
 Event=Alternative splicing; Named isoforms=3;
 IsoId=Q60680-1; Sequence=Displayed;
 SUBCELLULAR LOCATION: Cytoplasmic. ALTERNATIVE PRODUCTS:
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 EMBL; U12473; AAC52589.1; -.
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7476
743
29
444
23
 similarity).
 15
738
738
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21
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 BINDING
ACT SITE
MOD_RES
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MOD\_RES

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ö
MLSLLRYNANLTKMKNTLIS -> IFRKNVKSMERNGRKGH
 Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;
"IkappaB kinase-beta: NF-kappaB activation and complex formation with
IkappaB kinase-alpha and NIK.";
 014920, 075327, 16-007-2011 (Rel. 40, Created) 16-007-2001 (Rel. 40, Last sequence update) 16-007-2001 (Rel. 40, Last sequence update) 15-SEP-2003 (Rel. 42, Last amnotation update) 11-SEP-2003 (Rel. 42, Last amnotation update) (INAppa-B-kinase beta (INAppa-B-kinase beta) (INAppa-B-kinase beta) (INAppa-B-kinase beta) (INAPpa-B-Kinase beta) (INAPpa-B-Kinase beta) (INAPPA-B-Kinase beta) (INAPPA-B-KINAB-B-K
 Gaps
 Mihara M., Okumura K.;
to human chromosome band
 SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181. ISSUB-Cervical carcinoma; TaSSUB-cervical carcinoma; MEDLINE-98008B13; Pubmed-9346484; Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L., Mercurio F., Zhu H., Murray B.W., Mann M., Manning A., Rao A.; ILK-1 and IKK-2: cytokine-activated IkappaB kinases essential for NF-kappaB activation."
 Missing (in isoform 2).
/FTId=VSP 004867.
/FTId=VSP 004867.
/FTId=VSP 004868.
Missing (in isoform 3).
/FTId=VSP 004869.
K -> E (IN REF. 3).
S -> Y (IN REF. 3).
 Hu M.C.-T., Wang Y.-P.;
embrapa8 kinase-alpha and -beta genes are coexpressed in adult and
embryonic tissues but localized to different human chromosomes.";
Gene 222:31-40(1998).
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 ö
 100.0%; Score 40; DB 1; Length 745; 100.0%; Pred. No. 32; ive 0; Mismatches 0; Indels
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 SLF (in isoform 2). /FTId=VSP 004866.
 SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
MEDLINE=98008814; PubMed=9346485;
 756 AA.
 SEQUENCE FROM N.A., AND GENE MAPPING.
MEDLINE=98438415; PubMed=9763654;
Shindo M., Nakano H., Sakon S., Yagita H.,
"Assignment of IkappaB kinase beta (IKBKB)
8p12-->p11 by in situ hybridization.";
 TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932;
 TISSUE=Heart;
MEDLINE=99032998; PubMed=9813230;
 84728 MW;
 SEQUENCE OF 1-256 FROM N.A.
 Science 278:860-866(1997).
 Science 278:866-869(1997).
 6; Conservative
 STANDARD;
 745
 745
 236
471
 584
 400
 Homo sapiens (Human)
 400
745 AA;
 738 LDWSWL 743
 Local Similarity
 SEQUENCE FROM N.A.
 1 LDWSWL 6
 NCBI_TaxID=9606;
452
 472
 577
 585
 IKKB_HUMAN
 CONFLICT
CONFLICT
SEQUENCE
VARSPLIC
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 VARSPLIC
 VARSPLIC
 Query Match
 IKKB HUMAN
 Best Loc
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INTERVITE CALCION IN A COMPLEX WITH CREBBP; NCOA2; NCOA3; IKKA AND IKBKG. MEDLINE-21968797; PubMed-11971985; RA MEDLINE-21968797; PubMed-11971985; RA MEDLINE-21968797; PubMed-11971985; RA O'Malley Bu.W.; Valley Bu.W.; Valley Bu.W.; Rapulation of SRC-3 (pcIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator activity by I kappa B Kinase."; R. Mol. Cell. Biol. 22:3549-3561(2002).

R. Mol. Cell. Biol. 22:3549-3561(2002).

R. Mol. Cell. Biol. 22:3549-3561(2002).

R. Mol. Cell. Biol. 22:3549-3561(2002).

C. -I-FUNCTION: Phosphorylates inhibitor/NF-kappa-B complex and the dissociation of the inhibitor. Also phosphorylates (CC Ultimately the degradation of the inhibitor. Also phosphorylates (CC NCOA3 (By similarily) found as a heterodimer with IKK-alpha but also as a homodimer. Directly interacts with IKK-alpha but also bind to MEKK1, MAPSIK1/NIK, IKAP and IKB-alpha-P65-P50 complex. Phosphorylated IKB-alpha is further released from the complex. Pound in a complex composed of NCOA2, NCOA3, IKKA, IKBKG
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Attachul S.F., Zeeberg B., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Habith F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Willano D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., M., Pahey J., Helton E., Ketham M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Generation and initial analysis of more than 15,000 full-length Human and mouse cDNA sequences.";
 MEDLINE=99038238; PubMed=9819420; Nemoto S., Dibonato J.A., Lin A.; Nemoto S., Dibonato J.A., Lin A.; Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase Land MPF-kappaB-inducing kinase."; Mol. Cell. Biol. 18:7336-7343(1998).
 skeletal
 SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: Highly expressed in heart, placenta, skelet
muscle, kidney, pancreas, spleen, thymus, prostate, testis and
 -!- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
Weakly autophosphorylated.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 MEDLINE-20178139; PubMed=10712233;
Jobin C., Sartor R.B.;
"The I kappa B/NF-kappa B system: a key determinant of mucosal
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 or send an email to license@isb-sib.ch).
 J. Physiol. 278:C451-C462(2000).
 EMBL, AF029684; AAC51860.1; -. EMBL, AF080158; AAD08977.1; -. EMBL, AF091416; AAC646511; -. EMBL, BC066231; AAH06231.1; -.
 IKAPPAB KINASE SUBFAMILY.
 inflammation and protection
 peripheral blood
 IKK PHOSPHORYLATION.
 REVIEW.
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SEQUENCE FROM N.A.
 REVIEW
 ö
 K-AA: LOSS OF KINASE ACTIVITY AND NO EFFECT ON BINDING TO NIK.
S-AA: DECREASE OF ACTIVITY.
S-AB: FULL ACTIVATION.
S-AA: DECREASE OF ACTIVITY.
S-AB: FULL ACTIVATION.
WHISKVRQKEEVDIVVEEDLAGTYKF -> CVRMWPGTVAHS
CNPSTLGGRGRMI (IN REF. S).
 088351; 09R1J6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last annotation update)
18-FEB-2003 (Rel. 41, Last annotation update)
1nhibitor of nuclear factor kappa B kinaee beta subunit (EC 2.7.1.-)
(I-kappa-B-kinase beta) (IkBKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIKB)
 Gaps
 Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
 "Differential regulation of IkappaB kinase alpha and beta by two upperream kinases. NF-kappaB-inducing kinase and mitogen-activated
 GO; GO:0005737; C:cytoplasm; NAS.
GO; GO:0005524; F:ATP binding activity; NAS.
GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.
GO; GO:0016563; F:transcriptional activator activity; NAS.
GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser Ehr pkinase.
Pfam; PF00069; pkinase; 1.
 .
0
 ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION.
PHOSPHORYLATION.
 100.0%; Score 40; DB 1; Length 756; 100.0%; Pred. No. 32;
 Serine/threonine-protein kinase; ATP-binding,
 0; Indels
 LEUCINE-ZIPPER (POTENTIAL)
NEMO-BINDING.
 -> H (IN REF. 1).
F9CADF671AE9E14E CRC64;
 SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEKKI.
STRAIN=CS7BL/6; TISSUE=Spleen;
MEDLINE=98188238; PubMed=9520401;
 protein kinase/ERK kinase kinase-1.";
Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 Pfam; PP00240; ubiquitin; 1.
ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
PROSITE; PS00101; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP
 PROTEIN KINASE.
 Mismatches
 ö
 Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
NCBI_TaxID=10090,
 425 425 C
 Conservative
 STANDARD;
 HGNC: 5960; IKBKB.
 300
447
742
29
44
145
123
 44
 Mus musculus (Mouse)
 737 LDWSWL 742
 Query Match
Best Local Similarity
 1 LDWSWL 6
 IKBKB OR IKKB
 603258;
 .
9
 IKKB MOUSE
 Okumura K.
 DOMAIN
DOMAIN
NP BIND
BINDING
ACT SITE
MOD_RES
 SEQUENCE
 CONFLICT
 CONFLICT
 MOD_RES
MOD_RES
MUTAGEN
 MUTAGEN
MUTAGEN
 MUTAGEN
 AUTAGEN
 Matches
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H. M. C.-T., Wang Y.-P., Mithial J., Old W.R.;

H. M. C.-T., Kang Y.-P., Mithial J., Old W.R.;

H. WARTINESSER, STARCE

B. SUDRICOMMENTAL STARCE

M. SUDRICOMMENTAL STARCE

M. SUDRICOMMENTAL STARCE

M. M. M. C.-T., WAND. Y.-P. Old W.R.; Mithal A., Mayer C.P., Tan T.-H.;

Hench colocitic progenitor Kinase I (HRK1) stress response signaling at developmentally regulated protein Kinase. The Memory of Starce Impages Minase Mix-bland Mix-beta is a membrane signal star developmentally regulated protein Kinase. The Memory of Starce Impages Minase Mix-beta and IKK-beta is a memory of Minase Kinase in and Mix-beta is a memory of Minase
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SUBCELLULAR LOCATION: Cytoplasmic.
PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
 737 LDWSWL 742
 757 AA;
 Local Similarity
 SEQUENCE FROM N.A.
 1 LDWSWL 6
 CYOA BUCAI
P57544;
 ACT_SITE
MOD_RES
 Query Match
 DOMAIN
NP BIND
BINDING
 SEQUENCE
 RES
 DOMAIN
 DOMAIN
 CYOA_BUCAI
 Matches
 RESULT
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 Nemoto S., DiDonato J.A., Lin A.; "Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase tinase 1 and NF-kappaB-inducing kinase."; Mol. Cell. Biol. 18:7336-7343(1998).
 SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but talso as a homodimer. Directly interacts with IKK-gamma/NEMO. Heterodimers a homodimer active complex. The tripartite complex can also bind to MEKKI, MAPSKI4/NIK, IKAP and IKB-alpha-P65-P50 complex. Phosphorylated IKB-alpha is further released from the complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKBKG and CREBBP (By similarity).
 "The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";
Am. J. Physiol. 278-1645(2000).
-!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to the dissociation of the inhibitor/NF-kappa-B complex and ultimately the degradation of the inhibitor. Also phosphorylates
 Gaps
 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last annotation update)
Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
(I-Kappa-B-kinase beta) (IkBKB) (IKK-beta) (IKK-B) (I-Kappa-B kinase 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIKB)
IKBKB OR IKKB.
 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 K -> R (IN REF. 2).
TLDWSWLQMEDEERCSLEQACD -> VTA (IN REF.
 ö
 SIMILARITY)
SIMILARITY)
 100.0%; Score 40; DB 1; Length 757; 100.0%; Pred. No. 33;
 Indels
 Zhang Y., Sun S., Ravid K.;
"IKK beta in megakaryocyte differentiation.";
Submitted (DEÇ-1998) to the EMBL/GenBank/DDBJ databases.
PROTEIN KINASE.
LEUCINE-ZIPPER (POTENTIAL)
 FED962F095449C5E CRC64;
 (BY SIMILARITY). (BY SIMILARITY).
 (BY
(BY
(BY
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0
 ATP (BY SIMILARI'
BY SIMILARITY.
PHOSPHORYLATION
 (IN REF.
(IN REF.
(IN REF.
(IN REF.
 PHOSPHORYLATION PHOSPHORYLATION
 757 AA.
 0; Mismatches
 NEMO-BINDING
 0 C
1 1 N
2 N
 Х 1.
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Э. Б.
 о -- a
 MEDLINE=20178139; PubMed=10712233;
 MEDLINE=99038238; PubMed=9819420;
 86690 MW;
 Conservative
 STANDARD;
 356
390
406
573
757
 181
56
343
 Jobin C., Sartor R.B.;
 737 LDWSWL 742
 PHOSPHORYLATION
 757 AA;
 Local Similarity
 SEQUENCE FROM N.A.
 1 LDWSWL 6
 NCBI_TaxID=10116;
 356
390
406
 181
56
 9
 DOMAIN
DOMAIN
NP BIND
BINDING
ACT SITE
 CONFLICT
CONFLICT
CONFLICT
CONFLICT
 NCOA3
 MOD_RES
MOD_RES
MOD_RES
CONFLICT
CONFLICT
 IKKB RAT
 SEQUENCE
 Query Match
 Matches
 RESULT
 IKKB F
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 ö
 16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome O subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase
 subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase subunit 2). Cyok OR BU472.

Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 Gaps
 Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Buchnera.
NCBI_TaxID=118099;
Weakly autophosphorylated.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
IKAPPAB KINASE SUBFAMILY.
 0;
 BY SIMILARITY.
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
 100.0%; Score 40; DB 1; Length 757; 100.0%; Pred. No. 33; cive 0; Mismatches 0; Indels
 Transferase; Serine/threonine-protein kinase; ATP-binding;
Phosphorylation.
 LEUCINE-ZIPPER (POTENTIAL) NEMO-BINDING.
 ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
 PRINTS; PR00109; TYRKINASE.

Prodom; PD000001; Prot kinase; 1.

PROSITE; PS00101; PROTEIN KINASE ATP; FALSE NEG.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE DOM; 1.
 PROTEIN KINASE.
 296 AA.
 InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR01245; Tyr_pkinase.
 EMBL; AF115282; AAF21978.1; -.
HSSP; Q63450; 1A06.
 MW;
 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seg
 86866
 6; Conservative
 STANDARD;
 Pfam; PF00069; pkinase;
 181
 symbiotic bacterium).
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
40-MAY-2000 (Rel. 39, Last annotation update)
40-MAY-2000 (Rel. 39, Last annotation update)
50-MAY-2000 (Rel. 39, Last annotation update)
51-MAY-2000 (Rel. 39, Last annotation update)
52-MAY-2000 (Rel. 39, Last annotation update)
53-MAY-2000 (Rel. 39, Last annotation update)
 Pseudomonas putida.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 ö
 II.
 UBIQUINOL OXIDASE POLYPEPTIDE N-ACYL DIGLYCERIDE (POTENTIAL) POTENTIAL.
 Score 36; DB 1; Length 307;
 TIGRFAMB; TIGRO1433; ČYOĀ; 1.
PROSITE; PSO0013; PROKAR LIPOPROTEIN; 1.
Oxidoreductase; Transmembrane; Respiratory chain; Signal;
 1; Indels
 E66734B84410996D CRC64;
 314 AA.
 0; Mismatches
 POTENTIAL.
 POTENTIAL
 Pred. No.
 BUT LACK HEME-BINDING DOMAIN.
 PIR; A36885; A36885.

HSSP; P18400; 1CYW.

InterPro; IPR001505; Copper CuA.

InterPro; IPR005333; CyoA_II.

InterPro; IPR002429; Cyt_c_ox_2.

Pfam; PF00116; COX2; 1.
 CuA; 1.
 23 PO
307 UB
24 N-
66 PO
107 PO
33921 MW;
 PRINTS; PR01166; CYCOXIDASEII.
ProDom; PD000131; Copper CuA;
 Pseudomonadaceae; Pseudomonas.
 EMBL; D13185; BAA02480.1; -.
 90.06
 83.3%;
 5; Conservative
 STANDARD;
 135 LDWKWL 140
 307 AA;
 Local Similarity
 SEQUENCE FROM N.A.
 1 LDWSWL 6
 NCBI_TaxID=303;
 Lipoprotein
 CYOA_PSEPU
 FRANSMEM
 SEQUENCE
 Query Match
 TRANSMEM
 SIGNAL
 CHAIN
 LIPID
 CYOA_PSEPU
 Matches
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 ö
 HSSP; P18400; 1CYW.
InterPro; IRR001505; Copper CuA.
InterPro; IRR001505; CyoA II.
InterPro; IRR002429; CyoA II.
InterPro; IRR002429; Cyt Cox 2.
InterPro; IRR00437; Prok Iipoprot.
Probom; P0001131; COX2; 1.
Propom; P0000131; CyOA; 1.
TIGRFAMS; TIGR01433; CyOA; IIPOPROTEIN; FALSE NEG.
Oxidoreductage; Respiratory chain; Electron transport; Transmembrane;
 Gaps
 CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O. SUBCELLULAR LOCATION: Integral membrane protein (By similarity). SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS. BUT LACK HEME-BINDING DOMAIN.
 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome Al subunit 2) (Oxidase BA13) subunit 2).
 MEDLINE=9332308; PubMed=8392509;
Fukaya M., Tayama K., Tamaki T., Ebisuya H., Okumura H.,
Kawamura Y., Horinouchi S., Beppu T.;
"Characterization of a cytochrome al that functions as a ubiquinol oxidase in Acetobacter aceti.";
D Bacteriol. 175:430-4314(1991).
-!- PATHWAY: TERMINAL OXIDASE FOR ETHANOL OXIDATION.
-!- SUBGINIT: HETEROTETRAMER OF THE SUBGINITS 1, 2, 3 AND 4.
-!- SUBGINIT: SOME. In Integral membrane protein.
-!- SUBGINITS: SOME. TO MITOGRONDRIAL OR BACTERIAL COX2 SUBUNITS.
BUT LACK HEMB-BINDING DOMAIN.
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Acetobacteraceae; Acetobacter
 ö
 II.
 UBIQUINOL OXIDASE POLYPEPTIDE N-ACYL DIGLYCERIDE (POTENTIAL) EXTRACELLULAR (POTENTIAL).
 90.0%; Score 36; DB 1; Length 296;
 EXTRACELLULAR (POTENTIAL)
 1AB2B4F0408FFBAC CRC64;
 CYTOPLASMIC (POTENTIAL).
 307 AA
 ed. No. 54;
Mismatches
GROWN AT HIGH AERATION (BY SIMILARITY)
 Complete proteome
 POTENTIAL
 POTENTIAL
 EMBL; AP001119; BAB13169.1; -.
 34180 MW;
 83.3%;
 Local Similarity 83.3
 STANDARD;
 gnal; Lipoprotein;
 125 LDWKWL 130
 296 AA;
 SEQUENCE FROM N.A.
 1 LDWSWL 6
 Acetobacter aceti.
 NCBI_TaxID=435;
 QOX2_ACEAC
P50653;
 STRAIN=1023
 DOMAIN
TRANSMEM
 RANSMEM
 SEQUENCE
 Query Match
 IGNAL
 DOMAIN
 DOMAIN
 CHAIN
 QOX2_ACEAC
 Best Loc
Matches
 CYAB.
 RESULT 7
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Gaps

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5; Conservative
 STANDARD;
 Local Similarity
 279 LDWSW 283
 2
 NCBI_TaxID=9031;
 LDWSW
 CHICK
 Query Match
Best Local S
 EPA3 CHI
P29318;
 Gallus
 EPA3_CHICK
 Matches
 RESULT 10
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 oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
 InterPro; IPR001505; Copper CuA.
InterPro; IPR00433; CyoA_II.
InterPro; IPR004429; Cyt_c_ox_2.
Prom; PR00116; Copper CuA; 1.
IIGRPAMS; TIGR01433; CyoA; 1.
PROSITE; PS000131; PROKAR LIPOPROTEIN; 1.
Oxidoreductase; Respiratory Chain; Electron transport; Transmembrane; Signal; Lipoprotein.
SIGNAL
 Gaps
 Diflumeri C., Larocque R., Keng T.;
"Molecular analysis of HEM6 (HEM12) in Saccharomyces cerevisiae, the gene for uroporphyrinogen decarboxylase.";
Yeast 9:613-623(1993).
 "Uroporphyrinogen decarboxylase in Saccharomyces cerevisiae. HEM12 gene sequence and evidence for two conserved glycines essential for
 MEDLINE=92249304; PubMed=1576986;
Garey J.R., Labbe-Bois R., Chelstowska A., Rytka J., Harrison L.,
Kushner J., Labbe P.;
 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 ;
 UBIQUINOL OXIDASE POLYPEPTIDE II. N-ACYL DIGLYCERIDE (POTENTIAL). PERIPLASMIC (POTENTIAL).
 Rajandream M.A.;
 Score 36; DB 1; Length 314;
Pred. No. 57;
 01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD)
HEM12 OR PDP3 OR YD5609.03.
Saccharomyces cerevisiae (Baker's yeast).
 MEDLINE=93111946; PubMed=1471989;
Chelstowska A., Zoadek T., Garey J.R., Kushner J., Rytka
Labbe-Bois R.;
 1; Indels
 SEQUENCE FROM N.A.
STRALN-82186 / AB972;
Hunt S., Bowman S., Harris D., Barrell B.G., Rajandream
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
 96EE04FC3AA77F07 CRC64;
 CYTOPLASMIC (POTENTIAL).
 PERIPLASMIC (POTENTIAL)
 362 AA.
 Mismatches
 entities requires a license agreement (Se or send an email to license@isb-sib.ch).
 POTENTIAL.
 enzymatic activity.";
Bur. J. Biochem. 205:1011-1016(1992)
 PRT;
and this statement is not
 SEQUENCE FROM N.A.
MEDLINE=93348774; PubMed=8346678;
 ;
 EMBL; AB016787; BAA76356.1; -. HSSP; P18400; 1CYW.
 34702 MW;
 90.0%;
 Conservative
 STANDARD;
 LDWKWL 138
 314 AA;
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 1 LDWSWL 6
 WCBI_TaxID=4932;
 'n
 DCUP_YEAST
ID _DCUP_YEAST
 DOMAIN
TRANSMEM
 DOMAIN
TRANSMEM
 133
 SEQUENCE
 MUTANTS
 P32347;
 DOMAIN
 CHAIN
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Matches
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 ö
"Identification of amino acid changes affecting yeast uroporphyrinogen decarboxylase activity by sequence analysis of hem12
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 Gaps
 MEDLINE=92031278; PubMed=1657122;
MEDLINE=92031278; PubMed=1657122;
Sajjadi F.G., Pasquale E.B., Subramani S.;
"Identification of a new eph-related receptor tyrosine kinase gene
Irom mouse and chicken that is developmentally regulated and encodes
at least two forms of the receptor.";
 01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor ETK1) (CEK4).
EPHA3 OR ETK1 OR CEK4.
Gallus gallus (Chicken).
 mutant alleles.";
Biochem. J. 288:753-757(1992).
-!- CATALYTIC ACTIVITY: Uroporphyrinogen-III = coproporphyrinogen
 SGD; S0002454; HEM12.
GO; GO:0004853; F:uroporphyrinogen decarboxylase activity; IMP.
GO; GO:0006783; P:heme biosynthesis; IMP.
InterPro; IPR006361; HemE.
InterPro; IPR000257; Uro_decarbxyls.
 .;
0
 DB 1; Length 362;
65;
 0; Indels
 983 AA
 100.0%; Pred. No. ...
 PRT;
 EMBL, X63721, CAA45253.1; -.
EMBL, Z19089; CAA79514.1; -.
EMBL, Z49209; CAA89078.1; -.
PIR, S23471; S23471.
HSSP, P06132; 1URO.
SGD, S0002454; HEM12.
 01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last seq
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 LYTOSINE phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TSSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING BRAIN AND EMBRYONIC TISSUES. IN ADULT THE GREATEST LEVELS OF EXPRESSION OCCURS. IN THE BRAIN. IT IS EXPRESSED IN A GRADED MANNER ACROSS THE RETINA WITH THE HIGHEST EXPRESSION AT ITS TEMPORAL POLE.
-!- SIMILARITY: Contains 1 serile alpha motif (SAM) domain.
-!- SIMILARITY: Contains 2 fibronectin type III domains.
-!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 Pfam; PF01404; EPH 1bd; 1.

R Pfam; PF010404; EPH 1bd; 1.

R Pfam; PF010604; EPH 1bd; 1.

R Pfam; PF001041; fn3; 2.

R Pfam; PF001061; EPH 1bd; 1.

R PRINTS; PR00104; TYRKIMASE.

R PRINTS; PR00109; TYRKIMASE.

R PRODOM; PD0010495; EPH 1bd; 1.

R SMART; SM00615; EPH 1bd; 1.

R SMART; SM00615; RN3; 2.

R SMART; SM0019; PR07EIN KINASE DOM; 1.

R R SMART; SM0019; PR07EIN KINASE DOM; 1.

R R ROSITE; PS00109; PR07EIN KINASE DOM; 1.

R RROSITE; PS00109; PR07EIN KINASE DOM; 1.

R PROSITE; PS00109; PR07EIN KINASE TYR; 1.

R PROSITE; PS00109; PR07EIN KINASE TYR; 1.

R PROSITE; PS00109; PR07EIN KINASE TYR; 1.

R PROSITE; PS00109; PR07EIN KINASE TYR; 1.

R PROSITE; PS00109; PR07EIN KINASE TYR; 1.

R PROSITE; PS00109; PR07EIN KINASE TYR; 1.

R PROSITE; PS00109; PR07EIN KINASE TYR; 1.

R PROSITE; PS00109; PR07EIN KINASE TYR; 1.

R PROSITE; PS00109; PR07EIN KINASE TYR; 1.

R PROSITE; PS00109; PR07EIN KINASE TYR; 1.

R PROSITE; PS00109; PR07EIN KINASE TYR; 1.

R PROSITE; PS00109; PR07EIN KINASE TYR; 1.

R PROSITE; PS00109; PR07EIN KINASE TYR; 1.

R PROSITE; PS00109; PR07EIN KINASE TYR; 1.

R PROSITE; PS00109; PR07EIN KINASE TYR; 1.
New Biol. 3:769-778 (1991).
-!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A2, -A3, -A4 AND -A5.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 (AUTO-) (POTENTIAL).
(AUTO-) (POTENTIAL).
(AUTO-) (POTENTIAL).
 PDZ-BINDING MOTIF (POTENTIAL). ATP (BY SIMILARITY).
 EPHRIN TYPE-A RECEPTOR 3. EXTRACELLULAR (POTENTIAL)
 Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
SIGNAL 1 19 BY SIMILARITY.
 (AUTO-)
(AUTO-)
 CYTOPLASMIC (POTENTIAL).
 FIBRONECTIN TYPE-III 1. FIBRONECTIN TYPE-III 2.
 (BY SIMILARITY).
 BY SIMILARITY.
PHOSPHORYLATION (
PHOSPHORYLATION (
PHOSPHORYLATION (
 PROTEIN KINASE
 CYS-RICH.
 InterPro; IPR006209; EGF like.
InterPro; IPR001090; Ephrin_receptor.
InterPro; IPR003961; FN III subd.
InterPro; IPR003962; FnIII subd.
InterPro; IPR003719; Prot_Kinase.
 InterPro; IPR001660; SAM.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001426; YKase_receptorV.
 EMBL; M68514; AAA48666.1; -.
 RECEPTOR SUBFAMILY
 PIR; B45583; B45583.
HSSP; P00523; 2PTK.
 ACT SITE
MOD RES
MOD RES
MOD RES
 DOMAIN
TRANSMEM
 BIND
 DOMAIN
DOMAIN
SITE
 DOMAIN
 BINDING
 DOMAIN
```

```
SECUENCE OF 21-29 AND 840-860, AND CHARACTERIZATION.
MEDLINE-92147681; PubMed=1737782;
MEDLINE-92147681; PubMed=1737782;
MEDLINE-92147681; PubMed=1737782;
MEDLINE-92147681; PubMed=1737782;
MISOLATION. Wicker I.P., Simpson R.J., Salvaris E., Wilks A., Welch K., Loudovaris M., Rockman S., Busmanis I.;
"Isolation and characterization of a novel receptor-type protein tyroslatic kinses (hek) from a human pre-B cell line.";
J. Biol. Chem. 267:326-3267(1992).
-I. FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A2, -A3, -A4 AND -A5. COULD PLAY A ROLE IN LYMPHOID
 Isold=P29320-2; Sequence-VSP 002995, VSP 002996;
TISSUB SPECIFICITY: WIDELY EXPRESSED. HIGHEST LEVEL IN PLACENTA.
SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
SIMILARITY: Contains 2 tibronectin type III domains.
SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
 P29320; Q9H2V3; Q9H2V4; Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-2001 (Rel. 24, Last sequence update)
Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor ETK1) (HEK4).
 Chiari R., Hames G., Stroobant V., Maillere B., Texier C., Mach B., Boon T., Coulie P.G.;
 Boon I., Coulie P.G.,
"Identification of a tumor specific shared antigen derived from an
Eph-receptor and presented to CD4 I cells on HLA class II
 Bukaryoca, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
 SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=92179233; PubMed=1311845;
Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W.;
Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W.;
"Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expressed by human lymphoid tumor cell lines.";
Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615 (1992).
 FUNCTION.
 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
 ö
 LYTOSINE phosphate.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1);
SECRETED (ISOFORM 2).
ALTERNATIVE PRODUCTS:
 90.0%; Score 36; DB 1; Length 983; 100.0%; Pred. No. 1.7e+02;
 0; Indels
231 N-LINKED (GLCNAC. . .) (POT
336 N-LINKED (GLCNAC. . .) (POT
390 N-LINKED (GLCNAC. . .) (POT
492 N-LINKED (GLCNAC. . .) (POT
109910 MW; E8895F0BDF77651E CRC64;
 Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 Event=Alternative splicing; Named isoforms=2;
 983 AA.
 100.0%; Pred. No. ...
 IsoId=P29320-1; Sequence=Displayed;
 FROM N.A. (ISOFORMS 1 AND 2).
 5; Conservative
 STANDARD;
 RECEPTOR SUBFAMILY
 Homo sapiens (Human)
231
336
390
403
492
983 AA;
 Local Similarity
 LDWSW 346
 1 LDWSW 5
 TISSUE=Melanoma;
 NCBI_TaxID=9606;
 molecules."
 HUMAN
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
 342
 SEQUENCE
 Query Match
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 PRINTS; PROD1091; SAW; 1.1.

PRINTS; PRO0109; TRYTYPEIII.

PRINTS; PRO0109; TRYTYPEIII.

PRODOM; PD001091; PROFILE receptor; 1.

ProDOM; PD001091; PROFILE receptor; 1.

ProDOM; PRO01091; PROFILE RINASE AIP.

SMART; SM004619; SAM; 1.

SMART; SM004619; SAM; 1.

RAGIT; PRO0119; PROFILE RINASE AIP, 1.

PROSITE; PS00110; PROFILE RINASE AIP, 1.

PROSITE; PS00109; PROFILE RINASE AIP, 1.

PROSITE; PS00109; PROFILE RINASE AIP, 1.

PROSITE; PS00109; PROFILE RINASE AIP, 1.

PROSITE; PS00109; PROFILE RINASE AIP, 1.

PROSITE; PS00109; PROFILE RINASE AIP, 1.

PROSITE; PS00109; PROFILE RINASE AIP, 1.

PROSITE; PS00109; PROFILE RINASE AIP, 1.

PROSITE; PS00109; PROFILE RINASE AIP, 1.

PROSITE; PS00109; PROFILE RINASE AIP, 1.

PROSITE; PS00109; PROFILE RINASE AIP, 1.

PROSITE; PS00109; PROFILE RINASE AIP, 1.

PROSITE; PS00109; PROFILE RINASE AIP, 1.

PROSITE; PS00109; PROFILE RINASE AIP, 1.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROSITE; PS00109; PROFILE RINASE, I.

PROFILE RINASE AIP RINASE, I.

PROFILE RINASE AIP RINASE, I.

PROFILE RINASE AIP RINASE, I.

PROFILE RINASE AIP RINASE, I.

PROFILE RINASE AIP RINASE, I.

PROFILE RINASE
 ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY).

BY SIMILARITY).

PHOSPHORYLATION (AUTO-) (POTENTIAL).

PHOSPHORYLATION (AUTO-) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

SFSIEGES -> CMYYENAV (in isoform 2).

/FTIG=VSP_002995.
 (POTENTIAL).
 PDZ-BINDING MOTIF (POTENTIAL)
 GO; GO:0002887; C:integral to plasma membrane; TAS.
GO; GO:0007165; P:isignal transduction; TAS.
InterPro; IPR0016209; EGF like.
InterPro; IPR001090; Ephrin receptor.
InterPro; IPR001961; FN III.
InterPro; IPR001961; FN III.
InterPro; IPR001962; FN III.
InterPro; IPR001919; Prot Kinase.
InterPro; IPR001245; TYT Dkinase.
InterPro; IPR001245; TYT Dkinase.
InterPro; IPR001245; TYT Dkinase.
InterPro; IPR001426; YKase_receptorV.
Pfam; PP00404; EPH-lbd; 1.
Pfam; PP00404; EPH-lbd; 1.
Pfam; PP00636; SAM; 1.
 EPHRIN TYPE-A RECEPTOR 3.
EXTRACELLULAR (POTENTIAL)
 CYTOPLASMIC (POTENTIAL).
 FIBRONECTIN TYPE-III 1. FIBRONECTIN TYPE-III 2.
 Missing (In isoform 2)
 PROTEIN KINASE.
 EMBL, M83941; AAA58633.1; ---
EMBL, AF213459; AAG43576.1; --
EMBL, AF21460; AAG43577.1; ---
EMBL, A28003; CAA01906.1; ---
PIR, A38224; A38224.
HSSP, P00523; ZPTK,
Genew, HGNC:3387; EPHA3.
 983
 540
 TRANSMEM
DOMAIN
 SITE
NP BIND
BINDING
ACT SITE
MOD RES
 MOD_RES
MOD_RES
CARBOHYD
 CARBOHYD
CARBOHYD
 VARSPLIC
 CARBOHYD
 MRSPLIC
 CHAIN
 DOMAIN
DOMAIN
DOMAIN
DOMAIN
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 Name=Short;
Isold=P29319-2; Sequence=VSP_002997;
Isold=P29319-2; Sequence=VSP_002997;
Isold=P29319-2; Sequence=VSP_002997;
Isold=P29319-2; Sequence=VSP_002997;
Insold=P29319-2; Sequence=VSP_002997;
Insold=P29319-2; Sequence=VSP_002997;
Isold=P29319-2; Sequence=VSP_002997;
Isold=P29319-2; Sequence=VSP_002997;
Isold=P29319-2; Sequence=VSP_002997;
Isold=P29319-2; Sequence=VSP_002997;
Insold=P29319-2; Sequence=VSP_0029997;
Insold=P293
 Gaps
 tyrosine phosphate.
 01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor ETK1) (MEK4).
EPHA3 OR ETK1 OR MEK4 OR TYRO4.
Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
 ;
0
/FTId=VSP 002996.

507 507 F -> L (IN REF. 1; CAA01906).

724 724 V -> L (IN REF. 1; CAA01906).

911 911 S -> T (IN REF. 2).

924 924 R -> W (IN REF. 2).

983 AA; 110096 MW; BBD900FAB0FF5121 CRC64;
 Similarity 100.0%; Score 36; DB 1; Length 983; Similarity 100.0%; Pred. No. 1.7e+02; 5; Conservative 0; Mismatches 0; Indels
 Event=Alternative splicing; Named isoforms=2;
 SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
STRAIN=ICR X Swiss Webster; TISSUE-Embryo;
MEDLINE=92031278; PubMed=1657122;
 983 AA.
 Name=Long;
IsoId=P29319-1; Sequence=Displayed;
 EMBL; M68513; AAA39521.1; -.
EMBL; M86515; AAA39522.1; ALT_SEQ.
PIR; A45583; A45583.
HSSP; P00523; 2PTK.
MGD; MGI: 99612; Epha3.
INCEPPC; IPR006209; EGF like.
InterPrc; IPR001090; Ephrin_receptor.
 IS SECRETED.
 STANDARD;
 Query Match
Best Local Similarity
 343 LDWSW 347
 1 LDWSW 5
 EPA3 MOUSE
ID EPA3 MOUSE
 CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
 Matches
 RESULT 12
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InterPro; IRR006209; EGF like.
InterPro; IRR001090; Ephrin receptor.
InterPro; IRR003961; FN III.
InterPro; IRR003962; FnIII subd.
InterPro; IRR00119; Prot Kinase.
InterPro; IRR001149; Yr pkinase.
InterPro; IRR001446; Yr pkinase.
 POTENTIAL
 EMBL; U69278; AAC06273.1; -. HSSP; P00523; 2PTK.
 Pfam; PF01404; BPH 1bd; 1. Pfam; PF00041; fn3; 2. Pfam; PF00069; pkinase; 1. Pfam; PF00536; SAM; 1.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10116;
 CHAIN
DOMAIN
TRANSMEM
DOMAIN
 DOMAIN
DOMAIN
DOMAIN
DOMAIN
 ö
 PRINTS; PROUDSU; SAM; 1.

R PRINTS; PROUDSU; PYRKINASE.

R PYDOOM; PD00149; EDAITIN receptor; 1.

R PRODOM; PD00109; EDAITIN receptor; 1.

R SMART; SM00601; EDH_lDd; 1.

R SMART; SM00601; ENJ; 2.

R SMART; SM00219; TyrKc; 1.

R SMART; SM00219; TyrKc; 1.

R RPGSTTE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS00790; RECEPTOR_TYR KIN V 1; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 1; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 2; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 2; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 2; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 2; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 2; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 2; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR KIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR XIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR XIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR XIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR XIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR XIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR XIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR XIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR XIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR XIN V 3; 1.

R PROSITE; PS00791; RECEPTOR_TYR XIN V 3; 1.

R
 Gaps
 EPA3 RAT STANDARD; PRT; 984 AA.
008680;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ephrin type-A receptor 3 precursor (RC 2.7.1.112) (Tyrosine-protein Kinase receptor REK4) (TYRO-4).
 PDZ-BINDING MOTIF (POTENTIAL).
ATP (BY SIMILARITY).
BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (POTENTIAL).
PHOSPHORYLATION (AUTO-) (POTENTIAL).
PHOSPHORYLATION (AUTO-)
 (POTENTIAL).
 N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
 ö
 90.0%; Score 36; DB 1; Length 983;
 0; Indels
 983 AA; 109955 MW; BE44A6655D8107A2 CRC64;
 Missing (in isoform Short)
 EPHRIN TYPE-A RECEPTOR 3. EXTRACELLULAR (POTENTIAL)
 CYTOPLASMIC (POTENTIAL).
 FIBRONECTIN TYPE-III 1. FIBRONECTIN TYPE-III 2.
 Pred. No. 1.7e+02;
 PROTEIN KINASE
 BY SIMILARITY.
 0; Mismatches
 POTENTIAL.
 FTIG=VSP
 CYS-RICH.
 InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001426; Ykase_receptorV.
Pfam; PF00404; BPH lbd; 1.
Pfam; PF00041; fin3; 2.
Pfam; PF00069; pkinase; 1.
Pfam; PF00536; SAM; 1.
 IPR003962; FnIII subd.
IPR000719; Prot Kinase.
 100.08;
 IPR001660; SAM.
 Best Local Similarity 100.
Matches 5; Conservative
 342 LDWSW 346
 1 LDWSW 5
 InterPro;
 DOMAIN
TRANSMEM
 ACT_SITE
MOD_RES
MOD_RES
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
 CARBOHYD
VARSPLIC
 DOMAIN
DOMAIN
DOMAIN
 SEQUENCE
 Query Match
 BIND
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SITE
 SIGNAL
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 RESULT 13
 EPA3 RAT
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 PRINTS; PRO0109; TYRKINASE.

R PRINTS; PRO0109; TYRKINASE.

R PRODOM; PRO0109; TYRKINASE.

R PRODOM; PRO0109; TYRKINASE.

R PRODOM; PRO0101; Proc Kinase; 1.

R SWART; SM004615; EBH_1bd; 1.

R SWART; SM004615; EAH_1bd; 1.

R SWART; SM0018; SAM; 1.

R SWART; SM0018; SAM; 1.

R SWART; SM0019; PROTEIN KINASE ATP; 1.

R RASITE; PS00107; PROTEIN KINASE TYR; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.

R PROSITE; PS00109; RECEPTOR TYR KIN V 1; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.

R PROSITE; PS00109; RECEPTOR TYR KIN V 1; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.

R PROSITE; PS00109; RECEPTOR TYR KIN V 1; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.

R PROSITE; PS00109; PROTEIN TYPE-A RECEPTOR 3.

T CHAIN TYPE-A RECEPTOR 3.

DOMAIN 21 SERIRAL TYPE-A RECEPTOR 3.

PROMAIN 21 SERIENT TYPE-A RECEPTOR 3.

PROMAIN 21 SERIENT TYPE-A RECEPTOR 3.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
 MYOCYTES.
--- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
--- SIMILARITY: Contains 2 fibronectin type III domains.
--- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN RECEPTOR SUBFAMILY.
 tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUB SPECIFICITY: MOST ABUNDANT IN THE HEART, BRAIN, AND LUNG.
-!- INDUCTION: DOWN-REGULATED BY IL1-BETA IN NEONATAL CARDIAC
 FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
PROTEIN KINASE.
 CYTOPLASMIC (POTENTIAL)
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us-09-643-260-2.rsp

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 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, lichenin and cereal beta-D-glucons. CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages in cellulose and cellotetrace, releasing cellobiose from the non-reducing ends of the chains.

SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO CELLULASE FAMILY FIRMILARITY: IN THE C-FERMINAL SECTION, BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL HYDROLASES).
 01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Endoglucanase/excglucanase B precursor [Includes: Endoglucanase
(EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)
(Cellobiohydrolase); Excglucanase (EC 3.2.1.91) (Exccellobiohydrolase)
 Caldocellum saccharolyticum (Caldicellulosiruptor saccharolyticus).
Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;
Caldicellulosiruptor.
 Gaps
 (POTENTIAL).
 (POTENTIAL) . (POTENTIAL) . (POTENTIAL) .
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
 (POTENTIAL)
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0
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 DB 1; Length 984;
 0; Indels
 MW; F170C49312F7A0AB CRC64;
 1.7e+02;
 PRT; 1039 AA.
 100.0%; Pred. ...
 or send an email to license@isb-sib.ch).
 90.0%; Score 36;
 HSSP; Q06851; INBC.
InterPro; IPR001956; CBD_3.
InterPro; IPR001000; Glyco_hydro_10.
 (1,4-beta-cellobiohydrolase)].
 EMBL; X13602; CAA31936.1; -.
 110227
 Conservative
 STANDARD;
 391
 AN ENDOGLUCANASE
 S02711; S02711.
 984 AA;
 Best Local Similarity
Matches 5; Conserv
 343 LDWSW 347
 NCBI_TaxID=44001;
 1 LDWSW 5
 603
780
232
 GUNB CALSA
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 P10474;
DOMAIN
 RESULT 14
GUNB_CALSA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the Buropan Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
 -i- FUNCTION: Cytochrome O terminal oxidase complex is the component of the aerobic respiratory chain that predominates when cells are grown at high aeration (By similarity).
-i- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.
-i- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-i- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
BUT LACK HEME-BINDING DOMAIN.
 28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ubiquinol oxidase polypeptide II precursor (EC 1.10.3.-) (Cytochrome subunit 2) (Oxidase BO(3) subunit 2) (Cytochrome O ubiquinol oxidase CYOA OR BUSG456.
 Gaps
 ENDOGLUCANASE/EXOGLUCANASE B.
THR/PRO-RICH, TANDEM REPEATS OF T-P.
CELLUCASE-BINDING (EW SIMILARITY).
THR/PRO-RICH, TANDEM REPEATS OF T-P.
PROTON DONOR (POTENTIAL).
 Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
 MEDLINE=22084549; PubMed=12089438; Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Briksson A.-S., Tamas I., Klasson L., Canbaeck B., Moran N.A., Andersson S.G.E.; Mernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.; Science 296:2376-2379 (2002).
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 90.0%; Score 36; DB 1; Length 1039; 100.0%; Pred. No. 1.8e+02; ive 0; Mismatches 0; Indels
 NUCLEOPHILE (BY SIMILARITY).
 0E0378171594DDAE CRC64;
 Pfam; PP00941; CBM 3; 1.
Pfam; PP00150; cellulase; 1.
Pfam; PP001150; cellulase; 1.
Pfam; PP00131; diyoc hydro 10; 1.
PRINTS; PR00134; diyochydrasE10.
ProDom; PD001947; CBD 3; 1.
PROSITE; PS00591; dirCoSYL HYDROL F10; 1.
PROSITE; PS00599; dixCoSYL HYDROL F5; 1.
Cellulose degradation; Hydrolase; Glycosidase; Repeat;
 290 AA.
 BY SIMILARITY
 InterPro; IPR001505; Copper CuA.
InterPro; IPR006233; CydA II.
InterPro; IPR002429; Cyt. C ox 2.
InterPro; IPR000437; Prok_Iipoprot.
 117641 MW;
 28-FEB-2003 (Rel. 41, Created)
 EMBL; AE014121; AAM67999.1; -
 5: Conservative
 STANDARD;
 416
570
618
 1039
 1039 AA;
 Query Match
Best Local Similarity
 540 DWSWL 544
 SEQUENCE FROM N.A.
 2 DWSWL 6
 BUCAP
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ACT_SITE
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 <u>овко</u>93;
 DOMAIN
 SIGNAL
 DOMAIN
 CHAIN
 CYOA_BUCAP
 Matches
 CYOA
 RESULT 15
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DR PEAM; PF00116; COX2; 1.

DR PRINTS; PR01166; CYCOXIDAGEII.

DR PRODOM; PR00101; COOPER Cut; 1.

DR PROSITE; PS000131; CyoĀ; 1.

DR PROSITE; PS000131; PS000131; CyoĀ; 1.

DR PROSITE; PS000131; PS000131; PS00ENTIAL.

DR PROSITE; PS000131; PS000131; PS00ENTIAL.

KW Signal; Lipoprotein; Complete proteome.

FT SIGNAL 1 24 POTENTIAL.

FT CHAIN 25 290 N-ACYL DIGLYCERIDE (POTENTIAL).

FT TRANSMEM 43 63 POTENTIAL.

FT TRANSMEM 48 109 290 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 109 290 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 333730 MM; 3D80A284732963 CRC64;

QUETY MATCH

RODOR 1 LDWSNL 6

Nismatches 1; Indels 0; Gaps 0;
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Search completed: February 18, 2004, 14:28:01 Job time : 5.55263 secs

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Matches
 ð
 Q8cbt3 mus musculu Q95kvO bos taurus Q8cs1 yersinia pe Q8c5u2 streptococc Q8c065 streptococc Q8c065 streptococc Q9c057 rhizobium 1 Q8g100 brucella mu Q8g100 brucella su Q8g100 brucella su Q8g100 brucella su Q8g100 streptomyce Q8fb18 escherichia Q9acr5 streptomyce Q8ixk8 homo sapien Q919k8 culex nigri
 Q95kvl bos taurus
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 February 18, 2004, 14:09:39; Search time 17.3684 Seconds (without alignments) 89.145 Million cell updates/sec
 Description
 830525
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 830525 seqs, 258052604 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 Q8CBT3
Q95KV0
Q8ESU1
Q8ESU1
Q8ESU1
Q9XBS7
Q9XBS7
Q9KRX
Q9KRX
Q9KRX
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Gapop 10.0 , Gapext 0.5
 sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 US-09-643-260-2
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1 LDWSWL 6
 Length DB
 SPTREMBL 23:*
 645
85
205
227
242
 Query
Match I
 Scoring table:
 Title:
Perfect score:
 Score
 Database :
 Sequence:
 Searched:
 Run on:
 Result
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| ç                  | AT. T.CHIMENTO |    |      |         |     |      |  |
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| Usagg4 calaicellui | Q9AQG4         | 7  | 16/1 | y<br>0. |     |      |  |
| caldicel           | 09X3P6         | 7  | 1426 | 90.0    | 36  | 44   |  |
| 0                  | Q9CD30         | 16 | 1329 | 90.0    |     |      |  |
| u                  | Q9AQH0         | 7  | 966  | 90.0    |     | 42   |  |
| -                  | QBBRB1         | 11 | 984  | 90.0    |     | . 41 |  |
|                    | Q8C3U1         | 11 | 984  | 90.0    |     | 40   |  |
|                    | Q97UH8         | 17 | 803  | 90.0    |     | 39   |  |
|                    |                | 16 | 747  | 90.0    |     | 38   |  |
|                    |                | 10 | 703  | 90.0    |     | 37   |  |
|                    |                | 10 | 703  | 90.0    |     | 36   |  |
| Q8c9k6 mus musculu |                | 11 | 538  | 90.0    | 36  | 35   |  |
| Q9btv6 homo sapien | Q9BTV6         | 4  | 484  | 90.0    | 36  | 34   |  |
| Q9cyu6 mus musculu | 09CXU6         | 11 | 477  | 90.0    | 36  | 33   |  |
| рошо               | •              | 4  | 452  | 90.0    | 36  | 32   |  |
| Q9m3f6 arabidopsis |                | 10 | 409  | 90.0    | 36  | 31   |  |
|                    |                | 16 | 393  | 90.0    | 36. | 30   |  |
|                    |                | 16 | 386  | 90.0    |     | 29   |  |
|                    |                | 11 | 355  | 90.0    |     | 28   |  |
|                    |                | 16 | 353  | 90.0    | 36  | 27   |  |
|                    |                | 16 | 344  | 90.0    |     | 26   |  |
|                    |                | 16 | 341  | 90.0    |     | 25   |  |
| Q91427 pseudomonas |                | 16 | 331  | 90.0    |     | 24   |  |
| ralstonia          |                | 16 | 329  | 90.0    |     | 23   |  |
| 8                  |                | 16 | 318  | 0.06    |     | 22   |  |
| o.                 | 900.480        | ~  | 313  | 0.06    | 36  | 21   |  |
|                    | Q8KZS2         | ~  | 308  | 90.0    | 36  | 20   |  |
|                    | Q8VTT4         | ~  | 288  | 90.0    | 36  | 19   |  |
| Q8d354 wiggleswort | Q8D354         | 16 | 282  | 0.06    | 36  | 18   |  |
| Q9agg7 caldicellul | Q9AQG7         | 7  | 261  | 0.06    | 36  | 17   |  |
|                    |                |    |      |         |     |      |  |

## ALIGNMENTS

| ESULT 1<br>95KV1 | D Q95KV1 PRELIMINARY; PRT; 740 AA. | Q95KV1; | 01-DEC-2001 (TrEMBLrel. 19, Creat | 01-DEC-2001 (TrEMBLrel. | 01-MAR-2003 (TrEMBLrel. | IkB kinase-a] | N BIKKALPHA. | S Bos taurus (Bovine). | C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | Mammalia, Eutheria, |  |  |  | P SEQUENCE FROM N.A. | A Rottenberg S., Dobbelaere D.A.E., Heussler V.T.; |  |  | L Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. |  | R EMBL; AJ414555; CAC93686.1; |  | R InterPro; IPR002290; Ser_thr_pkinase. |  |  |  | R PROSITE; PS00107; PROTEIN KINASE ATP; 1. |  | R PROSITE; PS00108; PROTEIN KINASE ST; 1. |  | Q SEQUENCE 740 AA; 84343 MW; 01903BEIlF44D176 CRC64; | 100.04; | Best Local Similarity 100.0%; Pred. No. 2.18+02;<br>Matches 6: Conservative 0: Mismatches 0: Indels 0: Gabs |  |
|------------------|------------------------------------|---------|-----------------------------------|-------------------------|-------------------------|---------------|--------------|------------------------|---------------------------------------------------------------------|---------------------|--|--|--|----------------------|----------------------------------------------------|--|--|------------------------------------------------------------|--|-------------------------------|--|-----------------------------------------|--|--|--|--------------------------------------------|--|-------------------------------------------|--|------------------------------------------------------|---------|-------------------------------------------------------------------------------------------------------------|--|
|------------------|------------------------------------|---------|-----------------------------------|-------------------------|-------------------------|---------------|--------------|------------------------|---------------------------------------------------------------------|---------------------|--|--|--|----------------------|----------------------------------------------------|--|--|------------------------------------------------------------|--|-------------------------------|--|-----------------------------------------|--|--|--|--------------------------------------------|--|-------------------------------------------|--|------------------------------------------------------|---------|-------------------------------------------------------------------------------------------------------------|--|

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us-09-643-260-2.rspt

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Enterobacteriaceae; Yersinia.
NCBI_TaxID=632;
 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2003 (TrEMBLrel. 23,
 5; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Hypothetical protein. GBS0887.
 :|||||
480 MDWSWL 485
 737 LDWSWL 742
 Best Local Similarity
 1 LDWSWL 6
 1 LDWSWL 6
 Streptococcus.
NCBI_TaxID=216495;
 fersinia pestis
 Bacteria;
 Query Match
 Q82C91
Q82C91;
 Q8E5U2;
 Q8E5U2
 Matches
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Q8E5U2
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 Tottenberg S., Dobbelaere D.A.E., Heussler V.T.,
"Identification and characterisation of the bovine IkB kinases (IKKs)
alpha, beta and gamma."; Buttenberg Submitted (SEP-201) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL. AJ14556; CAC93687.1; -..
InterPro; IPR0012919; Prot Kinase.
InterPro; IPR001295; Tyr Dkinase.
InterPro; IPR001295; Tyr Dkinase.
Pfam; PR00069; pkinase; Tyr Dkinase.
PRINTS; PR00199; TYRKINASE.
 Gaps
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
 Prodom; PD00001; Prot kinase; 1.
PROSITE: PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE-ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 756 AA; 86647 MW; A072D15614A176ES CRC64;
 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Conserved helix-loop-helix ubiquitous kinase.
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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 ;
 100.0%; Score 40; DB 11; Length 745; 100.0%; Pred. No. 2.1e+02; ive 0; Mismatches 0; Indels (
 100.0%; Score 40; DB 6; Length 756; 100.0%; Pred. No. 2.2e+02; ive 0; Mismatches 0; Indels
 Last annotation update)
 Last sequence update)
 745 AA.
 756 AA.
 STRAIN=C57BL/67; TISSUE=Urinary bladder;
MEDLINE=22354683; PubMed=12466851;
 Created)
 Created)
 PRT;
 PRT;
 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2003 (TrEMBLrel. 23,
 01-MAR-2003 (TrEMBLrel, 23, 01-MAR-2003 (TrEMBLrel, 23, 01-MAR-2003 (TrEMBLrel, 23,
 Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
 Best Local Similarity 100.
Matches 6; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Bos taurus (Bovine).
 733 LDWSWL 738
 738 LDWSWL 743
 1 LDWSWL 6
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 IkB kinase-beta.
 NCBI_TaxID=9913;
 BIKKBETA.
 Query Match
 Q8CBT3
 Q95KV0
 RESULT 3
 095KV0
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 Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.B., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 MEDLINE=21470413; PubMed=11566360; Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Barker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davies P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Freshina pestis, the causative agent of plague."; Nature 413:523-527(2001).
 Gaps
 Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative potassium efflux system (Putative alpha helix protein)
YP03129 OR AEFA OR Y1054.
 ö
 95.0%; Score 38; DB 16; Length 1139; 83.3%; Pred. No. 6.5e+02;
 0; Indels
 7B54108BFC39A6B1 CRC64;
 Streptococcus agalactiae (serotype III).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
 01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
PRT; 1139 AA
 173 AA.
 "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
EMBL; A2141155; CAC92364.1; -.
EMBL; AE013709; AAW84635.1; -.
 1; Mismatches
 Hypothetical protein; Complete proteome SEQUENCE 1139 AA; 128409 MW; 7B54108
 Created)
 Interpro; IPR006685; MSion_channel.
Interpro; IPR006686; MS channel_dom.
Pfam, PF00924; MS_channel; 1.
PROSITE; PS01246; UPF0003; 1.
 MEDLINE=22137863; PubMed=12142430;
 SEQUENCE FROM N.A.
STRAIN=CO-92 / Biovar Orientalis;
 SEQUENCE FROM N.A.
STRAIN=KIM5 / Biovar Mediaevalis;
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Best Loc Matches

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RESULT 6 Q8E065

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SETAIN=16M / ATCC 21456 / Biotype 1;
MEDLINE=20020109; PubMed=1175668B;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
"The genome sequence of the facultative intracellular pathogen
Brucella melitensis."
Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 Um H.W., Kang H.S.; "The sequence analysis of 42D7 fosmid clone of Zymomonas mobilis
 Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales,
Sphingomonadaceae, Zymomonas
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 92.5%; Score 37; DB 16; Length 322; 83.3%; Pred. No. 2.7e+02; ive 1; Mismatches 0; Indels
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
 Score 37; DB 2; Length 310;
Pred. No. 2.6e+02;
1; Mismatches 0; Indels
 Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF157493; AAD42398.1; -.
InterPro; IPR002925; DLH.
InterPro; IPR00379; Ser_estrs_site.
Fram; PF01738; DLH; 34092 WW; 34AC821E1F91259D CRC64;
 InterPro; IPR01694; Resp.NADH_dhl.
Pfam; PF00146; NADHdh; 1.
PROSITES; PS00668; COMPLEX1 ND1_2; 1.
Oxidoreductase; Complete protecome.
SEQUENCE 322 AA; 35966 MW; D5858123AB2C13E7 CRC64;
 01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
NADH-quinone oxidoreductase chain H (EC 1.6.5.3).
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative carboxymethylenebutenolidase.
 322 AA.
 347 AA.
 1; Mismatches
 PRT;
 92.5%;
83.3%;
 Query Match
Best Local Similarity 83.33.
 5; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Brucella melitensis.
 153 VDWSWL 158
 174 LDWNWL 179
 Best Local Similarity
 Zymomonas mobilis.
 SEQUENCE FROM N.A.
 1 LDWSWL 6
 1 LDWSWL 6
 NCBI_TaxID=29459;
 NCBI_TaxID=542;
 STRAIN=ZM4
 Q8YGK7
 08YGK7
 Q98KR3
 RESULT 8
Q8YGK7
 RESULT 9
 Q98KR3
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 STRAIN=2603 V/R / Serotype V;
STRAIN=2203 U/R / Serotype V;
STRAIN=2203 U/R / Serotype V;
MEDLINE=2222988; PubMed=1220547;
Tettelln H., Masignan V., Cieslewicz M.J., Eisen J.A., Peterson S., Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.E., Madupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
 SEQUENCE FROM N.A.
STRAIN=NEW316 / Serotype III;
MEDLINE=22245269; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
Kunst F.;
 Gaps
 Genome sequence of Streptococcus agalactiae, a pathogen causing
 "Complete genome sequence and comparative genomic analysis of ar emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
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 92.5%; Score 37; DB 16; Length 173; 83.3%; Pred. No. 1.5e+02;
 92.5%; Score 37; DB 16; Length 173; 83.3%; Pred. No. 1.5e+02; Live 1; Mismatches 0; Indele
 Streptococcus agalactiae (serotype V).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 Hypothetical protein; Complete proteome.
SEQUENCE 173 AA; 20135 MW; F5F34044F0224CD1 CRC64;
 Transferase, Complete proteome.
SEQUENCE 173 AA, 20135 MW, 0081677125975921 CRC64;
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Acetyltransferase, GNAT family.
 Q9XBS7;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 1; Mismatches
 invasive neonatal disease.";
Mol. Microbiol. 45:1499-1513(2002).
EMBL; AL766847; CAD46531.1; -.
 PRT;
 Local Similarity 83.3%;
les 5; Conservative
 Local Similarity 83.3
168 5, Conservative
 PRELIMINARY;
 PRELIMINARY;
 SagaList, gbs0887; -.
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LDWAWL 130
 125 LDWAWL 130
 NCBI_TaxID=216466;
 1 LDWSWL 6
 1 LDWSWL 6
 SAG0870;
 Fraser C.M.;
 Query Match
 Query Match
 Q8E065
 Q9XBS7
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RESULT 7 Q9XBS7

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Created)
 EMBL; AE012305; AAM41300.1; -.
InterPro; IPR002656; Acyl transf_3.
Pfam; PF01757; Acyl_transf_3; 1.
 PRT;
 Xanthomonadaceae; Xanthomonas
 01-OCT-2002 (TrEMBLrel. 22,
 Local Similarity 83.3
nes 5; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Nature 417:459-463 (2002)
 199 LDWNWL 204
 117 LDWSWV 122
 Beta-galactosidase
 SEQUENCE FROM N.A.
9
 Complete proteome.
SEQUENCE 361 AA;
 1 LDWSWL 6
 NCBI_TaxID=56956;
 NCBI_TaxID=340;
 Query Match
 08P955;
 09x6C6;
 Q8P955
 929X60
 Matches
 RESULT 11
 RESULT 12
 08P955
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 Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., "Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizohim loti"
 Paulsen I.T., Sechadri R., Nelson K.E., Eisen J.A., Heidelberg J.F., Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J., Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Nelson W.C., Ayodeji B., Kraull M., Shetty J., Malek J., Van Aken S.E. Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.; "The Brucella suis genome reveals fundamental similarities between proc. Natl. Acad. Sci. US.A. 99:13148-13153(2002).
 Gaps
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 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
 Query Match 92.5%; Score 37; DB 16; Length 347; Best Local Similarity 83.3%; Pred. No. 2.9e+02; Matches 5; Conservative 1; Mismatches 0; Indels
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
NCBI_TaxID=29461;
 92.5%; Score 37; DB 16; Length 347; 83.3%; Pred. No. 2.9e+02; ive 1; Mismatches 0; Indels
 PROSITE; PS00668; COMPLEXI ND1_2; 1.
Ubiquinone; Complete protecme.
SEQUENCE 347 AA; 38370 MW; 1092F351BD97EC57 CRC64;
 347 AA; 38428 MW; DA7F7471FD34D127 CRC64;
 01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
NADH-ubiquinone dehydrogenase chain 8.
 Last sequence update)
Last annotation update)
 347 AA.
 Rhizobium loti (Mesorhizobium loti).
 Created)
 DNA Res. 7:331-338 (2000).
EMBL, AP002997; BAB48751.1; -.
InterPro; IPR001694; Resp_NADH_dhl.
Pfam, PF00146; NADHdh; 1.
 STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
 STRAIN=1330 / Biovar 1;
MEDLINE=22247741; PubMed=12271122;
 01-MAR-2003 (TrEMBLrel. 23, Creat 01-MAR-2003 (TrEMBLrel. 23, Last 01-MAR-2003 (TrEMBLrel. 23, Last NADH dehydrogenase I, H subunit. NUOH OR BR0809.
 5; Conservative
 PRELIMINARY;
 Best Local Similarity
Matches 5; Conservat
 |||:||
199 LDWNWL 204
 Complete proteome. SEQUENCE 347 AA;
 SEQUENCE FROM N.A.
 1 LDWSWL 6
 SEQUENCE FROM N.A.
 NCBI_TaxID=381;
 Brucella suis
 BR0809;
 Query Match
 Q8G1B0;
 Q8G1B0
 rigR;
 RESULT 10
Q8G1B0
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TO 33937 NCPPB 528;

MEDLINE=22022145; PubMed=12024217;

MEDLINE=22022145; PubMed=12024217;

RA a Silva A.C.R., Ferro J.A., Rethach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

Ranarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., El-Dorry H.,

Raria J.B., Ferreira A.J.S., Ferreira R.C.C., Fruber A.,

Rormighieri B.F., Franco M.C., Greggio C.C., Gruber A.,

Rormighieri B.F., Madeira A.M.B.M., Mayaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Rereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Retubal J.C., Kitajima J.P.,

Sapinola L.A.F., Takita M.A., Tanara R.B., Teixaira B.C., Tezza R.I.D.,

Retubal J.C., Kitajima J.P.,

St. "Comparison of the genomes of two Xanthomonas pathogens with differing context of the genomes of two Xanthomonas pathogens with differing
 STRAIN=ITI360;
MEDLINE=99402735; PubMed=10473401;
Fridjonsson O., Watzlawick H., Gehweiler A., Rohrhirsch T., Mattes R.;
 Gaps
 Thermus brockianus.
Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 ;
0
 92.5%; Score.37; DB 16; Length 361;
83.3%; Pred. No. 3e+02;
iive 1; Mismatches 0; Indels
 361 AA; 39147 MW; 37AB21791BE0393F CRC64;
 Last sequence update)
Last annotation update)
 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
361 AA
 645 AA
 01-OCT-2002 (TrEMBLrel. 22, Last sequent 01-OCT-2002 (TrEMBLrel. 22, Last annotal Exopolysaccharide biosynthesis protein.
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Streptomyces coelicolor.
 STRAIN=A3(2)
 SEQUENCE
 QBIXKB;
 QBIXKB
 RESULT 15
 NAME OF STREET O
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"Cloning of the gene encoding a novel thermostable alpha-galactosidase
 SEQUENCE FROM N.A.

STRAIN=06:H1 / CFT073 / ATCC 700928;

MEDLINE=22380234; PubMed=12471157;

MEDLINE=22380234; PubMed=12471157;

Melch R.A., Burland V., Plunkett G.

Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).

EMBL, AE016769; AAN83187.1; -

Hypotherical procein; Complete proteome.

SEQUENCE 85 AA; 9675 MW; 47DADB502F570A8B CRC64;
 Gaps
 Gaps
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
 Fridjonsson O., Warzlawick H., Mattes R.;
"The structure of the alpha-galactosidase gene loci in Thermus brockianus ITI360 and Thermus thermophilus TH125.";
Extremophiles 4:33-31(200).
EMBL; AF135398; AAD33667.1; ...
InterPro; IPR001554; Glyco_hydro_14.
InterPro; IPR001376; Glyco_hydro_42.
Pfam; PF01373; Glyco_hydro_42; 1.
SEQUENCE 645 AA; 73420 MW; C79A9EIC0020EC40 CRC64;
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 90.0%; Score 36; DB 16; Length 85; 66.7%; Pred. No. 1e+02; ive 2; Mismatches 0; Indels
 Length 645;
 92.5%; Score 37; DB 2; Length 645
83.3%; Pred. No. 5.3e+02;
ive 1; Mismatches 0; Indels
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
C4754.
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein SCP1.253.
 Appl. Environ. Microbiol. 65:3955-3963(1999).
 205 AA
 PRT;
 STRAIN=ITI360;
MEDLINE=20203878; PubMed=10741834;
 from Thermus brockianus ITI360.";
 5; Conservative
 Best Local Similarity 66.7
Matches 4; Conservative
 PRELIMINARY;
 Escherichia coli 06.
 Query Match
Best Local Similarity
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48 LDWAWL 53
 19 IDWSWM 24
 SEQUENCE FROM N.A.
 1 LDWSWL 6
 1 LDWSWL 6
 Query Match
 Q9ACR5;
 Q9ACR5
 Matches
 RESULT 13
 RESULT 14
 Q9ACR5
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 Bentley S.D., Chater K.E., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
Thomson N.R., James A., Hidalgo J., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Asbinowitsch E., Rajandream M.A., Rutherford K., Ruter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
Complete genome sequence of the model actinomycete Streptomyces
T. (Complete genome sequence of the model actinomycete Streptomyces
T. Mature 417:141-147(2002).
EMBL; ALS90464; CAC36779:1;
REBL; ALS90464; CAC36779:1;
REBL; ALS90464; A., 23051 MW; 6602396CFF93F2D9 CRC64;
 Gaps
 Gaps
 Homo sapiens (Human), bustanta, Craniata; Vertebrata; Euteleostomi; Bukaryota; Metarazoa; Chordates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycese; Streptomyces
 90.0%; Score 36; DB 16; Length 205; 100.0%; Pred. No. 2.4e+02; ive 0; Mismatches 0; Indels
 90.0%; Score 36; DB 4; Length 227; 100.0%; Pred. No. 2.7e+02; tive 0; Mismatches 0; Indels
 Straubberg R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC040173; AAH40173.1; -.
Hypothetical protein.
SEQUENCE 227 AA; 25487 MW; F11A71EA57062A05 CRC64;
 01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
 227 AA
 Similar to hypothetical protein BC017335.
 Search completed: February 18, 2004, 14:35:34
Job time : 19.3684 secs
 PRT;
 MEDLINE=21996410; PubMed=12000953;
 Query Match
Best Local Similarity 100...
Best Local Si Conservative
 Query Match
Best Local Similarity 100.v.
Best Local Si Conservative
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 SEQUENCE FROM N.A. TISSUE=Brain;
 114 DWSWL 118
 FROM N.A.
 11 DWSWL 15
 2 DWSWL 6
 2 DWSWL 6
 NCBI_TaxID=1902;
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